north dakota state university

ndsu

student research days

2026

welcome

MESSAGE FROM RESEARCH AND CREATIVE ACTIVITY

Welcome to the 2026 NDSU Student Research Days! We are pleased to have you join us as we showcase the outstanding work of our undergraduate researchers, with more than 100 presentations—the highest level of participation in the event's history. These projects reflect the depth, rigor, and innovation of student-led research at North Dakota State University.

At NDSU, undergraduate research is a cornerstone of our academic mission, contributing impactful advancements to the university, the region, and the nation. Student Research Days provides an important forum for students to present their findings, engage with peers and stakeholders, and foster interdisciplinary dialogue and collaboration.

Your presence and participation are vital to the success of this event, and we sincerely appreciate your continued support of undergraduate research excellence. The Office of Research and Creative Activity remains committed to advancing these efforts through NDSU EXPLORE.

Thank you for your support of Student Research Days and enjoy celebrating student research!

Ying Huang, Ph.D.
Undergraduate Research Director
Professor, Chair and Welch Faculty Fellow
Civil, Construction, and Environmental Engineering

MESSAGE FROM GAMMA SIGMA DELTA

Gamma Sigma Delta wishes to welcome everyone to the NDSU 2026 Student Research Days. Gamma Sigma Delta was founded in 1913 as an international honor society to advance agriculture. The NDSU chapter is pleased to participate in Student Research Days. We look forward to learning about the great research that our students are doing.

Sergio Cabello Leiva
Gamma Sigma Delta, NDSU Chapter President

MESSAGE FROM THE GRADUATE SCHOOL

The NDSU Graduate School and Graduate Student Council welcome you to NDSU Student Research Days! This annual celebration honors the vibrant research community thriving across our campus. This year's event features the innovative and creative research of nearly 200 graduate students representing 32 programs from across all six NDSU colleges. We are excited as this marks the highest level of participation, in terms of both number of presentations and number of participating programs! History, landscape architecture, business administration, coatings and polymeric materials, civil and environmental engineering, plant sciences, public health, natural resource sciences, pharmaceutical sciences and more, the breadth and depth of the NDSU research enterprise is on display today.

Graduate student research sits at the heart of NDSU's identity as a high-intensity research university and reflects our Land Grant commitment to making innovative scholarship open and accessible to all. Today's event is a testament to that mission.

Thank you for your attendance supporting NDSU graduate students. Your presence means a great deal to our graduate students as they grow into accomplished scholars and communicators, and we hope you depart inspired by their remarkable research.

Yueh-Ting "YT" Lee, Ph.D.
Dean and Professor
College of Graduate and Interdisciplinary Studies
North Dakota State University

Muhammad Muzamal Ashfaq
President, Graduate Student Council
Doctoral Student, Mechanical Engineering
North Dakota State University

2026

schedule

ALL SESSIONS WILL BE HELD IN THE MEMORIAL UNION

WEDNESDAY, APRIL 8

EXPLORE (UNDERGRADUATE) SCHEDULE

10 a.m. – noon
Poster Session
Ballroom B

Noon – 1:30 p.m.
Break

1:30 – 3 p.m.

Oral Presentation Sessions
Hidatsa and Sahnish Rooms

3:30 – 4 p.m.

Awards Ceremony
Ballroom A

THURSDAY, APRIL 9

GRADUATE STUDENT SCHEDULE

10 a.m. – noon
Poster Session
Oceti Sakowin Ballroom

Noon – 1 p.m.
Break

1 – 3 p.m.
Oral Presentations
Various Rooms

3:30 – 4:30 p.m.
Awards Ceremony
Ballroom A

undergrad participants

EXPLORE ORAL PRESENTATIONS:

Ella Berger
Mechanical Engineering

Paige Cmelik
Biological Sciences, CHANGE RaMP

Nora Daub
Biotechnology

Jack Leone
Environmental Engineering

Evelyn Lewis
Anthropology

Sohum Mallik
Pharmaceutical Sciences

Shawna Nix
Crop and Weed Science

Madison Patterson
Biochemistry and Molecular Biology

Alexa Ruberte
Biological Sciences, CHANGE RaMP

Miriam Sullivan
Biochemistry and Molecular Biology

EXPLORE POSTER PRESENTATIONS:

Andres Aasheim
Mechanical Engineering

Josie Abel
Psychology

Maryum Adnan
Pharmaceutical Sciences

Ebenezer Agbenyegah
Civil Engineering

Andrew Ahiable
Cybersecurity

Thomas Allmer
Mechanical Engineering

Zachary Arendt
Electrical Engineering

Thomas Banley
Natural Resources Management

Kianna Bannerman
Biological Sciences

Lolana Bath-Thurstin
Biological Sciences, CHANGE RaMP

Maral Bayarmagnai
Crop & Weed Science

Alexa Bendixen
Psychology

Caedmon Benson
Biological Sciences

Amy Berg
Psychology

Jo Berger
Microbiology

Kolbie Bernu
Environmental Engineering

Olivia Boyd
Biological Sciences

Alyssa Boyko
Biological Sciences

Kyren Brahos
Microbiology

Maddy Cartelli
Interior Design

Austin Chase
Electrical Engineering

Andrea Clarisse Corrales
Biochemistry and Molecular Biology

Madelyn Craft
Biochemistry and Molecular Biology

Noah Douglas
Mechanical Engineering

Hayden Durand
Electrical Engineering

Parker Ehrman
Biological Sciences

Avery Folsom
Microbiology

Anevay Foote
Biological Sciences

Kaitlyn Forehand
Psychology

Brooklyn Fortier
Chemistry

Gage Fossen
Anthropology

Elizabeth Frias
Biological Sciences, CHANGE RaMP

Jordan Friske
Biological Sciences

Louis Gaytan
Mechanical Engineering

Javier Gomez Atilano
Agricultural and Biosystems Engineering

Kalen Gordon
Mechanical Engineering

Abigail Graham
Athletics

Jada Griffin
Biological Sciences

Lauren Gunderson
Biological Sciences

Rylie Gustafson
Natural Resources Management

Alyssa Hall
Interior Design

Olivia Hollerich
Biological Sciences

Ahmad Itani
Physics

Hannah Johnson
Psychology

Daniel Jones
Agricultural Sciences

Adam Kalina
Psychology

Wyatt Kalliokoski
Construction Engineering

JoMarie Kelly
Construction Engineering

Derek Kittilson
Psychology

Mason Kornezos
Computer Science

Chloe Lamb
Electrical Engineering

Jamison Lang
Chemistry

Cora Larson
Psychology

Evelyn Lewis
Anthropology

Samuel Lies
Biological Sciences

Somi Lim
Biotechnology

Connor Lukkari
Electrical Engineering

Kathryn Mack
Accounting and Finance

Elliot Magcalas
Biological Sciences

Taylor McElroy
Biological Sciences

Brayden McLean
Biological Sciences

Mac Mclellan
Interior Design

Alexis Meredith
Microbiology

Andrew Meyer
Economics

Courtney Mitchell
Biological Sciences, CHANGE RaMP

River Olson
Electrical Engineering

Jacie Osier
Biological Sciences, CHANGE RaMP

Zubin Park
Chemistry

Evan Paulson
Mechanical Engineering

Kaia Paulus
Animal Science

Ariana Pfaff
Anthropology

Erin Pitmon
Interior Design

Nathan Rateau
Mathematics and Statistics

Olivia Rosenthal
Animal Science

Anna Rothfusz
Microbiology, CHANGE RaMP

Lucas Rutten
Biotechnology

Liv Schroeder
Biological Sciences, CHANGE RaMP

Melody Sen
Biological Sciences, CHANGE RaMP

Georgina Sieh
Computer Science

Ethan Skott
Mechanical Engineering

Hailey Smith
Animal Science

Maya Sohail
Physics

Jack Stoppleworth
Biological Sciences

Stella Strong
Chemistry

Skylar Sundeen
Anthropology

Tess Taloumis
Biological Sciences, CHANGE RaMP

Eva Tastad
Animal Science

Jared Tesch
Biological Sciences

Marissa Tiegen
Agricultural Sciences, CHANGE RaMP

Samuel Tipka
Business Administration

Sophie Viger
Mechanical Engineering

Sara Wheatley
Biological Sciences, CHANGE RaMP

Noah Wilson
Biological Sciences, CHANGE RaMP

Griffin Winstead
Computer Science

Piper Zander
Biological Sciences, CHANGE RaMP

Ella Zanetti
Biological Sciences

Kouma Zoungrana
Biochemistry and Molecular Biology

undergrad advisors + mentors

COLLEGE OF AGRICULTURE, FOOD SYSTEMS, AND NATURAL RESOURCES

Thomas Krumel, Ph.D.
Agribusiness and Applied Economics

Xinhua Jia, Ph.D.
Agricultural and Biosystems Engineering

Ahmed Rabia, Ph.D.
Agricultural and Biosystems Engineering

Pawel Borowicz, Ph.D.
Animal Sciences

Christopher Byrd, Ph.D.
Animal Sciences

Carl Dahlen, Ph.D.
Animal Sciences

Kendall Swanson, Ph.D.
Animal Sciences

Ahmad Al-Amad
Plant Pathology, Microbiology and Biotechnology

Thomas Baldwin, Ph.D.
Plant Pathology, Microbiology and Biotechnology

Samiran Banerjee, Ph.D.
Plant Pathology, Microbiology and Biotechnology

Glenn Dorsam, Ph.D.
Plant Pathology, Microbiology and Biotechnology

Barney Geddes, Ph.D.
Plant Pathology, Microbiology and Biotechnology

Zhaohui Liu, Ph.D.
Plant Pathology, Microbiology and Biotechnology

Eglantina Lopez-Echartea, Ph.D.
Plant Pathology, Microbiology and Biotechnology

Shahidul Islam, Ph.D.
Plant Sciences

Simardeep Kaur, Ph.D.
Plant Sciences

Juan Osorno, Ph.D.
Plant Sciences

Dillon Fogarty, Ph.D.
School of Natural Resource Sciences

Lindsay Malone, Ph.D.
School of Natural Resource Sciences

Bethany Roberton, Ph.D.
School of Natural Resource Sciences

Travis Seaborn, Ph.D.
School of Natural Resource Sciences

COLLEGE OF ARTS AND SCIENCES

Laura Aldrich-Wolfe, Ph.D.
Biological Sciences

Korie Debardlabon
Biological Sciences

Ned Dochtermann, Ph.D.
Biological Sciences

Kendra Greenlee, Ph.D.
Biological Sciences

Timothy Greives, Ph.D.
Biological Sciences

Emily Hackerson
Biological Sciences

Britt Heidinger, Ph.D.
Biological Sciences

Giancarlo López-Martínez, Ph.D.
Biological Sciences

Jennifer Momsen, Ph.D.
Biological Sciences

Katie Reindl, Ph.D.
Biological Sciences

Sarah Signor, Ph.D.
Biological Sciences

Tara Slominski, Ph.D.
Biological Sciences

Ethan Strom
Biological Sciences

Uwe Burghaus, Ph.D.
Chemistry and Biochemistry

Christopher Colbert, Ph.D.
Chemistry and Biochemistry

Stuart Haring, Ph.D.
Chemistry and Biochemistry

Rebecca Huss
Chemistry and Biochemistry

Ariana McDarby
Chemistry and Biochemistry

Mukund Sibi, Ph.D.
Chemistry and Biochemistry

Kajalben Somani
Chemistry and Biochemistry

Pinjing Zhao, Ph.D.
Chemistry and Biochemistry

Eugene Caldona, Ph.D.
Coatings and Polymeric Materials

Bakthiyor Rasulev, Ph.D.
Coatings and Polymeric Materials

Durbek Usmanov
Coatings and Polymeric Materials

Janet Page, Ph.D.
Mathematics

Timothy Ryan, Ph.D.
Mathematics

John Buncher, Ph.D.
Physics

Idris Malik
Physics

Sylvio May, Ph.D.
Physics

Jonathan Owen
Physics

William Riihiluoma
Physics

Benjamin Balas, Ph.D.
Psychology

Katherine Duggan, Ph.D.
Psychology

Anna Finley, Ph.D.
Psychology

Odalis Garcia
Psychology

Susan Ray Degges, Ph.D.
School of Design, Architecture and Art

Kristen Fellows, Ph.D.
Sociology and Anthropology

COLLEGE OF BUSINESS

Ricky Feir, MS
Challey Institute

COLLEGE OF ENGINEERING

Armstrong Aboah, Ph.D.
Civil, Construction and Environmental Engineering

Achintya Bezbaruah, Ph.D.
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Adam Ding, Ph.D.
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Syeed Iskander, Ph.D.
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Youjin Jang, Ph.D.
Civil, Construction and Environmental Engineering

Kathryn Quenette
Civil, Construction and Environmental Engineering

Luyang Xu, Ph.D.
Civil, Construction and Environmental Engineering

Yao Yu, Ph.D.
Civil, Construction and nvironmental Engineering

Ajay Jha, Ph.D.
Computer Science

Sumitha George, Ph.D.
Electrical and Computer Engineering

Qifeng Zhang, Ph.D.
Electrical and Computer Engineering

Harun Pirim, Ph.D.
Industrial and Manufacturing Systems Engineering

Ali Amiri, Ph.D.
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Adam Gladen, Ph.D.
Mechanical Engineering

Long Jiang, Ph.D.
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Selvakumar Parthiban Prakash, Ph.D.
Mechanical Engineering

William Refling, Ph.D.
Mechanical Engineering

Majura Selekwa, Ph.D.
Mechanical Engineering

Annie Tangpong, Ph.D.
Mechanical Engineering

Chad Ulven, Ph.D.
Mechanical Engineering

Yan Zhang, Ph.D.
Mechanical Engineering

COLLEGE OF HEALTH AND HUMAN SCIENCES

Wen Wang, Ph.D.
Human Development and Family Science

Roberto Gomes, Ph.D.
Pharmaceutical Sciences

Estelle Leclerc, Ph.D.
Pharmaceutical Sciences

Elisabetta Liverani, Ph.D.
Pharmaceutical Sciences

Sijo Mathew, Ph.D.
Pharmaceutical Sciences

Stefan Vetter, Ph.D.
Pharmaceutical Sciences

OTHER NDSU MENTORS

Benjamin Noonan, MD, MS
NDSU Athletics and Sanford Health

Sharijad Hasan, Ph.D.
Upper Great Plains Transportation Institute

EXTERNAL MENTORS

Loren Miller, Ph.D.
Minnesota Department of Natural Resources; University of Minnesota

Colin Bond, Ph.D.
Sanford Health

Jeremy Guinn, Ph.D.
United Tribes Technical College

Mandy Guinn, Ph.D.
United Tribes Technical College

Sheri Dorsam, Ph.D.
USDA Agricultural Research Service

Jarrad Prasifka, Ph.D.
USDA Agricultural Research Service

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USDA-APHIS Wildlife Services National Wildlife Research Center

Kristen Ellis, Ph.D.
USGS Northern Prairie Wildlife Research Center

Kyle McLean, Ph.D.
USGS Northern Prairie Wildlife Research Center

Siddharth Singhal, MD, FACP, SFHM
Veterans Affairs Medical Center

Elution of Lidocaine from UHMWPE under Gait Loading

ANDRES AASHEIM
Mechanical Engineering
Project Mentor: Chad Ulven, Ph.D.

Musculoskeletal disorders such as rheumatoid arthritis and spinal degeneration affect millions of patients worldwide and represent a rapidly growing healthcare crisis. Drug-eluting orthopedic materials offer a potential strategy for improving localized pain management and therapeutic delivery following implant procedures. Most in vitro drug-elution studies are performed under static conditions, typically involving simple immersion of drug-incorporated materials in solutions without any mechanical loading. However, these conditions do not accurately represent the dynamic mechanical environment experienced by implants in the human body, particularly within load-bearing systems such as the spine.

This project aims to develop a more physiologically relevant in vitro testing method to evaluate drug elution under cyclic mechanical loading conditions. Ultra-high-molecular-weight polyethylene (UHMWPE) specimens manufactured with lidocaine will be subjected to cyclic compressive loading using a Bose ElectroForce 3200 series III load frame for simulating gait-like conditions. During testing, specimens will be immersed in a simulated buffer solution (SBS) bath, and time-dependent elution samples will be collected. Elution samples will be collected during testing, and lidocaine concentrations will be quantified using UV–Vis spectrophotometry to generate release profiles from lidocaine-incorporated UHMWPE specimens under cyclic loading conditions.

By incorporating controlled mechanical cyclic loading into drug-elution experiments, this work aims to establish a more representative in vitro methodology for studying mechanically-influenced drug transport from orthopedic biomaterials.

Beyond Growth Mindset--Parents' Beliefs and Approaches to Support Children to Deal with Setbacks

JOSIE ABEL
Psychology
Project Mentor: Wen Wang, Ph.D.

Growth mindset refers to the belief that intelligence can be developed through effort and learning, which is a positive predictor to children's academic and social-emotional adjustment. In contrast, a fixed mindset sees intelligence as something set in stone. Parents aim to raise a child who has a growth mindset and is resilient to learning setbacks. Recent research suggests that parents' failure mindsets influence how they respond to their children's setbacks (Haimovitz & Dweck, 2016), but it is still unclear how parental support during challenging experiences. Our study uses qualitative methods to understand parents' responses to their children's failure. In the in-person interview, we gave parents a scenario of their children failed in some learning tasks, and asked 4 questions: what is your immediate reaction; how would you feel about your child's wish to not continue; what do you think you would do; and what role do you think children's experience of failure have in their learning? We used thematic analysis to code 25 parents' answers and found that 90% of parents used emotional coaching (validating children's frustrating feelings) and supportive approaches (including creating a positive learning environment, providing scaffolding, and seeking for other professional help). And 95% of parents had a growth mindset on their children's failure, believing that failure/setback is a learning opportunity for children. However, despite the commonality, their parenting styles vary in navigating their children to deal with failure. We coded two axis to classify parents: a) whether the parent is parent-led, shared-led, or child-led style; b) whether the parent is confident or anxious in handling this situation. For example, some parents confidently lead and help their children; and some other parents would standby and go with children's pace in solving the problems. And a few parents felt anxious and were inconsistent in their strategies. Previous studies only focused on one dimension: growth or fixed mindsets, which cannot capture this diversity among parents. Our study unwraps the complexity of parents' approaches to children's failure. These findings highlight the impact of different parenting styles and call for future research on how they affect children's outcomes.

Focus on the Immune Response to Sepsis by Analyzing Bacterial Clearance in the Spleen in a Mouse Model

MARYUM ADNAN
Pharmaceutical Sciences
Project Mentor: Elisabetta Liverani, Ph.D.

Sepsis is a life-threatening condition caused by an extreme immune response to bacterial infection, leading to widespread inflammation and organ damage. My research focuses on the immune response to sepsis by analyzing spleen pathology in a mouse model. I specifically studied the spleen in my research because it plays a crucial role in filtering blood, mounting an immune response, and promoting bacterial clearance.

Sepsis is induced in healthy laboratory mice by injection, followed by organ harvesting 24 hours later. In my previous projects, I examined structural damage and differences in specific immune cell content between septic and healthy mice, as well as sex-based variation. In this project, I will analyze whether the changes noted in the spleen contribute to bacterial clearance. The tissue was weighed and then chopped on a glass platform, and the cell suspension is transferred into labeled tubes with HBSS to maintain cell integrity. The labeled tubes

(1-6) are placed into a centrifuge to ensure proper identification and preparation for separation. The Ultrasonicator uses ultrasonic waves to break apart cells or bacteria, while the centrifuge applies high-speed spinning to separate cellular components based on density. I made serial dilutions of the generated homogenates using sterile saline. An open flame was used to create an aseptic environment when plating the samples. After a 24-h incubation at 37°C, I manually counted the colony of bacteria that formed on the blood agar plate. Each colony is considered a colony-forming unit (cfu), and the data will be shown as CFU/gram of spleen tissue.

Conclusion: Overall, this experiment reinforced my understanding of labeling and staining techniques, and microbiology, which are essential tools for immunological analysis in sepsis and infectious diseases in general.

High Temperature Performance and Mechanical Characterization of Wire Arc Sprayed Al-Zn Metallized Polymer Coating Systems

EBENEZER AGBENYEGAH
Civil Engineering
Project Mentors: Luyang Xu, Ph.D.
Kathryn Quenette

Polymer-based coatings are widely used to protect Department of Defense (DOD) infrastructure; however, their inherently low operational temperatures and susceptibility to flammability limits the coatings' performance in harsh environments. This study investigates the high temperature behavior and mechanical properties of a metallized polymer coating system produced by wire arc spraying Al-Zn alloys onto polymer primer layers applied to cold-rolled steel substrates. Wire arc spraying was selected for its portability and cost-effectiveness for potential field application. Two metallization material combinations, Al-15Zn alloy and Al-Zn pseudo alloy, were deposited at one thickness and evaluated for tensile bond strength, hardness, Young's modulus, and fracture toughness. High temperature performance was assessed by exposing the metallized coating samples to elevated temperatures ranging from 50°C to 500°C, with thermal cycle testing conducted to evaluate coating stability and degradation behavior. Surface morphology and coating microstructure were characterized using profilometry to quantify surface texture, roughness, and topographical changes resulting from elevated temperature exposure.

Road Crack Detection Using YOLO-Based Deep Learning

ANDREW AHIABLE
Cybersecurity
Project Mentor: Armstrong Aboah, Ph.D.

Road infrastructure maintenance is essential for ensuring transportation safety and reducing long-term repair costs. Traditional methods of road inspection are manual, time-consuming, and prone to human error. This project addresses the need for an efficient and automated system for detecting road cracks using modern computer vision techniques.

To solve this problem, a deep learning-based approach was implemented using the YOLO (You Only Look Once) object detection framework. A labeled dataset obtained from Zenodo was used to train the model to identify and classify different types of road cracks. The training process was conducted using the Ultralytics YOLO environment, where images were processed and annotated to improve detection accuracy. The model learned to detect crack patterns through multiple training iterations, optimizing performance through validation metrics such as precision and recall.

The trained model demonstrated strong performance in detecting road cracks across various images, achieving high accuracy in identifying crack regions. The results indicate that the system can perform real-time detection and can generalize well to unseen data. These outcomes highlight the effectiveness of deep learning in automating infrastructure monitoring tasks.

The implications of this project are significant for transportation systems and smart city development. By reducing reliance on manual inspections, this approach can improve efficiency, lower maintenance costs, and enhance road safety. I plan on making future improvements such as expanding the dataset, optimizing the model for deployment on mobile devices, and integrating the system into real-world monitoring applications.

Unsteady Aerodynamics

THOMAS ALLMER
Mechanical Engineering
Project Mentor: William Refling, Ph.D.

Dynamic stall remains a critical challenge in the aerodynamic performance of rotorcraft and other highly maneuverable aircraft. Flow separation at high angles of attack leads to significant lift reduction, large unsteady aerodynamic loads, and performance degradation. Investigation into this phenomenon requires simulation of the active pitching motion seen by wings on rotor craft. This project investigates the design, construction and analysis of performance of a sinusoidal pitching mechanism to be mounted on the wind tunnel. To elucidate and quantify the full motion of the airfoil, rigorous testing has been performed making use of high-speed imaging techniques to track the motion of the pitching wing in the tunnel. Further validation of this motion will be validated using a 9 degree of freedom inertial measurement system on board of the wing. Advanced flow diagnostics will be performed to understand the interactions of the fluid with the wing if time allows.

3D Printable and Implantable Soy Protein and MXene-Based Crosslinked Bioink Hydrogel for Cancer Detection Application

ZACHARY ARENDT
Electrical Engineering
Project Mentor: Long Jiang, Ph.D.

Early detection and accurate monitoring of cancer growth remain significant challenges in modern medicine. Current diagnostic techniques often rely on intermittent imaging or invasive procedures, limiting the ability of clinicians to monitor tumor progression or regression during treatment continuously. This gap highlights the need for implantable sensing technologies that are biocompatible, low-cost, and capable of providing real-time measurements of cancer development. Currently explored MXene and other 2D nanomaterialbased sensors have a major limitation: instability at the wet surface, which makes their use as implantable sensors impractical. To resolve this limitation, in this project, we are exploring a biocompatible, conductive hydrogel bioink housing derived from soy protein, cellulose, and MXene for use in implantable cancer-detection devices. This work comprises two steps: first, to develop 3D-printable conductive bioink and an implantable scaffold using this bioink; and second, to detect resistance fluctuations by applying a cancer protein on the scaffold surface, specifically Prostate-specific antigen (PSA) and its antibody in this case. To develop a structurally stable network, chemically modified cellulose in nanofiber form will be used, along with a functional group-specific crosslinker. Our preliminary trials have allowed us to determine the optimal ratios of modified cellulose nanofiber, crosslinker, and soy protein for supporting a 3D-printable, implantable scaffold without sacrificing structural integrity. In addition, the MXene content ratio in the bioink at which cancer detection is most notable, along with the required sensitivity efficiency, must be high for resistance-based detection. We are further investigating the 3D printing parameters to develop a structurally stable, free-standing scaffold from this bioink. As we progress, we expect to learn more about which specific ratios and triggers will be most notable during detection, as well as the properties of MXene that may provide even greater utility for internal sensing applications in the wet environment. The successful development and exploitation of this sensing scaffold will provide crucial knowledge on cancer detection and monitoring by enabling real-time measurement of tumor activity. Such technology has the potential to support earlier detection, more precise treatment options, benefit current detection/removal systems, and improve patient outcomes while maintaining affordability and environmental sustainability.

Genetic Diversity and Inbreeding Depression of Elk in North Dakota

THOMAS BANLEY
Natural Resources Management
Project Mentor: Travis Seaborn, Ph.D.

Inbreeding decreases genetic diversity, fitness, and viability of offspring and measuring and minimizing it is often a management goal. Due to their polygynous nature and the patchy distribution of their range, elk are susceptible to inbreeding, which can reduce reproductive capability. In this study, we analyzed elk herds found in North Dakota, mostly in the Badlands and Pembina regions, to look for signs of inbreeding. This genetic data, provided by United Tribes Technical College, was compared to prior data from North Dakota Game and Fish, Minnesota Department of Natural Resources, University of Manitoba, and Memorial University of Newfoundland. We hypothesized that inbreeding would be higher or lower depending on the population size of the herd the sample came from. The genetic data were formed using genotyping by sequencing (GBS) to identify identical single nucleotide polymorphisms (SNPs) for genetic analyses, such as estimating the coefficient of inbreeding (FIS). In 157 samples, there were 58,841 markers on 29,566 loci. After filtering for missing data and data quality, we had 145 samples with 8,223 markers on 5,400 loci. We then calculated heterozygosity, FIS, and relatedness metrics. This research will enhance our comprehension of elk herd relatedness and movement which will serve to better inform partner conservation strategies.

Unpacking Students' Thinking About Mutation: Insights for Teaching Undergraduate Biology

KIANNA BANNERMAN
Biological Sciences

OLIVIA BOYD
Biological Sciences
Project Mentor: Jennifer Momsen, Ph.D.

Statement of the Problem: Mutation underpins genetic variation and enables evolution by natural selection. A strong understanding of mutation is critical to understanding family medical history, genetic testing, and even vaccine development. However, the research on student understanding of mutation is surprisingly thin. In this exploratory study, we sought to understand and describe students' conceptions of mutation and how those conceptions vary over their academic career.

Methods: We focused on General Biology II (n=301) and Evolution (n=92), courses where mutation is a key concept. Students were asked to define mutation as completely as possible, and to state whether mutation is positive, neutral, or negative for an organism. We are using emergent coding to analyze students' responses. We will compare how students in Evolution and General Biology think about mutation.

Results: We expect to see that students in Evolution will understand that mutation can be good, bad, or neutral for an organism, whereas we expect to see that General Biology II students might think that mutation is only negative for an organism.

Implications: This project will present some of the first research describing students' ideas about mutation, especially at the advanced level. We aim to help students develop a more robust understanding of mutation, specifically by designing instruction that enables students to connect mutation to its effects or outcomes, such as new alleles, genes, and proteins.

New Transposable Element Invasions in *Drosophila simulans*

LOLANA BATH-THURSTIN
Biological Sciences; CHANGE Research and Mentoring for Post-Baccalaureates

Project Mentor: Sarah Signor, Ph.D.

Transposable elements (TEs) are mobile genetic elements capable of moving within and between genomes, selfishly increasing copy number in the host genome, altering gene expression, and reshaping genome architecture. Despite their potential deleterious effects, TEs are also major drivers of evolutionary change. Recent work indicates a high frequency of TE invasions in *D.simulans* over the past century, making it an ideal system to study. Investigating the dynamics of TE invasions should help us better understand host genome responses to these selfish genes.

This project investigates patterns of recent TE invasions in *D. simulans* populations. Using publicly available whole-genome sequencing data, we analyzed TE prescence, copy number variation, and insertion frequency across individuals. We identified novel insertions and compared their distribution across populations. We examined whether newly invading TEs show signatures of rapid speed, population structure, or evidence of host suppression mechanisms such as piRNA-mediated silencing.

Preliminary results indicate variation in TE copy numbers among populations, consistent with ongoing invasion dynamics. Several TE families appear at low to intermediate frequencies, suggesting they are still spreading and have not yet reached equilibrium. Patterns of insertion distribution suggest both stochastic processes and potential selective pressures shaping TE dynamics.

These findings contribute to our understanding of genome evolution by providing insight into the early stages of TE invasion. Studying TE dynamics in *D. simulans* offers a window into how natural populations respond to genomic conflict in real time. More broadly, this work improves our understanding of how mobile DNA influences adaption, genome stability, and evolutionary innovation.

Functional Characterization of a Bacterial Effector Triggering Resistance in Wheat

MARAL BAYARMAGNAI
Crop & Weed Science
Project Mentor: Zhaohui Liu, Ph.D.

Bacterial leaf streak (BLS) is an important disease of wheat caused by *Xanthomonas translucens* pv. *undulosa* (Xtu). Despite its economic impact on wheat production, the molecular mechanisms underlying bacterial virulence and host resistance remain poorly understood. In this work, we conducted functional characterization of a candidate type III effector gene, XopAF1, as an avirulence factor Polymerase chain reaction amplification results showed that XopAF1 is present in strains LB10 and B1FA while it is absent in Cr31 and P3. A suicide plasmid carrying a gene-specific fragment of XopAF1 was used to disrupt the gene in LB10 by bacterial conjugation. The mutants were verified with gene-specific primers and whole genome sequencing. The confirmed mutants were tested on the resistant genotype TA10105 and the results showed the mutants became virulent. This confirms that XopAF1 is an avirulence factor triggering resistance in TA10105. Understanding the role of this effector will improve our knowledge of plant–pathogen interactions and may contribute to the development of wheat cultivars with enhanced resistance to bacterial leaf streak.

Does Authenticity Mediate the Relationship Between Sense of Belonging on a College Campus and Loneliness?

ALEXA BENDIXEN
Psychology
Project Mentor: Anna Finley, Ph.D.

The relationship between loneliness, authenticity, and sense of belonging on a college campus have been examined separately, however the relationship between the three is under researched. Universities are hoping to improve student retention and experience by deepening their understanding of the factors that contribute to a sense of belonging on campus and reduce student loneliness and distress. Additionally, loneliness is recognized as an important social determent of health, making loneliness an important primary intervention target for public health programs. I am hoping to understand how authenticity may contribute to the relationship between belonging and loneliness. If we can gain a further understanding of this topic, then we can design campus wide interventions to reduce loneliness in college students. We examined this question by conducting a self-report study on n = 201 undergraduate students at North Dakota State University, utilizing the 20-item UCLA Loneliness Scale, 12-item Authenticity scale, 24-item University Belonging Scale. I hypothesize that people who feel less university belonging will report higher loneliness, and authenticity will mediate this relationship such that lower university belonging will be related to lower authenticity, which in turn will be related to higher levels of loneliness. We preregistered our hypothesis and analysis plan. Conducting this research will help us understand how authenticity impacts a student's sense of belonging on campus and the relationship with loneliness. This will suggest strategies to help students feel authentically themselves on campus to reduce loneliness.

Effects of Time on Viability of Thawed Monarch Butterfly Sperm

CAEDMON BENSON
Biological Sciences
Project Mentors: Kendra Greenlee, Ph.D.
Korie DeBardlabon

The western monarch butterfly (*Danaus plexipus*) has a >99% chance of being extinct by 2080. Biotechnological tools such as cryopreservation may serve as a safeguard against species extinction. Cryopreserved storage of germplasm, like sperm cells from genetically diverse populations, in liquid nitrogen could be used in downstream applications such as artificial insemination. In this study, we assessed the effects of time on the quality and activation potential of monarch butterfly sperm. The seminal duplex, the primary storage organ for mature sperm cells, contains two types of sperm, parasperm and eusperm. Parasperm does not contain a nucleus and therefore cannot fertilize an egg. Eusperm are stored in bundles of 256 nucleated sperm cells that dissociate and become motile after being transferred to the female during mating. Although bundles dissociate automatically during mating, they must be chemically activated for artificial insemination of cryopreserved samples. This activation is done through an enzyme called trypsin that breaks down the protein that binds the bundle, releasing the individual sperm cells. In this study, the seminal duplex was removed from the male butterfly, cryopreserved through vitrification, and stored in liquid nitrogen. After thawing, sperm cell viability was assessed by using fluorescent labels (Helixyte™ and propidium iodide). We scored bundles on their state of dissociation over time in response to different concentrations of trypsin. Finding the optimal concentration of trypsin to induce bundle dissociation and sperm motility without affecting viability is a crucial step in developing an artificial insemination protocol for monarch butterflies where the naturally occurring sperm activator is not available to us.

The Role of Loneliness on College Freshmen Retention

AMY BERG
Psychology
Project Mentor: Anna Finley, Ph.D.

The act of dropping out of college incurs economic cost to the individual, university, and society as a whole. Freshmen year is a critical period for college student dropout. We wanted to understand what factors contribute to student retention, dropout, and success within the first semester. We hypothesized that persistent feelings of loneliness play a major role in a student's intentions to continue enrollment, and university belonging will mediate this relationship. We assessed this in a sample of n = 30 (of whom n = 8 completed Wave 1 and Wave 4 of data collection) first semester freshman enrolled in UNIV 100 freshmen experience course during the Fall 2025 semester. We used the 20 item UCLA loneliness scale, 24 item University Belonging, and 3 item measurements of intent to continue enrollment. We preregistered our hypotheses that people who have less persistent feelings of loneliness will have higher intentions of re-enrollment; and feelings of university belonging will mediate this relationship. Our results were consistent with our hypotheses, but a formal mediation analysis could not be completed due to a low sample size. This research contributes to the understanding of how student loneliness, isolation, and lack of social integration with the university may mediate students' enrollment choice and help understand what social factors contribute to student success, particularly in a first-year freshmen experience seminar.

Synthesis and Characterization of Gelatin Methacrylate Hydrogel Microparticles With Various Aspect Ratios By Digital Light Processing 3D Printer

ELLA BERGER
Mechanical Engineering
Project Mentor: Selvakumar Parthiban Prakash, Ph.D.

Hydrogel microparticles are widely used in tissue engineering, drug delivery, and biomaterials research due to their tunable mechanical and biological properties. An ongoing challenge in this field is achieving precise control over microparticle geometry, which significantly influences cellular interactions and material performance. This project seeks to address this limitation by synthesizing gelatin methacrylate (GelMA) hydrogel microparticles with controlled aspect ratios using a digital light processing (DLP) 3D printer.

GelMA solutions are prepared and photopolymerized through a layer-by-layer DLP printing process to fabricate microparticles with defined geometries. Printing parameters such as exposure time, layer thickness, and light intensity are currently being refined to improve resolution and consistency. Ongoing characterization includes optical microscopy and dimensional analysis to evaluate particle shape accuracy, structural integrity, and repeatability. Printing fidelity is also being assessed to understand how fabrication conditions influence final particle quality.

Preliminary testing suggests that DLP-based fabrication has the potential to produce hydrogel microparticles with reproducible aspect ratios and stable geometries. Continued experimentation is focused on refining printing parameters and quantifying dimensional precision. The desired outcome is a reliable process for generating microparticles with predictable shapes suitable for biomaterials research.

The ability to engineer hydrogel microparticles with controlled geometries may expand opportunities to study cell–material interactions and design advanced biomedical systems. This work aims to demonstrate how additive manufacturing techniques can overcome geometric limitations in hydrogel fabrication and contribute to future applications in tissue scaffolding, drug delivery, and microscale biomedical devices.

The Case of the Missing Exon: Disentangling Intestinal VPAC1 Signaling

JO BERGER
Microbiology
Project Mentor: Glenn Dorsam, Ph.D.

VIP is a neuropeptide that serves critical roles as an anti-inflammatory, metabolic, and master circadian regulator whose amino acid sequence has remained unchanged since the dinosaurs. Given its evolutionary importance and influence on human health, a better understanding of its molecular actions is important for highlighting its essential role in gut health. Previously, our lab reported gut dysbiosis in mice deficient for VIP, implicating its role as a key regulator for gut homeostasis. VIP works by binding to a surface receptor, called VPAC1, however this protein is expressed throughout the GI tract in many cell types, including intestinal epithelial cells (IECs), immune cells, and muscle cells. Therefore, there is a critical gap in the knowledge base explaining how cell-specific VIPàVPAC1 signaling regulates gut homeostasis. We hypothesized that IEC VPAC1 signaling drives gut homeostasis. To this end, we developed a conditional VPAC1 IEC knockout mouse using a Cre-recombination system to study cell-specific signaling in the gut. The objective of this research was to quantify, at the DNA level, the excision of exon 2 in the VPAC1 gene. We analyzed wild-type, heterozygous, and conditional knockout VPAC1 mouse tissue from the jejunum and kidney (negative control) for exon 2 by qPCR. This work in progress is expected to reveal a reduction in jejunum or enriched IECs compared to the kidney. The successful completion of this undergraduate research experience will help validate a mouse model for studying IEC-specific VPAC1 signaling and its influence on gut homeostasis and overall host health.

Other contributors: Teala Matiur, Savanah Klegon, Razia Dawlaty

Enhancing Nanoparticle Stability through Protein-Based Surface Modification of Layered Double Hydroxides

KOLBIE BERNU
Environmental Engineering
Project Mentor: Achintya Bezbaruah, Ph.D.

Layered double hydroxide (LDH) nanoparticles, a class of anionic clay materials, are promising adsorbents for water purification due to their large interlayer spacing, positively charged lamellar structure, and exchangeable interlayer anions. However, bare LDH nanoparticles are prone to aggregation because of their high surface-to-volume ratio and strong interparticle interactions, which can reduce colloidal stability and adsorption performance. In this study, LDH nanoparticles were surface-modified with ovalbumin (OVA), an egg white-derived protein, to investigate protein-mediated stabilization under varying experimental conditions. Mg-Al LDH nanoparticles were synthesized via a co-precipitation strategy. The LDH:OVA mass ratio was systematically optimized to identify conditions that maximize surface modification efficiency. In addition, the effects of the sequence and rate of LDH addition into the OVA solution, stirring speed, and aging time on nanohybrid formation were evaluated. OVA coating efficiency was quantified by UV-visible absorbance at 280 nm, while colloidal stability was assessed by particle size distribution and zeta potential measurements. The results showed that dropwise addition of LDH into the OVA solution under vigorous stirring produced a more homogeneous and well-dispersed suspension. Increasing the OVA ratio enhanced protein adsorption up to an optimal level, beyond which only marginal improvement was observed, likely due to saturation and possible aggregation induced by protein bridging. The higher zeta potential value of the LDH-OVA nanohybrids relative to bare LDH nanoparticles confirmed successful surface modification and improved colloidal stability, arising from combined steric hindrance and electrostatic repulsion. These findings suggest that protein-based surface modification offers an effective strategy for stabilizing LDH nanoparticles for environmental remediation and related applications.

The use of AKR1B1 Inhibitors for PDAC Treatment

ALYSSA BOYKO
Biological Sciences
Project Mentor: Roberto Gomes, Ph.D.

The AKR1B1 protein is an aldose reductase widely expressed throughout the body. It plays an important role in the polyol pathway where it acts as a catalyst to reduce glucose to sorbitol. Because this can cause sorbitol accumulation, AKR1B1 is associated with diabetic complications. However, more recent studies have shown that AKR1B1 also plays a key role in cancer growth and metastasis such as liver, lung, and breast cancer. However, no study has been reported in pancreatic adenocarcinoma (PDAC). In this study, we will observe the effects of AKR1B1 inhibition in PDAC cell lines.

Epalrestat is a well-known inhibitor of AKR1B1, commonly used to treat diabetic neuropathy. We will use Epalrestat in comparison studies and in combination with our own compounds to inhibit AKR1B1. Using Epalrestat as a guide, we did molecular docking studies to show our compounds were binding to the same pocket in the AKR1B1 protein. The results from our molecular docking studies show that our compounds have a higher binding affinity than Epalrestat, making them more selective for AKR1B1. We will assess cytotoxicity of Epalrestat, our compounds, and their combination through MTT (cell viability assay). By testing our compounds in conjunction with Epalrestat, we will be able to confirm our molecular docking studies and show that they are in competition to bind in the same pocket. However, if they do not bind in the same pocket, results from the MTT assays will show a larger decrease in cell viability when used together. Based on the results, we aim to create an optimized molecule which will have high binding affinity to AKR1B1, high toxicity to PDAC cell lines, and minimal toxicity to healthy pancreatic cell lines.

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Experimental Evolution of Engineered Rhizobia Adapting to a Novel Legume Host

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Microbiology
Project Mentor: Barney Geddes, Ph.D.

Creating new symbiotic partnerships between rhizobia and non-host legumes represents a major step toward reducing reliance on synthetic fertilizers and enabling sustainable nitrogen fixation in agriculture. One of the biggest challenges in building these synthetic partnerships is that rhizobia and plants must recognize one another through multiple checkpoints. These checkpoints range from root invasion to nodule colonization to nitrogen fixation. Although engineered symbioses can be established, we still lack a mechanistic understanding of how compatibility evolves once a new partnership is created. We recently engineered *Sinorhizobium meliloti* to establish a nitrogen-fixing symbiosis with *Vigna unguiculata* (cowpea), a legume it does not naturally associate with. Because this interaction is evolutionarily new, the partnership is unlikely to be fully optimized. In natural systems, mutualism is driven by long evolutionary histories. By recreating this process in the lab, we can identify the genetic and physiological traits that enhance rhizobia compatibility with novel legume hosts. By using experimental evolution (cycling engineered *S. meliloti* through repeated rounds of cowpea infection, nodule harvest, and re-inoculation), we hypothesize that the repeated passage through the host will select variants with enhanced nitrogen fixation efficiency and increased compatibility. To identify the genetic changes underlying improved symbiotic performance, we will perform whole-genome sequencing on the evolved *S. meliloti* lineages. This insight will provide foundational knowledge for engineering rhizobia for cereal crops and advancing the long-term goals in sustainable agriculture.

Other Contributors: Ahmad Al-Amad, Maryam Khan, and Lucas Rutten

Prenatal and Postnatal Wellness Experience that Respects Birthing Choice

MADDY CARTELLI
Interior Design

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Interior Design

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The purpose of this study was to gather and understand the experiences and desires of individuals during the prenatal, labor, and postpartum experience. The needs and desires of individuals during this time are underfunded and leaves many individuals without proper care, resources, and knowledge of how to take care of themselves, their partners, or their infants, especially if these individuals belong to any kind of minority group such as race, sexuality, gender identity, marital status, age, or religious ideology. A review of current literature centered around the prenatal, labor, and postpartum experience was conducted then followed with a Qualtrics survey aimed at individuals who have given birth as well as support people/family members who played a major role in an individual's prenatal, labor, and postpartum experience. Survey results indicated preferences in what types of spaces were desired during the prenatal, labor, and postpartum experience, improvement that could be made during the birthing experience, what changes could be made to birth plans, how much input an individual felt they had in their birthing location, and if individuals felt isolated during their pregnancy. When executed, this research and knowledge can improve the experiences of those receiving care at a birthing and family wellness center.

Modeling of a House to Simulate Electrical Systems

AUSTIN CHASE
Electrical Engineering
Project Mentors: Qifeng Zhang, Ph.D.
Yao Yu, Ph.D.

This presentation introduces a Modelica-based approach for modeling the electrical system of a real residential building. An approximate representation of the building's electrical layout is first developed and then translated into a simulation environment for analysis. Model parameters are calibrated using utility bill data and estimated appliance usage to achieve reasonable accuracy. This project serves as a proof of concept for extending the approach to develop building digital twin models for larger facilities, such as office buildings, to evaluate their performance under power grid stress and varying environmental conditions.

Investigating Local Adaptation in Minnesota Walleye Using Low Coverage Whole Genome Sequencing

PAIGE CMELIK
Biological Sciences; CHANGE Research and Mentoring for Post-Baccalaureates
Project Mentors: Travis Seaborn, Ph.D.
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Genomic tools have become increasingly important for understanding differentiation of natural and hatchery populations of fish. Walleye (*Sander vitreus*), a widely stocked and managed game species, represents a key species to apply these approaches due to previous research on survivorship and cost being impacted by choice of hatchery strain in certain environments. This study focused on Walleye strains found to have performance and cost differences in Minnesota. Eleven populations represented northern strains and 3 populations represented a southern strain. Using 208 fin clips collected by MNDNR, we used low-coverage whole genome sequencing to identify genetic differentiation by looking for single nucleotide polymorphisms (SNPs). Genotype likelihoods were generated using Analysis of Next Generation Sequencing Data (ANGSD). After filtering, we generated a dataset of the 5,670,882 SNPs for identifying differentiated regions. Following identification of these regions with outlier methods, we plan to use genotype environment association analyses to identify environmental variables that may be driving this differentiation. The results of our study will facilitate further identification of genomic regions under selection in Walleye and improve the understanding of environmental drivers of local adaptation. These results may provide information on genomically informed stocking strategies for present and future environmental conditions for Walleye in Minnesota.

Improving Tobacco Etch Virus NIa Protease for Improved Fusion Protein Cleavage Efficiency

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Tobacco Etch Virus NIa protease (TEVp) is a cysteine protease commonly used in molecular biology for cleaving fusion proteins, allowing for the removal of common affinity tags like Maltose Binding Protein (MBP) and polyhistidine (His6). Wild-Type (WT) TEV protease offers favorable biochemical properties as it remains active over a broad pH range (approximately 6.0-9.0) and is routinely used at temperatures ranging from 4 to 30 depending on the use case. However, a significant limitation of WT TEVp is its ability to undergo autoproteolysis, a self-cleavage phenomenon that generates truncated, catalytically inactive fragments that reduce overall catalytic activity and efficiency To address this limitation, mutations such as S219V, which suppresses autoproteolytic activity, in combination with solubility enhancing mutants such as T17S, N68D, I77V, are commonly used to improve yield and stability. Mutated TEV variants were generated via site-directed mutagenesis, expressed in *Escherichia coli* and purified through a variety of chromatographic methods. Catalytic efficiency of the TEV mutants was then compared to Wild-Type to document the observed effect of the mutations; these mutants are expected to demonstrate improved stability and sustained catalytic activity relative to WT, with reduced formation of autoproteolytic degradation product and enhanced yield upon expression. Collectively, these efforts aim to establish an optimized TEVp variant with enhanced stability, solubility, and sustained catalytic activity for routine application in fusion protein purification pipelines.

Structure-Function Insights from Reintroducing a Disulfide Bond in a Low Potential Rieske Ferredoxin, BphF

MADELYN CRAFT
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Project Mentor: Christopher Colbert, Ph.D.

Rieske Ferredoxins are a subclass of [2Fe-2S] clusters that are critical to electron transfer in various processes across all domains of life, including photosynthesis, cellular respiration, and bacterial catabolism of aromatic compounds. Rieske Ferredoxins are distinguished from other Ferredoxins by coordination of a cluster Iron via two histidines opposed to canonical cysteine coordination. Additionally, Rieske clusters possess an expansive range of midpoint potentials (E_m: +360 to -160 mV) compared to canonical [2Fe-2S] Ferredoxins (E_m: -250 to -450 mV). High Potential Rieske Ferredoxins have distinct structural features lacking in Low Potential Rieske Ferredoxins, a prime example is the presence of a disulfide bond between two of the cluster coordinating loops. The presence of the disulfide bond allows for delocalization of negative charge density in the Rieske [2Fe-2S] cluster, which in turn increases cluster potential and stabilizes the reduced state. In previous studies, removal of this disulfide bond from High Potential Rieske Ferredoxins resulted in a decrease in both midpoint potential and overall catalytic activity. Our protein of interest, BphF, is a low potential Rieske Ferredoxin that is a key component in the first step of biphenyl metabolism seen in gram negative bacteria. The goal of our research is to probe the structural and kinetic effects of altering the electrostatic/hydrogen bond environment around the Rieske cluster through the reintroduction of the disulfide bond.

In Vitro Characterization of Fluorescent Biosensors in Nitrogen-Fixing Bacteria

NORA DAUB
Biotechnology
Project Mentor: Barney Geddes, Ph.D.

Biological nitrogen fixation plays a crucial role in sustainable agriculture by reducing reliance on synthetic fertilizers. This has the potential to be especially impactful in cereal crop production. However, understanding gene expression dynamics of nitrogen-fixing bacteria within varying environmental conditions remains a significant challenge. My research addresses this gap by characterizing fluorescent biosensors in three model nitrogen-fixing bacterial species—*Sinorhizobium meliloti*, *Rhizobium leguminosarum*, and *Sinorhizobium medicae*—to establish baseline expression profiles for future plant-associated applications.

Each bacterial strain was engineered with a fluorescent biosensor inserted at one of two genomic loci: upstream of nitrogen fixation (*nif*) genes or decarboxylate transport (*dct*) genes. Additionally, all strains contained a plasmid encoding mScarlet fluorescence to allow comparison in the quantification of gene expression. Cultures were grown under controlled variations in carbon source, carbon concentration, and oxygen availability. Fluorescence intensity was measured using flow cytometry to assess biosensor activity across environmental conditions.

Results demonstrated that biosensor expression responded consistently to environmental changes. Increased carbon concentrations were associated with higher fluorescence levels, while lower concentrations resulted in reduced expression. Different carbon sources produced distinct yet comparable expression patterns across all strains. Oxygen availability also significantly influenced fluorescence output. Notably, biosensors positioned upstream of *nif* genes exhibited minimal sensitivity to carbon conditions but responded to oxygen variation, reflecting the regulatory mechanisms governing nitrogen fixation.

These findings confirm that the engineered biosensors function reliably and provide a robust framework for interpreting gene expression in future plant-microbe interaction studies. Establishing these baseline fluorescence values enables more accurate assessment of bacterial behavior in plant environments and supports ongoing efforts to engineer more efficient nitrogen-fixing microbes for agricultural use.

Development of a Benchtop Pulsatile Flow Tester for the Next-Gen Pulmonary Visceral Pleural (PVP) Aortic Valve

NOAH DOUGLAS
Mechanical Engineering
Project Mentor: Yan Zhang, Ph.D.

In recent years, research on biological materials and biomaterials has advanced significantly, particularly in the context of their potential use in human organ replacement. This advancement necessitates the creation of testing environments to evaluate the effectiveness of candidate materials in these applications. This project aimed to design and construct a benchtop flow testing environment (FTE) to evaluate aortic valve replacements made from bovine pulmonary visceral pleura (PVP) as alternatives to traditional transcatheter aortic valve replacements. The FTE was constructed to support multiple flow testing methods, including particle image velocimetry (PIV) laser measurements and ultrasonic measurements. Given the limitations of these measurement techniques, the FTE was designed as an octagonal tank made of PMMA (acrylic/plexiglass), allowing for perpendicular laser/camera views necessary for PIV measurement. Inlet and outlet ports were incorporated into the tank to facilitate a pulsatile flow loop that simulated the dynamic flow conditions within the testing environment. The tank was filled with a 65% water and 35% glycerol solution to closely match the rheological properties of human blood and ensure accurate PIV measurements. Additionally, the FTE was designed with sufficient space to accommodate an ultrasound transducer, enabling ultrasound flow measurement without significant modification to the chamber. Following construction, the octagonal structure and size of the FTE were found to allow accurate and versatile measurements of pulsatile flow through the PVP-derived valve. The configuration provided nine distinct PIV views (eight side views and one top-down view) and supported ultrasound measurement, enabling flow testing at various angles and locations along the downstream. This FTE design offers a promising platform for evaluating replacement aortic valves and could contribute to the development of more effective, long-lasting heart valves for implantation. Furthermore, the versatility of the FTE's structure suggests its potential use in flow testing for other surgical applications, such as vascular grafts and vessel stents.

Design & Exploration of FeFET Based Logic & Memories

HAYDEN DURAND
Electrical Engineering
Project Mentor: Sumitha George, Ph.D.

Ferroelectric field-effect transistors (FeFETs) have emerged as a promising research focus due to their nonvolatile characteristics and their ability to integrate memory and logic functionalities. FeFETs enable the development of logic-in-memory circuits capable of performing essential computational tasks efficiently. Modern applications such as deep neural networks (DNNs) rely heavily on large numbers of addition operations, motivating the need for optimized and area-efficient adder designs.

In this work, we explore various adder architectures and logic circuits utilizing FeFET technology to achieve improved area efficiency. We specifically leverage key FeFET properties, including tunable threshold voltage, nonvolatile storage capability, and multi-bit storage within a single device, to develop compact circuit designs. These designs significantly reduce the number of transistors compared to traditional CMOS-based implementations.

Comparing Slow-Freezing and Vitrification for Cryopreservation of Female Lepidopteran Ovarian Primordial Cells

PARKER EHRMAN
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Project Mentors: Kendra Greenlee, Ph.D.
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Studies on several lepidopteran (moths and butterflies) species worldwide have shown evidence of declining populations. Cryopreservation is a conservation method that safeguards a species' genetic material by storing cells at cryogenic temperatures for future restoration. To determine the most viable cryopreservation techniques for lepidopteran germplasm, we assessed the effects of two cryopreservation methods, slow freezing and vitrification, on the ovarian primordial cells isolated from ovariole tips of the adult painted lady butterfly (*Vanessa cardui*). The butterflies were anesthetized, and the abdominal contents were removed and placed in a petri plate with phosphate-buffered saline. The primordial cells were isolated from the tips of four ovarioles and immediately frozen (frozen-thawed samples) using either vitrification or slow-freeze methods. They were later thawed and assessed for cell viability, and the control samples were immediately assessed for cell viability (never-frozen). To measure percent viability, samples were stained using Helixcyte™ (ex/em) and counterstained with propidium iodide (ex/em). Under a fluorescent microscope, the nuclei of cells with intact membranes fluoresce green, while those of cells with compromised membranes appear red. Our initial findings demonstrate that both slow-freeze and vitrification cryopreservation methods effectively preserve cell viability in frozen-thawed samples. Optimization of both protocols is ongoing. This work represents some of the first applications of vitrification techniques to lepidopteran germplasm. Comparison of the two cryopreservation methods contributes to the field of cryobiology for lepidopterans and establishes a foundation for the future development of insect germplasm cryobanks.

Other Contributors: Cade Benson

Phage-Based Manipulation of Salinity Stressed Synthetic Microbial Communities

AVERY FOLSOM
Microbiology
Project Mentor: Samiran Banerjee, Ph.D.

Soil microbial communities drive essential ecosystem functions through complex interaction networks that support nutrient cycling, plant growth, and soil stability. Environmental stressors such as salinity stress can disrupt these networks, reducing community resilience and overall soil function. To evaluate the effects of salinity stress, field samples were analyzed and showed a decrease in microbial diversity and network complexity with increasing salinity, reflected by a reduction in nodes (taxa) and edges (interactions) within the networks. Microbial isolates from high-salinity soils were cultured to reconstruct representative synthetic communities, where in vitro analysis produced similar trends, with increasing salinity corresponding to reduced community complexity. Network analysis of both field and synthetic communities identified taxa with high connectivity, suggesting a potentially greater influence on community structure. To experimentally investigate the role of these highly connected taxa, bacteriophages were isolated from soil samples and tested for host specificity. Bacteriophages targeting Arthrobacter oryzae, a highly connected taxon in our networks, were successfully isolated, and transmission electron microscopy (TEM) was performed to characterize phage morphology. Phage assays demonstrated strong specificity to target taxa, with no observable effects on non-target members of the community. This specificity enables targeted perturbation of microbial communities, providing a controlled approach to evaluate how the removal of highly connected taxa impacts community structure and stability. This approach provides a framework for experimentally evaluating how highly connected taxa influence microbial community structure and stability under salinity stress.

Effects of Macronutrient Diet on Cricket Behavior

ANEVAY FOOTE
Biological Sciences
Project Mentor: Ned Dochtermann, Ph.D.

Energy is a fundamental requirement, but it is often limited and must be allocated among physiological processes and behavior. The energy allocation model explains how organisms distribute energy to support functions such as growth, reproduction, and movement. Variation in macronutrients can influence how energy is used, which may ultimately affect behaviors such as activity levels, exploration, and risk-taking. In crickets, differences in dietary protein-to-carbohydrate ratios have been shown to influence traits including growth, reproduction, flight, and locomotion. However, studies regarding the effects of macronutrient balance on behavioral traits such as boldness and exploratory activity are often overlooked, particularly in crickets. I will be testing how different diet treatments influence exploratory behavior and boldness in crickets. The crickets are assigned to one of three diet treatments: a high-carbohydrate diet, a high-protein diet, or a standard diet. Behavioral responses will be measured using latency trials, which assess boldness and curiosity, and open-field trials that measure exploratory activity and total distance traveled. Open-field trials are recorded and analyzed using EthoVision software. I predict that the crickets on a high-carbohydrate diet will exhibit shorter latency times, greater exploratory movement, and increased risk-taking behavior compared to crickets on high-protein or standard diets due to the immediate energy availability provided by carbohydrates. Additionally, males may allocate more energy to calling for a mate and moving less while doing so, whereas females may show higher levels of activity due to searching for the male's mating call. These findings can contribute to our overall understanding of how macronutrients can influence behaviors and trade-offs in energy allocation.

P,N Ligands Synthesis to Allow Asymmetric Synthesis

BROOKLYN FORTIER
Chemistry
Project Mentors: Mukund Sibi, Ph.D.
Kajalben Somani

P,N ligands have emerged as a versatile class of ligands in asymmetric synthesis due to their ability to coordinate metals through both soft (phosphorus) and hard (nitrogen) donor sites. This dual coordination mode enables fine control over the electronic and steric environment at the metal center, making them highly effective in promoting enantioselective transformations. In this work, a series of novel P,N ligands were designed and synthesized. These ligands are intended for application in asymmetric catalysis, where their structural features may influence enantioselectivity and catalytic efficiency. This study contributes to the development of new ligand frameworks and provides insight into the role of P,N ligands in controlling stereochemical outcomes in catalytic reactions.

Not Throwing Away My Shot: How the Expansion of Vaccine Services Affect Rural Pharmacies

GAGE FOSSEN
Anthropology
Project Mentor: Kristen Fellows, Ph.D.

In North Dakota, independent community pharmacies operate differently from chain pharmacies, one difference being how they offer immunization services. Independent pharmacies are not required to offer vaccination services, but many began to implement them to help their local community and generate more revenue. Something that has not been a focus is the physical space within the pharmacies to accommodate immunizations. This poster draws on existing qualitative research completed by members of the North Dakota Pharmacy Service Enhancement Project (PSEP) team. The goal of PSEP is to enhance and expand clinical services provided in North Dakota community pharmacies while ensuring sustainability through billing and reimbursement of services. There are six pharmacies that participate in this research as pilot sites to help guide the future of the project. The ethnographers on the project visited these pharmacies and collected data through interviews, site visits, and peer learning meetings. Through an independent study class working with the ethnographers, I gained a better perspective of the field. For my final research poster I coded their existing findings, focusing on one aspect by picking out specific data related to the physical adaptations made to implement vaccine services in North Dakota community pharmacies. What was found was an increase in vaccine administration which caused change in the physical environment and workflow. Each pharmacy used their space differently to accommodate these changes. Immunization rooms need to be private, so some pharmacies had fully enclosed spaces and others had partially enclosed spaces. This shows the different mindsets pharmacies have to make these adaptations. Vaccines were very important for pharmacies to thrive and they changed the entire processes of the workplace. This poster focuses on what the rooms look like at different pharmacies, which leads to possible examination for the future of why they chose these setups specifically.

Interactions Between Diet and Immune Challenge on Life History Trade-Offs in *Gryllodes sigillatus*

ELIZABETH FRIAS
Biological Sciences; CHANGE Research and Mentoring for Post-Baccalaureates
Project Mentors: Ned Dotchermann, Ph.D.
Timothy Greives, Ph.D.

Exposure to pathogens and parasites is a constant threat to insects in the wild. With climate change, both periods of exposure to pathogens and environmental stressors are on the rise. Although insect immune responses have been widely studied, the role of nutritional intake in shaping these responses is often overlooked. This project addresses this gap by examining how immune challenge interacts with different diet treatments in the tropical house cricket, *Gryllodes sigillatus*. I will be reviewing the procedures for several techniques used in data collection, including nylon insertions, ovary dissections, live/dead sperm analysis, and aggression trials. Crickets were provided with one of three test diets–high protein, high carbohydrate, and a standard diet–during development and then infected with the DH5α strain of *Escherichia coli* at maturation. To investigate the interaction between diet and immune challenge, physiological, immunological, and behavioral traits will be measured. Ovary mass and live/dead sperm analyses will be used to evaluate reproductive trade-offs. These analyses will also be paired with aggression trials to test for potential correlations between reproductive quality and behavior. Immune responses will be assessed through nylon insertion assays, which measure melanization ability. I expect individuals on a high-protein diet to exhibit stronger immune responses and higher overall fitness. Individuals on a high-carbohydrate diet are expected to show reduced immune responses but minimal changes in fitness. Additionally, I predict that males on a high-carbohydrate diet will display increased aggression but lower sperm quality. This work will contribute to our understanding of the impacts of environmental stressors on insect communities and how individuals allocate resources under stressful conditions.

Adsorption of Methanol on Graphene/Silicon

JORDAN FRISKE
Biological Sciences
Project Mentor: Uwe Burghaus, Ph.D.

Graphene is a promising material for metal-free catalysis, offering an alternative to traditional metal catalysts. In addition, it is used as a component of direct liquid fuel cells and sensors. Therefore, understanding how organic molecules interact with graphene surfaces is important. In this study, we investigated the adsorption of methanol (CH3OH) on graphene/Si(111) using multi-mass thermal desorption spectroscopy (TDS), Auger electron spectroscopy (AES), X-ray photoelectron spectroscopy (XPS), and Raman spectroscopy. Our results show that methanol adsorbs molecularly on Gr/Si(111). In contrast, small sulfur molecules dissociate on the same catalyst [Proc. Natl. Acad. Sci. U.S.A. 123 (10) 2026, e2524790123].

Other Contributors: Md Arif Uddin (NDSU); Trung T. Pham, Jean-François Colomerd, and Robert Sporken (Department of Physics, University of Namur, Belgium)

Internal Jugular and Subclavian Vein Flow Design and Analysis

LOUIS GAYTAN
Mechanical Engineering
Project Mentor: Yan Zhang, Ph.D.

Human venous circulation is highly sensitive to gravity and body position, making these factors essential for understanding how the cardiovascular system adapts to both Earth and spaceflight conditions. Vessels, including the internal jugular, subclavian, and brachiocephalic veins, play large roles in cerebral and upper-body venous drainage. Because these veins have thin, flexible walls, gravity and pressure changes can dramatically impact flow distribution. This study investigates how changes in body position influence blood flow within a physical mock-loop model of these vessels. Flow through each conduit is controlled using pumps and valves to simulate the hydrostatic gradients of different postures. A flow sensor and video imaging of dye-injection patterns are used to measure changes in flow behavior under simulated conditions. Although this model does not fully replicate human physiology, it serves as a proof of concept for studying venous flow. This work serves as a foundation for future research into stagnant blood flow in the brachiocephalic junction under microgravity.

Other Contributors: Santu Golder

Building an Annotated Drone Imagery Dataset for Agricultural AI Applications

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The goal of this project is to show the progress made in analyzing drone imagery datasets by comparing strategies such as manual annotations and the use of a smart annotation tool powered by the Segment Anything Model (SAM) in Roboflow. Dataset annotation is an important step in developing machine learning and computer vision models for agricultural applications. The growing use of unmanned aerial vehicles (UAVs) in precision agriculture has made it easier to observe crop health, weed populations, and crop development throughout the growing season, which contributes to maintaining high yields.

Artificial Intelligence (AI) has also played a major role in analyzing agricultural data, making annotations faster through tools like Roboflow. Its smart select feature allows for automatic segmentation of objects, improving efficiency. However, this method does not always generate bounding boxes, which are required for certain models. In these cases, manual annotation can be more accurate and reliable, although it is more time-consuming.

The dataset for this study was collected using a Tomcat IF800 Quadcopter UAV equipped with a Sentera 65R RGB sensor, flown at an altitude of 65 feet over a 0.36-acre agricultural field with prepared targets of varying shapes and areas. Because the original images exceeded the 20 MB upload limit and TIFF format is not supported by Roboflow, images were divided into four tiles to allow for annotation and upload.

This study compares manual and AI-assisted annotation methods to evaluate their efficiency, accuracy, and limitations, particularly in relation to object shape and size. The dataset was also used for biomass estimation of a cover crop, Winter Camelina, to determine ground coverage. Overall, the results highlight the importance of balancing manual and AI-assisted methods to improve dataset quality and support advancements in precision agriculture.

Environmental Testing of Compression Molded PET/ Fiberglass Composites

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Project Mentor: Chad Ulven, Ph.D.

Fiber-reinforced composites materials (FRC's) consist of reinforcing fibers within another material known as the matrix. The fibers are often incorporated to improve the mechanical properties of the matrix. The most common matrix materials are thermosetting polymers. However, in many applications such as in the automotive field another class of polymers, thermoplastic polymers, have shown promise as an alternative matrix material in FRC's. This is because thermoplastic composites offer useful advantages such as higher recyclability and toughness, as well as faster production times over their thermosetting counterparts. One potential thermoplastic matrix material is polyethylene terephthalate (PET). PET is the most recycled plastic in the world, and one of the most abundant – an example of its use being water bottles. A possible obstacle faced in implementing PET as an FRC matrix is its lower thermal stability in comparison to traditional materials. For this reason, in assessing its viability it is important to evaluate such a composite's mechanical properties in different environments. The aim of this study was to mechanically characterize a PET fiberglass composite over a range of temperatures from extreme cold to high heat following MIL 810. To do this, composites were made from E-glass and PET fibers in the form of a plain weave fabric of long continuous fiber from Concordia Composites, which was placed in a steel mold and heated under high pressure in a process known as compression molding. Specimens were then machined with a waterjet from this material and subjected to flexural, tensile, and impact testing at a variety of temperatures. Results indicated that flexural and tensile strengths decreased with increasing temperature, while modulus values remained relatively stable across the tested range. During impact testing, as energy increased, the material went from slight deformation to major cracking and eventual perforation, with damage spreading along the weave and showing more back-face bending and fiber separation.

The Effect of Autograft Type and Sex on Subjective Knee Function Following Anterior Cruciate Ligament Reconstruction

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The International Knee Documentation Committee Subjective Knee Evaluation Form (IKDC) assesses patient-reported knee function following anterior cruciate ligament reconstruction (ACLR). While patient sex has been shown to affect IKDC scores, the impact of graft selection is not as clear. Bone-patellar tendon-bone (BTB) and hamstring (HS) autografts are the predominant graft types. We hypothesized that there would be no difference in IKDC scores between graft types, but females would report lower scores.

Methods: This retrospective cohort study analyzed patients aged 15-23 years undergoing ACLR with BTB or HS autografts. Recorded variables included IKDC score, graft type, and sex. Inclusion criteria were an IKDC score collected between 5.5-8.5 months postoperatively. Patients were excluded if they had prior ACLR or used graft types other than BTB or HS. The effect of sex and graft type on IKDC was analyzed using a two-way ANOVA.

Results: The mean age at surgery was 17.4 ± 1.71 y. The effect of graft type on IKDC score was significant ($p < 0.001$), suggesting that HS grafts (88.9 ± 8.58) had higher scores than BTB grafts (81.7 ± 10.7). The effect of sex on IKDC score was significant ($p=0.032$), suggesting that males (87.0 ± 9.49) had higher scores than females (83.8 ± 10.8). The interaction between graft type and biological sex was not significant ($p=0.586$).

Discussion: Patients with HS grafts reported higher IKDC scores compared to those receiving BTB grafts, and males reported higher scores than females. Our findings partially support our hypothesis that females would report lower IKDC scores but counter our prediction that scores would not differ between graft type. One possible explanation for this difference is that BTB grafts are associated with increased donor site pain, resulting in lower IKDC scores. A possible explanation for the sex-based difference is that females have higher rates of joint laxity than males, which has been associated with decreased knee stability and neuromuscular control during high-risk movements. There is also a heightened awareness of knee injuries in females due to the high prevalence of ACL tears, which is intensified during the recovery process and may lead to decreased confidence.

Roots of Performance: The Role of Soil Microbial Communities in Field Pea Performance

JADA GRIFFIN
Biological Sciences
Project Mentor: Laura Aldrich-Wolfe, Ph.D.

Soil microbial communities strongly influence plant growth and nutrient dynamics and are often altered by agricultural practices compared to native ecosystems. These differences may be especially important for legumes such as field peas, which form symbiotic associations with nitrogen-fixing bacteria. Changes in microbial composition can influence root nodulation by these bacteria, nutrient acquisition, and ultimately plant growth and yield. This experiment examined how microbial communities from agricultural and native prairie soils affect field pea growth and performance. For the greenhouse study, soil samples collected from six different native prairie and agricultural sites were wet sieved to produce filtrates representing different components of the soil microbial community. Field pea seeds were surface-sterilized and planted in individual pots inoculated with one of five filtrate types from either agricultural or prairie soil: whole soil, arbuscular mycorrhizal fungi, fungal pathogen, bacteria, and control. After 10 weeks, above- and belowground biomass and yield were measured to assess plant performance. Nodulation of root systems by nitrogen-fixing bacteria was also quantified. Field peas were expected to exhibit greater biomass and nodulation when grown with microbial communities derived from native prairie compared to agricultural soils, indicating that increased microbial diversity and reduced pathogen pressure may improve plant performance. Plant responses were expected to vary among filtrate treatments, with bacteria and AMF treatments enhancing growth and nodulation, pathogen treatment reducing performance, and whole soil and control treatments producing intermediate and minimal responses, respectively. However, variation among filtrate treatment may indicate which soil microbial groups are most influential in driving plant performance.

Other Contributors: Ethan Strom

Assessment of Native Bee Utilization of Soybeans in North Dakota

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Bethany Roberton, Ph.D.

Soybeans are a major crop in North Dakota, covering several thousand acres of land. Soybeans self-pollinate to reproduce, but visitation from pollinators like bees can improve soybean yield and quality. However, it is relatively unknown what types of bees are visiting soybean flowers and what food sources (i.e. nectar and pollen) bees are specifically collecting. Therefore, we aim to identify the bee species that are visiting soybean flowers and pollinating them. We surveyed bees visiting soybean flowers in two 40-acre fields at the end of July and in early August 2023. One field was located at the Central Grasslands Research Extension Center near Streeter, ND, and the other was at Carrington Research Extension Center in Carrington, ND. Each field divided into eighteen sections and surveyed with a sweep-net for 10 minutes on four survey dates. For each bee caught, we photographed them for identification and swabbed them for a pollen sample. The collected pollen samples went through chemical acetolysis, were deposited onto microscope slides, photographed, and then sent through a machine learning program to identify the plant species. We caught a total of 59 bees in the two soybean fields: 11 honeybees and 48 bumble bees. Of these, there were 46 bees observed visiting a soybean flower. We have processed 19 pollen samples so far (two honeybees and seventeen bumble bees). The number of grains found on each bee ranged from one to eight thousand. We identified soybean grains on seven of the bumble bees. Each one had less than 10 soybean grains, making up less than 1% of the sampled pollen load. So far, our results indicate that female bees do not actively collect soybean pollen on their body to feed their young. Therefore, they must, coincidentally, pick up grains when foraging for nectar. The presence, although few, of the grains still support that honeybees and bumble bees are potentially pollinating soybean flowers for an additional food source in their diet. In conclusion, we have detected that soybean fields in North Dakota may be providing food for honeybees and bumble bees while also potentially benefiting from pollination services.

Does transition to migration alter seed oil preferences in Red-Winged Blackbirds: Potential for decoy crop fields to increase market crop yield

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Biological Sciences

Project Mentors: Page Klug, Ph.D.; USDA-APHIS Wildlife Services National Wildlife Research Center
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Red-Winged Blackbirds (*Agelaius phoeniceus*) are a migratory species that breeds locally in wetlands in North Dakota and migrate overwinter. During migration blackbirds undergo hyperphagia and put on fat to prepare for their long migratory flights. Prior to migration in the fall, sunflower fields are one main feeding source for red-winged blackbirds. This has a significant economic impact on sunflower farmers in the Dakotas. It's currently unknown if red-winged blackbirds can differentiate between the fatty acids in sunflower seeds. Our current study aims to determine if blackbirds preparing for migration display a preference for different types of oil fatty acid contents.

19 red-winged blackbirds (all male) were captured in October and held overwinter. We stimulated the migration phenotype in the birds by increasing photoperiod to 14 hours of light. For 5 days before and two weeks after increasing the photoperiod, we offered birds a choice of ground cornmeal that we combined with either high-Oleic (5g) or linoleic (5g) oil (35% fats). We assessed choice by recording the amount of each food type consumed during the first 3 hours of light to determine if they had a consumption preference during the various cycles and if it changed after photo-stimulation. We recorded body mass, blood samples, fat scores, and food consumption data for later analysis.

We predict that the birds preparing to migrate will prefer the high-oleic cornmeal crumble during the migratory phase because of its ability to produce the most energy and be used immediately. The results of this study should be able to inform farmers of 1) premium seed use in the bird seed market or 2) varieties to use in decoy crops (i.e., crops planted to offer alternative forage for blackbirds near their roost to keep them out of larger fields). That way red-winged blackbirds may be able to get fat faster with linoleic, reducing consumption and damage to the landscape.

Symmetry Breaking of Interacting Charge-regulated Planar Macroions at Low Salt Concentration

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When two chemically identical macroions interact across an electrolyte, charge regulation will typically lead to the same charge density on both macroion surfaces. However, it was recently demonstrated that a non-ideal, Frumkin-like adsorption behavior of the ions can lead to a spontaneous symmetry breaking, where the coupling of charge regulation leads to different surface charge densities on both macroions in thermal equilibrium. The focus of this work is on macroions with dissociable surface groups in the absence of salt, where the Poisson-Boltzmann equation can be solved analytically and the spontaneous emergence of uniform but different degrees of dissociation on both macroions signifies a symmetry breaking. Using a perturbation approach we derive analytic results for the local stability of the symmetric state. This not only provides a complete thermodynamic characterization of the symmetry breaking as function of all parameters, it also uncovers previously unrecognized features. First, depending on the degree of non-ideality, the symmetry breaking transition can be continuous or discontinuous. Second, metastable states do exist far away from critical points but not in their vicinity. And third, electrostatic interactions generally act toward weakening or suppressing the occurrence of symmetry breaking.

Microgreen Development for Enhanced Human Health in North Dakota

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Agricultural Sciences
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North Dakota crops—such as peas, lentils, soybeans, chickpeas, grains, and oilseeds—are well suited for microgreen production; limited research and awareness currently restrict their development. This project evaluated microgreen production using 15 North Dakota grown crop varieties in controlled environment systems. Two experiments were conducted: the first assessed overall growth performance and grouped microgreens based on seed size and growth duration. The second evaluated growth performance within these groups under controlled conditions. Microgreen yield, size, nutrient content, and water consumption were measured. Results showed that sunflower had the highest fresh yield (100.88 g per tray), while wheat, barley, and oats had the shortest growing period (6 days after germination). Nutritional analysis indicated that snow peas had the highest total dissolved solids (5.2%). Peas and beans also exhibited higher water use than other microgreens. These findings provide practical guidance for microgreen production in North Dakota.

Comparing Touch-Based and Vision-Based Drawings of Textures

ADAM KALINA
Psychology
Project Mentor: Benjamin Balas, Ph.D.

Texture can be experienced by feeling patterns or by seeing them. How does the information that we get from touching a textured pattern inform our understanding of what it might look like? We explored this question by asking observers to explore natural textures haptically and then estimate the visual appearance of those patterns. We created four pairs of unique plaster cast textures, and asked participants (N=43) to draw each pattern one at a time, first relying only on touch and then based on viewing the texture. Within each pair, we created both a "positive" and "negative" version of each pattern by casting the texture with raised vs. sunken features, which allowed us to investigate how edges of different polarity were interpreted both visually and haptically. We expect to see a significant difference between (1) touch-based drawings and vision-based drawings, and (2) between raised and sunken renditions of each pattern. We will test these hypotheses by comparing the power spectra and contour statistics of participants' drawings, both of which will be calculated using open-source programs. Our results will increase our understanding of how we create visual maps of objects using haptic and tactile sensation and help us discover if there are underlying biases in the way we create those maps.

Assessing Robot-Induced Distraction Through Physiological Monitoring in Human–Robot Coexistence on Construction Sites

WYATT KALLIOKOSKI
Construction Engineering
Project Mentor: Youjin Jang, Ph.D.

Construction sites are complex and dynamic environments where workers must maintain constant situational awareness to ensure safety. As autonomous robotic systems are increasingly deployed for tasks such as inspection, monitoring, and material transport, new safety considerations emerge regarding how these systems interact with human workers. A key concern is robot-induced distraction, where a robot's presence or movement unintentionally diverts a worker's attention from their primary task. This research investigated whether the presence and movement of an autonomous robotic dog operating in a shared construction environment influenced workers' physiological responses, serving as indicators of distraction. Participants performed simulated construction tasks while wearing health-monitoring wristbands that recorded heart rate (HR), electrodermal activity (EDA), and skin temperature. Subjective distraction ratings were also collected from participants to capture their perceived level of distraction caused by the robot's activities. Analysis of physiological data revealed observable patterns associated with robot-induced distraction. Participants who reported higher subjective distraction levels showed corresponding changes in heart rate, electrodermal activity, and skin temperature, suggesting shifts in autonomic arousal and cognitive load during the robot's presence and movement. These findings indicate that the robot's dynamic behavior may influence workers' physiological states, reflecting potential attentional disruption in shared workspaces. The findings also suggest that physiological signals can serve as reliable, objective markers of worker distraction in human–robot coexistence scenarios. By correlating subjective distraction reports with measurable biometric changes, this study establishes a foundation for developing adaptive robotic systems capable of detecting and responding to worker distraction in real time. Ultimately, this work supports the safer integration of autonomous robots into active construction environments where humans and machines must operate simultaneously.

Other Contributors: Hardik Chauhan

Practical Time-Cost Trade-Off Optimization for Engineering Project Management

JOMARIE KELLY
Construction Engineering
Project Mentor: Adam Ding, Ph.D.

The time-cost trade-off (TCT) problem, commonly known as schedule acceleration, is when reductions in project duration often result in an increase of cost and resource demands. TCT remains a significant challenge in engineering project management. Extensive research exists on heuristic and mathematical optimization methods; however, their industry adoption has been limited by high implementation complexity and lack of integration with standard project-scheduling tools. This study aims to develop an accessible, technology-enabled framework for analyzing and optimizing schedule acceleration decisions. By building on foundational models supported by NSF and DOE research, this work will create a simplified data-driven prototype tool that integrates automation, algorithmic decision-making, and compatibility with Microsoft Project, Primavera P6, and Building Information Modeling (BIM) environments. The prototype tool is tested using representative construction project data in Microsoft Project. From testing, the Practical TCT research is expected to result in a functional, early-stage prototype tool for practical schedule acceleration analysis. The favorable result is a prototype tool that successfully finds the optimal TCT. The Practical TCT research addresses nationally relevant research areas such as digital construction, advanced manufacturing, and computational decision support, which are all areas supported by principles central to NSF's EFRI, CMMI, and AI-in-construction initiatives, as well as DOE and DOD priorities in infrastructure resilience and optimized project delivery.

Is insect plastic bioremediation a reliable solution?

DEREK KITTILSON
Psychology
Project Mentor: Giancarlo López-Martínez, Ph.D.

Polystyrene (PS) is known as a commonly used product in our daily lives that is not biodegradable. Our daily high level of plastic production makes the waste management of these items unsustainable and as a result microplastic waste accumulates in the environment and up the food chain. Thus, looking for a solution could be beneficial for the future of the environment and human health. The mealworm beetle, *Tenebrio molitor*, uses gut microflora to digest PS, but it is unclear how a plastic-based diet can impact the beetle life cycle. Our goal was to determine whether these beetles can consume and recycle PS while continuing their life cycle (or if PS consumption would be lethal). Additionally, we wanted to investigate the effect of PS ingestion (at 50% and 100% dietary content) on various performance metrics. Adult beetles were sorted into 3 groups: A control group fed oats, a mixed diet group where polystyrene was mixed into the oats at a 1:1 ratio, and a group only fed PS. A preliminary experiment revealed that *T. molitor* beetles continue to eat regardless of diet (i.e., PS was not a feeding deterrent). Our data suggests that *T. molitor* adults can consume polystyrene and continue to live and reproduce. Diets containing PS did yield a reduction in lifespan, but not in a way that harmed their reproduction. Ongoing experiments are focused on nutrient stores and beetle walking activity. If *T. molitor* are able to continue reproducing on a partial or complete PS diet, it could potentially have practical effects on the disposal of polystyrene.

Bridging Language and Optimization: An AI-Powered Operations Research Assistant

MASON KORNEZOS
Computer Science
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Operations Research problems optimize business decisions, but creating mathematical models requires specialized expertise in optimization theory and programming. Small businesses and non-technical decision-makers face barriers when leveraging OR techniques, preventing organizations from benefiting from cost savings and improved efficiency. Our project develops an AI-powered assistant that translates natural language problem descriptions into solved optimization models, normalizing access to OR tools. We developed a four-stage hybrid pipeline processing natural language OR problems end-to-end. Stage 1 employs a custom classifier using regex text extraction and rules-based scoring to identify problem types (production planning, transportation, knapsack, assignment, scheduling, network flow) and extract parameters. This hybrid approach reduces LLM dependency to 40% of cases, invoking Claude AI use only when rule confidence falls below 0.6. Stage 2 converts classified problems into executable optimization models using custom builders for PuLP and CVXPY solvers. Stage 3 solves problems using open-source CBC or commercial-grade solvers. Stage 4 generates human-readable interpretations translating raw solutions into actionable business language. The system successfully solves 10 of 13 test problem types (77% success rate), including production planning, transportation, facility location, scheduling, and network flow. The classifier achieves >90% accuracy on objective detection and >80% on problem family classification. The pipeline processes problems in under 3 seconds and provides validated models with constraint verification. Current development focuses on migrating from toy problems with 10-20 parameters to industry-scale problems requiring data uploads from databases with thousands of parameters, enabling real-world deployment for supply chain optimization and production scheduling. This project demonstrates that AI-assisted OR tools significantly lower barriers to optimization techniques. By automating model formulation, we enable non-experts to solve complex problems requiring specialized knowledge. The hybrid architecture proves combining rule-based systems with LLM fallbacks increases accuracy and cost-efficiency. Future work includes scaling to enterprise datasets with 1,000+ variables and developing web interfaces. Applications span manufacturing, logistics, healthcare scheduling, and financial planning.

Electromagnetic Interference Shielding (EMI) Properties of High-Entropic Material Consisting of the Oxides of Cobalt and Nickel

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Electrical Engineering
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Electromagnetic Interference (EMI) occurs when an unwanted electrical noise or signal of one device disrupts the operation of another device. Such interference can lead to significant consequences, particularly in medical, military, and communication systems where reliability is critical. In the context of EMI, high-entropic materials are significant when considering EMI shielding due to their unique characteristics. In this work, high-entropy materials consisting of the oxides of cobalt and nickel were synthesized with the co-precipitation method and deposited onto substrates using doctor blading to form a film. Their EMI shielding performance will be evaluated using (1) a coaxial transmission line method coupled with a Hewlett Packard 8753E Network Analyzer, and (2) a coplanar waveguide fabricated on a PCB board. The absorption property of the materials to electromagnetic waves in the frequency range from 4-6 GHz will be measured and analyzed, revealing a great potential of the materials for EMI shielding applications. Based on the material's characteristics and the low frequency range tested at, the expected result coming from the experiment is that the majority of EMI waves will be absorbed and dissipated as heat rather than reflected off the surface of the material. The absorption and reflection behavior would indicate that the material has a high absorption capacity. Furthermore, the characteristics and observed EMI properties suggest that the high entropic material may be applicable to the biomedical field and high temperature applications. However, due to the low-frequency range studied during this experiment, the applicability of this material may be limited to low-frequency devices, unless otherwise tested. For future work, utilizing alternative measurement techniques and a wider range of substrate materials to perform the experiment is recommended to further explore EMI performance of high-entropic materials.

Hydroamination of Asymmetric Internal Alkynes

JAMISON LANG
Chemistry
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The Lenacapavir molecule has received significant attention in recent years due to its high effectiveness in HIV prevention. Much of this research is focused on modifications to the core structure. One attractive method for this modification is alkyne hydroamination as it has high atom efficiency, however traditional hydroamination (HAM) suffers from harsh conditions such as high temperatures, the use of strong acids and bases, and expensive late transition metal catalysts. The reason harsh conditions are typically seen in HAM reactions is due to a fundamental challenge of combining an alkyne and an amine, both of which are nucleophilic. The way in which we have chosen to address these problems are with a Ni(0) based catalytic system that is able to behave as both an early and late transition metal. This gives the benefits of being more affordable and less toxic, without sacrificing functional group tolerance. Herein we report a synthetic strategy that combines the broad accessibility of Sonogashira coupling with our two-step, one-pot hydroamination reaction to give a modular approach to the synthesis and modification of Lenacapavir.

The Relationship Between Social Support, Strain, and Anxiety in Undergraduate Students

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Psychology

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Psychology
Project Mentor: Anna Finley, Ph.D.

Anxiety is a common struggle for many college students around the United States. Although it is common, many college students don't know how to properly cope with anxiety or who to go to for support. We explore how familial and friend support and strain impact the presence and severity of anxiety in undergraduate college students. We examined this question by conducting a self-report study on n = 201 undergraduate students at North Dakota State University, utilizing the PROMIS Anxiety Scale, 8-item Family and 8-item Friend subscales of the Social Support and Strain Questionnaire. We performed a zero-order correlations analysis, along with follow-up exploratory regression analyses to better understand whether family or friend support relates more to anxiety, as well as whether family or friend strain relates more to anxiety. Overall, higher family and friend support were associated with lower levels of anxiety (family support $r(199) = -0.17$, $p = 0.008$; friend support $r(199) = -0.20$, $p = 0.004$), while greater family and friend strain were associated with higher anxiety levels (family strain $r(199) = 0.18$, $p = 0.005$; friend strain $r(199) = 0.15$, $p = 0.017$). Regression analyses suggest friend support is still related to anxiety even when controlling for family support ($p = 0.042$), while family strain is still marginally related to anxiety when controlling for friend strain ($p = 0.061$). These findings highlight the importance of social relationships in the context of anxiety among college students, particularly the unique role of both family and friends. Understanding how different sources of support and strain related to anxiety may help guide universities to develop targeted mental health resources for students.

How Microplastics Make Their Way into Your Cup of Coffee

JACK LEONE
Environmental Engineering
Project Mentor: Syeed Iskander, Ph.D.

Micro/nano-plastics has been getting more in the news and in our lives daily with research coming out every day about their effects, and how frequently we are ingesting them. Studies have shown that these plastics can make their way into your bloodstream, kidneys, lungs, and even your brain and heart, which is making the source and fate pathways, a vital area of research. One area less known for its contribution to microplastic intake is coffee, and since it is part of many people's morning routine to help them get ready for the day, it can be another common contributor to microplastic ingestion. To begin a study on the microplastic release you would see in your daily cup of coffee, we isolated the two main contributors, the stir sticks, and the lids. With the stir stick testing, we found that an average of 20 nanograms of PE are released from having a stir stick in your cup, from when it was poured, and brought down to room temperature. With the coffee lids, we did a pour-by-pour test, for six pours, to see if the first few sips will yield more plastic degradation than later sips. We found that the first sip released the most plastic, at 16.5 nanograms, to half that for the second. After which it goes down to a negligible amount and later rises again in the last two sips. To explain this, what is likely happening is that the hot water will degrade plastic in the first two sips, and later the condensation on the lid will begin to degrade the plastic and fall back into the water being poured into the beaker. In the future, we aim to run different types of lids, as well as doing tests into the condensation acting on the lid.

Health and Beauty at the Crystal Palace: Analysis of Specialty Bottles from a 19th-Century Brothel in North Dakota

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Anthropology
Project Mentor: Kristen Fellows, Ph.D.

In 2016, scholars from North Dakota State University led a salvage archaeology project on a 19th Century brothel known as the Crystal Palace. Melvina Massey, an African American madam, owned and operated this brothel in Fargo, North Dakota. Although the context of recovered materials was poor, the identification and dating of bottles collected from the site allowed for the exploration of health and medicinal practices within the brothel. Preliminary analysis of these materials demonstrate that the women working at the Crystal Palace used beauty, pharmaceutical, and medicinal products, as well as their femininity to their advantage while working. The differences in the products represented by the recovered bottles demonstrate how these sex workers navigated their health and well-being within the context of their work and daily lives. This project demonstrates how some women outside of social norms gained agency through the manipulation of their femininity, which changes previous narratives about them and their history.

"Before college, I didn't have to really study:" An interview study exploring student study approaches in STEM

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Undergraduate STEM students often carry a heavy courseload; as a result, they are often preparing for multiple high stakes exams at the same time. Students must decide not just how to study, but also how to adjust their study strategies for different courses. However, we still know relatively little about how students choose their study approaches or how they decide whether their strategies are effective. In this research project, we investigated why students study the ways they do; we specifically asked: What factors influence a student's study approach? How do these study approaches change or develop over time? We interviewed eight NDSU undergraduates co-enrolled in either BIOL 150 and CHEM 121 or BIOL 220 and PHYS 211. During the structured interview each student answered a series of open-ended questions designed to elicit how they studied in each course, their satisfaction with their performance, and whether they would change their study strategies for future exams. We also asked students to compare their study approaches and success across the two courses as we hypothesized course context would impact students' study approaches. Through qualitative thematic analysis, we developed a code book to capture common themes and compare answers across interview responses. We found that students rely on past successful experiences when deciding how to study. In addition, we found that students use very different strategies when studying for biology versus chemistry and physics courses and they adjust those strategies based on performance and perceived difficulty of course content. Our findings point to the importance of creating instruction that directly teaches students how to study for a particular course, to maximize student success in their STEM courses.

Nitrogen Fixation by Synthetic Microbial Communities on Barley and Corn: ARA Activity Detected by Oxygen Concentration Adjustment

SOMI LIM
Biotechnology
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Synthetic nitrogen fertilizers are widely used to enhance crop yields; however, excessive use leads to soil degradation, water pollution, and greenhouse gas emissions, posing risks to environmental and human health. Biological nitrogen fixation offers a natural alternative in which certain microorganisms convert atmospheric nitrogen (N_2) into ammonia (NH_3), a form of nitrogen that plants can utilize. Therefore, nitrogen-fixing microbial inoculants have the potential to supplement crop nitrogen needs and decrease reliance on synthetic fertilizers. However, the effectiveness of these microbial communities depends on interactions with host plants and environmental factors, which remain poorly understood.

This study investigated the responses and outcomes of a nitrogen-fixing synthetic microbial community (SynCom) inoculated on two host plants, corn and barley, under nitrogen- and carbon-free conditions. Microbial colonization was measured by counting colony-forming units (CFUs) from root samples. Nitrogenase activity was evaluated using the acetylene reduction assay (ARA), and microbial community composition was analyzed through 16S rRNA gene amplicon sequencing.

Inoculation with the live SynCom promoted early-stage plant growth compared to heat-killed controls under nitrogen- and carbon-free conditions. Nitrogenase activity, assessed using the ARA, appeared limited under the tested conditions. In contrast, significantly higher CFU counts in live treatments confirmed successful microbial colonization of plant roots. NMDS analysis revealed clear differences in microbial community composition based on host plant (corn vs. barley) and treatment (live vs. heat-killed). Notably, SynCom taxa constituted a greater proportion of the root microbiome in the live-corn treatment compared to other treatments, suggesting more efficient colonization in corn.

These findings highlight host-dependent dynamics of synthetic nitrogen-fixing microbial communities and emphasize the importance of plant–microbe interactions when evaluating microbial inoculants for sustainable nitrogen management in agriculture.

Integrin α2β1 inhibition upregulate Cubilin expression in renal epithelial cells

CONNOR LUKKARI
Electrical Engineering
Project Mentor: Sijo Mathew, Ph.D.

Fibrosis and chronic kidney disease are strongly linked to diabetes and obesity. A key feature of these conditions is albuminuria, where excess albumin in urine damages proximal tubular cells through inflammation, oxidative stress, and apoptosis, leading to progressive loss of kidney function. Cubilin is a major endocytic receptor expressed in proximal tubular epithelial cells that plays a critical role in albumin reabsorption. It functions with megalin and amnionless to internalize filtered albumin and maintain protein balance. However, increased albumin uptake leads to intracellular accumulation, triggering inflammatory and fibrotic responses.

Integrins are heterodimeric transmembrane receptors composed of α and β subunits that mediate cell–extracellular matrix (ECM) interactions. In the kidney, integrin β1-containing complexes are essential for cell adhesion, basement membrane signaling, and cell survival. In particular, integrin α2β1, a collagen-binding receptor, regulates downstream signaling pathways such as FAK, MAPK, and PI3K/Akt, which can influence cellular responses and protein handling.

In this study, we investigated whether ECM signaling regulates cubilin expression. We observed that female mice exhibited lower integrin β1 expression and higher cubilin levels than age matched male mice kidneys, suggesting an inverse relationship. This was further confirmed by Western blot analysis of kidney cortex samples from integrin β1 knockdown (Itgb1 KD) and control mice. *In vitro*, inhibition of integrin α2β1 in TKPTS (mouse proximal tubular epithelial) cells resulted in increased cubilin expression, as determined by RT-PCR analysis, further supporting the *in vivo* findings.

Overall, our findings indicate that integrin-mediated ECM signaling regulates cubilin and renal albumin reabsorption. Targeting integrin pathways, particularly integrin agonist, may help reduce albumin-induced tubular injury and protect against kidney damage in diabetes and obesity.

Other Contributors: Sreyasi Pal, Md Shafiqul Islam Sovon

AI-Assisted Identification of Road Users and Pavement Conditions on Low-Volume Roads

KATHRYN MACK
Accounting and Finance
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In rural North Dakota, managing transportation infrastructure is a significant challenge. While the traffic volume is generally low, local roads often bear the brunt of heavy, wide-axle trucks tied to agriculture and energy activities. This repetitive vehicular loading is the primary cause of rapid pavement distress. Many local agencies in these underserved regions struggle with limited staff and resources. This hinders those agencies from having the timely, detailed data needed for effective road monitoring and maintenance, and leads them to reactive, costly repairs.

To tackle this problem, this project focuses on creating an automated computer vision pipeline using the TensorFlow deep learning framework. By using the TensorFlow Object Detection API on low-powered edge devices, vehicles can be identified and classified by axle type and size under the challenging conditions of rural areas. Model accuracy and validation are achieved by comparing AI-generated vehicle counts with manually verified data, ensuring they meet the unique needs of North Dakota's roads.

The primary goal of this project is to produce a high-quality dataset that improves the reliability of AI-driven methodologies for traffic data collection on rural roads. Besides developing a robust machine learning model capable of accurately classifying vehicles, this project will document the technical challenges encountered during rural deployments, offering insights for engineers and researchers using open-source AI tools.

The goal of this work is to help rural transportation agencies adopt a more proactive maintenance approach by providing timely access to reliable data. This will also optimize their repair schedules, extend road lifespans, and equip local officials with data-driven insights and ultimately enhance the resilience of essential infrastructure in North Dakota.

Investigating Genetic Differentiation in Minnesota Walleye Hatchery Strains

ELLIOT MAGCALAS
Biological Sciences
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The advancement of genomic tools recently allowed for deeper investigation into differentiation of stocked fish populations underlying the relationship between performance and population locale. Special attention in previous work was given to Walleye (*Sander vitreus*) in Minnesota, as studies on stocking effort between hatchery strains revealed a significant effect on yearling survivorship and net cost, which may entail significant management considerations due to Walleyes' prominence as a stocked game fish. We studied genomic strain differentiation between northern Minnesota strain (MIS) and southern Minnesota strain (SMS) due to observed differences in survivorship and cost across the state. 208 fin clips from Minnesota Walleye populations provided by MNDNR were processed for sequencing. The sequence data was used to identify single nucleotide polymorphisms (SNPs), which were then used to call genotypes, and those genotypes were used to estimate genetic variation and differentiation. Genetic variation was determined using R packages adegenet, for multivariate and geospatial analyses, and hierfstat, to examine population structure and heterozygosity. We created and used a set of 23,000 high quality SNPs with a mean depth 12-22X aligned to a Walleye reference genome. We found some evidence of population differentiation. Further interrogation will involve genotype environment association analyses to identify the driving environmental factors of differentiation. The results of this study will reveal loci under selection in these strains of Walleye and assist in explaining the environmental mechanisms driving differential performance. Stocking strategies for Walleye using the desired genomic information will better account for local adaptation to environmental conditions across the state and lead to more successful management outcomes.

QSAR Modeling with Machine Learning Benchmarking for Anticancer Compound Discovery in Hepatocellular Carcinoma

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Pharmaceutical Sciences
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Hepatocellular carcinoma (HCC) is a major cause of cancer-related mortality worldwide, and treatment options remain limited, especially in advanced disease. Identifying compounds with potential anticancer activity is important, but experimental screening can be time- and cost-intensive. Quantitative structure–activity relationship (QSAR) modeling provides a way to predict biological activity based on molecular structure, which can help prioritize compounds before laboratory testing. However, many QSAR studies do not include thorough validation or direct comparisons with machine learning approaches on the same dataset, particularly for specific models such as Huh-7 cells.

In this study, a dataset of 55 structurally diverse compounds with reported IC_{50} values against Huh-7 cells was collected from the literature. Molecular descriptors (approximately 2,000 per compound) were generated using alvaDesc and then filtered to remove constant and highly correlated variables. A genetic algorithm–multiple linear regression (GA-MLR) model was developed using QSARINS, resulting in a final model with seven selected descriptors. Model performance was assessed using internal validation (Q^2_LOO and Q^2_LMO), external validation (R^2_ext and CCC), Y-scrambling, and applicability domain analysis to ensure reliability.

The final GA-MLR model showed strong predictive performance ($R^2 = 0.896$, Q^2_LOO = 0.848, R^2_ext = 0.826, CCC_ext = 0.888), and Y-scrambling results suggested that the model was not due to chance correlation. The selected descriptors indicate that electronic properties, molecular topology, and lipophilicity play an important role in anticancer activity for this dataset. Given the relatively small sample size, additional models including Random Forest, XGBoost, and Support Vector Regression were also evaluated using the same descriptors and data split. While these models performed well on the training data, they showed weaker performance on the test set, suggesting some degree of overfitting.

Overall, this study supports the use of interpretable GA-MLR QSAR models for predicting anticancer activity in HCC-related datasets. These results suggest that simpler, well-validated models may be more appropriate for smaller datasets and can still provide useful insight for compound prioritization in early-stage drug discovery.

Cover Crops and Grazing as Weed Seed Bank Management

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Project Mentor:
Lindsay Malone, Ph.D.

Weed seedbanks are a primary determinant of weed population dynamics within agroecosystems. Management practices like cover cropping and livestock grazing may alter seedbank composition, dormancy, and emergence patterns. Evaluation of these interactions is essential for improving the integration of weed management in semi-arid cropping systems.

Soil was collected from replicated field plots at the NDSU Central Grasslands Research Extension Center in Streeter, ND, with samples taken near fence lines to capture the representative seed bank inputs under contrasting management conditions. Treatments reflect different combinations of grazing: spring graze, dual graze, and no graze, as well as cover crop presence and absence. Collected soils were transferred to an NDSU greenhouse and placed in standardized 1 x 1 plots, where they were under controlled conditions. Cumulative weed emergence was quantified over time as a proxy for an active seedbank, with periodical counting used to track emergence rates and the total seed densities across treatments.

Cumulative emergence varied among the treatments; grazed systems generally exhibited greater total weed emergence than no-graze treatments. Soils collected from plots with no cover cropping showed reduced emergence relative to cover-cropped systems, suggesting that management practices influence both size and germination dynamics. Results from this study indicate interactions between grazing and cover cropping can shape weed expressions, implicating the importance of integrated weed management within the Northern Great Plains agroecosystems.

Other Contributors: Miranda Meehan, Kevin Sedivec, Katrina Kratzke, Josh Wianecki

Cytotoxic effects of a KRAS G12D inhibitor on pancreatic cancer cells

BRAYDEN MCLEAN
Biological Sciences
Project Mentor: Katie Reindl, Ph.D.

Pancreatic cancer is one of the deadliest cancers, with a 5-year survival rate of only 13%. Over 95% of pancreatic cancers have a mutation in the KRAS oncogene that drives tumor growth. Recently, a selective KRAS G12D inhibitor, MRTX1133, was discovered to have potent cytotoxic effects against pancreatic ductal adenocarcinoma (PDAC) cells. The purpose of our project is to evaluate the anti-cancer effects of MRTX1133 against KRAS-mutant PDAC cell lines. Two patient-derived PDAC cell lines, A09 and A19, and two commercial PDAC cell lines, PANC-1 and MIA-PaCa 2, were treated with increasing concentrations of MRTX1133 (0, 0.1 nM, 1 nM, 10 nM, 100 nM) for 48 hours and 96 hours. Alamar Blue assays were performed to measure the overall metabolic activity in the presence or absence of the KRAS G12D inhibitor. We next evaluated the effects of the KRAS inhibitor on downstream cell signaling. The 4 cell lines (A09, A19, PANC-1, MIA-PaCa 2) were treated with 10 nM MRTX1133 for 6 hours. Western blotting was used to measure total ERK and phosphorylated ERK expression in control vs. treated cells. Preliminary results of the Alamar Blue assays indicate significant reduction (up to <1% of control) in cell metabolic activity in KRAS G12D-mutant A09, A19, and PANC-1 after 48 and 96 hours of treatment with MRTX1133, but not in KRAS G12C-mutant MIA PaCa-2 cells. Further directions of this research will be to identify how KRAS inhibitors could sensitize PDAC cells to immunotherapy.

A Serendipitous Discovery: Characterizing the Zone of Inhibition Between a Black-Spored *Aspergillus* and the Phytopathogen *Fusarium graminearum*

ALEXIS MEREDITH
Microbiology
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Fusarium graminearum is the primary causal agent of Fusarium Head Blight (FHB), a devastating disease affecting barley, oats, rice, rye, and wheat. Infection leads to substantial yield loss and contamination of grain with harmful mycotoxins such as deoxynivalenol and zearalenone, posing serious risks to human and animal health. Historical epidemics in the United States have resulted in $2.7 billion in losses between 1998 and 2000, and continued outbreaks highlight the need for improved control strategies. Current management approaches, including resistant cultivars, fungicide application, and disease prediction tools, reduce risk but do not fully prevent infection. Here, we report the serendipitous discovery of a previously unidentified fungal contaminant that produces a zone of inhibition (ZOI) against *F. graminearum*. The contaminant has been provisionally characterized as a black spore *Aspergillus* (BSA) based on its morphological features. Experimental work has focused on reproducing the ZOI under controlled conditions and evaluating factors that influence its formation. Preliminary results suggest that a metabolite produced during the interaction by BSA may inhibit the growth of *F. graminearum*, dependent on temperature, maturity of BSA culture, and nutrient availability. Ongoing work includes genetic identification of the contaminant through Sanger sequencing and characterization of the inhibitory compound. This research emphasizes the potential of naturally occurring fungal interactions to guide new biological control strategies for FHB and enhances the broader understanding of antagonistic mechanisms among fungal species.

Farm Labor Shortages in the Midwest

ANDREW MEYER
Economics
Project Mentor: Thomas Krumel, Ph.D.

Farm labor shortages have become a persistent challenge across the Upper Plains region, particularly in North Dakota, South Dakota, and Minnesota. These shortages matter because agriculture depends heavily on timely labor during planting, harvest, and livestock-intensive periods, and even small labor gaps can reduce productivity, increase costs, and disrupt farm operations. Despite the importance of this issue, there is limited farm-level evidence on the severity of these shortages, the types of labor most affected, and whether common responses such as higher wages are enough to solve the problem.

This project examines the extent and consequences of farm labor shortages in the Upper Plains by developing and distributing a survey instrument to farmers in the region. The survey collects information on farm scale, labor demand during peak periods, wages paid, worker recruitment strategies, labor hours needed versus available, skill mismatches, turnover, and farm responses such as technology adoption or changes in production practices. In addition to survey data, the project is informed by existing research on agricultural labor markets and related workforce trends.

Expected results suggest that many farms experience meaningful labor shortages, especially during peak seasonal periods, and that wage increases alone may not be sufficient to attract and retain the workers farms need. Instead, shortages may reflect deeper structural issues, including seasonality, skill requirements, geographic constraints, and limited labor supply in rural areas. The project also expects to identify important differences in how farms cope with shortages, such as through cross-training, adjustments in acreage or livestock, custom hiring, and labor-saving technology.

The broader implication of this research is that policies designed to address labor shortages in other industries may not translate well to agriculture. More effective solutions will likely require programs tailored to the unique structure of farm labor markets, including targeted workforce development, improved recruitment pipelines, and policies that better account for the seasonal and skill-specific nature of agricultural work. By providing clearer evidence on these challenges, this project aims to support more practical and effective responses for farmers and policymakers in the Upper Plains.

Genetics of a Co-Managed Elk Herd on Tribal Lands within the Context of Regional Elk Genetics

COURTNEY MITCHELL
Biological Sciences; CHANGE Research and Mentoring for Post-Baccalaureates
Project Mentor: Jeremy Guinn, Ph.D.; United Tribes Technical College

Tribal lands, including those of the Standing Rock Sioux Tribe (SRST) in North Dakota and South Dakota, may function as important refuges or linkages for regional elk herds, yet their role in maintaining population connectivity has received limited scientific attention. Following their extirpation in North Dakota during the late 1800s, elk populations have gradually rebounded through restoration efforts led by tribal and federal partners. However, reintroduced populations often experience genetic challenges associated with small founder sizes and restricted gene flow, all of which can reduce genetic diversity and limit long-term adaptive potential. On SRST lands, an initial elk population established in the Porcupine Hills persisted for many years at a small population size before expanding to more than 200 individuals over the past decade. The objectives of this project are to (1) assess genetic diversity and population structure within the population and (2) identify genetic connectivity with neighboring herds across the state and surrounding region. We applied Genotype-by-Sequencing to oral mucosa samples, primarily collected from hunter-harvested individuals, to characterize genetic structure across multiple spatial scales. We will use RStudio to map migration and gene flow patterns using packages such as divMigrate and EEMS. Our initial results showed two distinct herds, one originating from Yellowstone National Park and the other from Canadian sources. Overall, this research will reveal temporal patterns in genetic diversity and provide insight into how reintroduced elk populations maintain or lose variation over time. This will support regional elk management, reinforce tribal sovereignty in wildlife research, and contribute to biodiversity conservation by promoting genetically resilient elk populations.

Non-Destructive Kernel Vitreousness Screening in Hard Red Spring Wheat via SWIR Hyperspectral Imaging and Machine Learning

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Crop and Weed Science
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Hard red spring (HRS) wheat is valued and marketed based on the percentage of dark hard and vitreous (DHV) kernel, which influence milling performance, flour yield, end-use functionality, and ultimately export acceptance and price premiums. Rapid categorization of HRS wheat into “Red Spring (RS)” (DHV < 25), “Northern Spring (NS)” (DHV = 25–75), and “Dark Northern Spring (DNS)” (DHV > 75) is therefore essential for quality segregation and contract compliance. However, conventional DHV grading is performed manually and requires a trained inspector to visually evaluate kernels. This approach is time-consuming and labor-intensive, and because it relies on human judgment, grading outcomes can be operator-dependent, increasing the risk of subjectivity and variability across inspectors and inspection sessions. To address this gap, we evaluated a hyperspectral imaging (HSI) and machine-learning workflow for classifying HRS wheat samples into the three DHV categories using SWIR reflectance spectra (1000-2500 nm range, 272 bands). We benchmarked various spectral preprocessing strategies- standard normal variate (SNV), multiplicative scatter correction (MSC), detrending (DT), Savitzky–Golay (SG) smoothing and derivatives, coupled with five classifiers (SVM, Random Forest, Extra Trees, k-NN, and logistic regression). The best-performing pipeline was Logistic Regression with SG second-derivative preprocessing, achieving an overall test accuracy of 56.2%. Class-wise results indicated stronger discrimination for higher-quality categories: DNS achieved precision 0.63, recall 0.65, and F1 0.64, while NS achieved precision 0.63, F1 0.54, and specificity 0.80. RS remained more challenging (precision 0.31, recall 0.53, F1 0.39), indicating confusion (accuracy 0.79 and specificity 0.83) near the DHV < 25 threshold and overlap with intermediate samples. Other high-ranking combinations, k-NN with SG first derivative, k-NN with detrending, SVM with DT+SNV, and logistic regression with MSC, also performed competitively, suggesting that derivative-based preprocessing and scatter-correction help capture vitreousness-related spectral signatures. This study demonstrates the potential of SWIR-HSI with machine learning as a scalable, non-invasive tool for rapid DHV screening and export-oriented lot segregation in HRS wheat supply chains. Future accuracy gains are expected by identifying key SWIR wavelength regions for targeted band selection and noise reduction and fusing visible range spectral information with SWIR spectra to better capture kernel characteristics.

Developing an in vitro Assay to Screen Ligand Specific RAGE Inhibitors

RIVER OLSON
Electrical Engineering
Project Mentors: Stefan Vetter, Ph.D.
Estelle Leclerc, Ph.D.

Objectives: The receptor for advanced glycation end products (RAGE) is activated by several structural distinct ligands. Ligand engagement leads to activation of specific cellular signaling cascades resulting in the up-regulation of pro-inflammatory genes, changes in cell-adhesion and motility, increased autophagy and other phenomena that are directly involved in the progression of several important human diseases. Therefore, RAGE is a target of drug development with a particular focus on ligand specific RAGE inhibitors.

The goal of this research project is to develop an in vitro assay to screen monoclonal anti-RAGE antibodies for their ability to block the binding of RAGE ligands to the receptor. We selected an enzyme complementation assay to monitor the protein-protein interaction between the extracellular VC1-domain of RAGE with S100B. We recombinantly expressed and purified the extracellular VC1-domain of RAGE tagged with the LgBiT-fragment of nano-luciferase and S100B tagged with the smBiT-fragment of luciferase. Binding of S100B-smBiT to VC1-LgBiT restores the enzymatic activity of luciferase and allows quantifying the interaction in a 96-well plate format. Assay conditions were optimized and the assay was applied to the screening of a panel of anti-RAGE antibodies to identify S100B specific RAGE antagonists. Results of the assay optimization and screening results will be presented.

Other Contributors: Jack Stoppleworth, Lora Ensign, Peyton Zaun, Anupom Nath

Using Multiple Drones with Various Threat Stimuli to Haze Nuisance Blackbird Flocks from Sunflower in North Dakota

JACIE OSIER

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Project Mentor: Page Klug, Ph.D.; USDA-APHIS Wildlife Services National Wildlife Research Center

Considering the economic loss blackbirds (*Icteridae*) inflict on sunflower crops, further investigation into effective management tools is needed. Drones as frightening devices are dynamic tools that cause antipredator behavior in birds. Hazing blackbirds with a drone reduces flock sizes and can cause complete field abandonment, but one drone is often not threatening enough to significantly impact large flocks. We evaluated if efficacy increased when using multiple drones with various threatening features. We used a larger yet slow drone (large; DJI Agras, 1,500 mm), a smaller yet fast and maneuverable drone (small; DJI Mavic, 400 mm), and a smaller fast drone with a loudspeaker (sound-broadcasting; Autel Evo 2 RTK Series V3, 427 mm) emitting threatening sounds (i.e., firecrackers, pyrotechnics, raptor calls, and blackbird distress calls; 88 dB at 60 m). Our six hazing treatments were individual drones and all combinations of paired drones. Overall, we saw a 65% decline in flock size (sound-broadcasting/small = 100%, sound-broadcasting/large = 77%, large/small = 70%, small = 73%, sound-broadcasting = 67%, large = 40%) with 55% of the flocks (15 of 27) fully abandoning the field after 20 min of hazing (sound-broadcasting/small = 100%, sound-broadcasting/large = 75%, sound-broadcasting = 67%, small = 57%, large/small = 40%, large = 0%,). We found that flock reduction after 20 min of hazing did not significantly differ by treatment but found a significant effect of temperature, ambient light, and day of year. Although not significant, greater flock reduction was observed when the large drone was absent and time to abandonment was quicker when the sound-broadcasting drone was present. Flight initiation distance (FID) of the flock with the drone approaching directly was not significantly different by treatment but was impacted by flock size and flock distance from drone launch. Multiple drones equipped with various negative stimuli did not elicit significant changes in FID or intensity of antipredator response, but evidence suggests the possibility of increased hazing efficacy. Low sample sizes (n=27) could have influenced significance. Our results inform producers about the effectiveness of hazing blackbirds with multiple drones and the most effective threat stimulus.

Polyaniline-Graphene Oxide Coating Primer for Automotive Applications

ZUBIN PARK

Chemistry
Project Mentor: Eugene Caldona, Ph.D.

Corrosion of carbon steel remains a critical durability challenge in the automotive industry, where multilayer coating systems must simultaneously provide adhesion, barrier protection, and compatibility with topcoats. Conducting polymer–nanocarbon hybrids offer a promising route to active–passive corrosion control, particularly when integrated into primer architectures. However, the mechanistic compatibility between electropolymerized polyaniline–graphene oxide interlayers and low-surface-energy fluoropolymer topcoats remains insufficiently understood. Here we show that an electropolymerized polyaniline–graphene oxide composite primer forms an adherent, electroactive interphase on carbon steel that is chemically and physically compatible with a poly(vinylidene fluoride–hexafluoropropylene) topcoat. Electrochemical measurements demonstrate suppressed corrosion kinetics and stabilized impedance response consistent with coupled barrier and redox-mediated protection mechanisms. Spectroscopic analysis confirms the incorporation of oxygen-functionalized graphene domains into the polyaniline matrix and the preservation of protonated emeraldine structures during anodic passivation. Wettability measurements reveal a moderate increase in surface polarity relative to neat polyaniline, promoting improved interfacial wetting and mechanical interlocking with the fluoropolymer overlayer. The resulting bilayer system integrates active corrosion inhibition from the conducting polymer with the low permeability and chemical resistance of the fluoropolymer topcoat, establishing a coherent processing–structure–property–performance relationship relevant to automotive primer design. This work positions polyaniline–graphene oxide composite primers as multifunctional interlayers for durable automotive coating stacks, offering a scalable strategy for coupling electrochemical corrosion control with fluoropolymer-based surface protection in next-generation vehicle platforms.

The Replication Factor A (RFA) complex participates in a unique pathway that while promoting cell growth, also leads to increased frequency of DNA mutation

MADISON PATTERSON

Biochemistry & Molecular Biology
Project Mentor: Stuart Haring, Ph.D.

All cells encounter stressors (environmental and chemical) that create lesions in DNA. While lesions are often temporary, if they are not repaired, they can lead to permanent changes in DNA called mutations, which are the leading cause of cellular dysfunction and diseases like cancer. Cells have pathways to recognize and deal with lesions while also regulating (preventing) cell growth to provide time to deal with the lesion(s). However, a unique pathway (checkpoint adaptation) exists where cells will attempt to grow despite still having a DNA lesion(s) present. While this may allow the cell to survive (good?), it also leads to mutations in the DNA (bad?). It appears that once cells have DNA damage, they are "on the clock" for repairing it. Once the timer is up, cells attempt to resume growth, whether or not the damage has been repaired. Replication Factor A (RFA) is a single-stranded DNA binding complex that when modified, appears to be the "timer" that influences the decision of when cells should resume growth following DNA damage.

To assess how RFA modification affects the decision to halt or continue cell growth when DNA damage is present, we mutated specific combinations of serine or threonine residues in the amino-terminus of the Rfa2 subunit. Upon inducing a non-repairable DNA damage in cells with various forms of Rfa2, I asked if cells remain arrested (non-growing) or if they adapt (resume growth) in the presence of this damage using microscopy. This allowed us to assay which specific serine/threonine residues are important in this unique, checkpoint adaptation pathway. The data in this presentation will make the distinction of whether it is more important where modification occurs or if it is simply important that the Rfa2 subunit be modified within the targeted region of the protein (with the exact amino acid location being unimportant). Knowledge of checkpoint activation, maintenance, and exit (especially when DNA damage is still present) is critical for understanding how this pathway might be manipulated to prevent cell growth in the face of excessive/irreparable DNA damage to ultimately prevent the formation of potential disease-causing mutations.

Creation of Nanoparticles from Biomass for Polymer Additives

EVAN PAULSON
Mechanical Engineering
Project Mentor: Ali Amiri, Ph.D.

There is a growing need for sustainable high-performance composites to replace currently used non-sustainable polymers and plastics. Many attempts have been made to create biomass-based composites as a solution, but these composites are difficult to work with and do not achieve the needed performance. This research investigates the creation of nanoparticles from biomasses using high shear homogenization. Those particles are to be evaluated as additives in composites to improve the processing and performance vs traditional biomass. The process involves milling particles to micron size using a planetary ball mill, followed by high shear homogenization to achieve nanoscale particles. The evaluated biomasses are soy hulls, wheat middlings, and wood flour. The resulting nanoparticles are studied to determine physical properties and evaluated for use as a polymer additive. Suitable particles are added to biopolymers to create sustainable composites, and the composite properties are evaluated for performance. The success of the research would result in the development of a repeatable process for the creation of nanoparticles from biomass, properties of the nanoparticle s created including size distribution and morphology, and insights into applications of biomass derived nanoparticles as additives in polymer composites. These deliverables will create new opportunities for sustainable bio composites to be used in industries as a superior alternative to the current polymer plastics.

Influence of feeding high-forage vs. high-concentrate diets to pregnant heifers on pancreatic α-amylase activity in offspring during the finishing period

KAIA PAULUS
Animal Science
Project Mentor: Kendall Swanson, Ph.D.

Maternal diet can influence fetal development and long-term productivity of the offspring in cattle. In finishing cattle, high-starch diets are fed to maximize gain and improve meat quality and therefore, developing approaches to improve starch digestion are important. α-Amylase is produced in the pancreas and is responsible for the initial hydrolysis of starch in the small intestine. However, α-amylase activity is negatively influenced by increasing starch flow to the small intestine in cattle. This study evaluated the influence of feeding high-forage versus high-concentrate diets to pregnant heifers on pancreatic α-amylase activity in finishing steers. Heifers ($n = 22$), predominately of Angus breeding, were blocked by initial BW and randomly assigned individually to either feeding a high-forage (75% forage) or high-concentrate (75% concentrate) diet using an Insentec feeding system to gain 0.45 kg/day from 15 days before breeding until two-thirds of gestation and 0.79 kg/day during the last third of gestation. Heifers were bred using artificial insemination with male-sexed semen from the same sire. Following calving, all cows and calves were managed similarly and after weaning steers were fed for approximately 3 months before entering the finishing phase. Steers (293 ± 21 kg) were blocked by BW, fed individually using Calan gates, and adapted to a common high-concentrate diet and fed until finished (140 ± 5.6 days). At the conclusion of the finishing period, steers were slaughtered and the pancreas was weighed and a sample collected for analysis of protein concentration and α-amylase activity. Data were analyzed as a completely randomized block design with treatment and slaughter day as the block using the MIXED procedure of SAS. Feeding pregnant heifers a high-forage vs. high-concentrate diet did not influence ($P \geq 0.15$) pancreatic mass (g and % of BW) and α-amylase activity (U/g, U/pancreas, and U/g protein) in steer offspring. These results suggest that feeding a high- vs low-concentrate diet to heifers during pregnancy does not influence pancreatic α-amylase activity, suggesting minimal effects on regulating the initial steps of starch hydrolysis in the small intestine.

Other Contributors: Christy Finck, Pauliane Pucetti, Carl Dahlen, Joel Caton, Kevin Sedivec, Samat Amat

"The clinical part of pharmacy is rising up:" Breaking the "Pill Packer" Myth

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Pharmacists are often perceived primarily as medication dispensers rather than as clinical healthcare providers, reinforcing the persistent "pill packer" stereotype. This perception overlooks the expanding clinical role of pharmacists in community settings and contributes to the underutilization of their services. This project explores the disconnect between pharmacists' actual clinical responsibilities and the public and professional narratives that continue to define their role. Thematic analysis was conducted on insights gathered through participation alongside the Pharmacy Service Enhancement Project (PSEP) as part of a field experience. The analysis focused on recurring themes related to professional identity, clinical labor, and institutional constraints. This methodology allowed for an in-depth examination of how pharmacists' clinical roles are experienced, perceived, and communicated in practice. Findings indicate that community pharmacists are among the most accessible healthcare providers and play a significant role in delivering clinical services beyond dispensing medications. These services include medication therapy management, immunizations, chronic disease management, tobacco cessation counseling, opioid education and naloxone distribution, and point-of-care testing. Despite these contributions, clinical work often remains underrecognized due to systemic barriers and limited public awareness. The results highlight ongoing challenges in shifting perceptions of pharmacy practice while emphasizing the critical role of pharmacists in improving access to care and supporting public health. Increasing visibility and understanding of pharmacists' clinical services may enhance patient engagement and utilization of these services. Addressing the "pill packer" myth is essential for strengthening pharmacists' identity as integral members of the healthcare system and for advancing the future of patient-centered care.

Surfaces and Skew Lines

NATHAN RATEAU

Mathematics and Statistics
Project Mentors: Timothy Ryan, Ph.D.
Janet Page, Ph.D.

A continuing area of interest in mathematical research is the number of lines contained in a surface. The surfaces we study will have a degree, defined by the maximum number of times it can intersect with a line. Generally speaking, the higher the degree, the curvier the surface is. We know that on surfaces without corners or sharp edges (of degree at least 3), there are a finite number of lines on the surface. As we increase the degree of our surfaces, these surfaces have more lines. Our project focuses on specific sets of lines, known as skew lines, which are lines that don't intersect. Since the total number of lines is finite, we have a finite number of skew lines on these surfaces. We seek to apply and modify computational algorithms such as the Bron-Kerbosch Algorithm to categorize our skew sets and count the sizes of skew sets of lines for our given surface. In our project, we hope to use these algorithms to see if there is a relationship between the degree of the polynomial of our given surface and the size of our skew sets. Our algorithm has broader applications in graph theory and coding theory, and our modification will not only help with finding our skew sets of lines but will also have these broader applications.

Effects of One Carbon Metabolite Supplementation on Placental Vascular Development at Mid-Gestation (Day 161 and Day 260) in Nutrient-Restricted Beef Heifers

OLIVIA ROSENTHAL

Animal Science
Project Mentor: Pawel Borowicz, Ph.D.

Forage quality and maternal nutrition are critical to placental vascular development and fetal growth in beef heifers. Placental vascularity supports the transfer of essential nutrients; amino acids, glucose, fructose, and growth factors. Nutrient restriction during gestation can impair placental function, resulting in reduced fetal growth, lower birth weights, and negative impacts on maternal condition, milk production, and immune function. This study evaluated the effects of one-carbon metabolite (OCM) supplementation, including methionine, folate, choline, and vitamin B12, on placental vascularity. Previous findings at Day (d) 63 of gestation demonstrated reduced placental vascularity under nutrient restriction; it was unclear whether these effects persisted later in gestation. Therefore, this study focused on mid-gestation (Day 161). Thirty-two Angus-crossbred heifers were estrous synchronized and bred to a single sire using female-sexed semen. A 2×2 factorial design was implemented with two levels of gain: control (CON; 0.6 kg/d ADG) and restricted (RES; −0.23 kg/d ADG), two supplementation groups: with OCM (+OCM) or without (−OCM). Placentas were collected, and vascularity was assessed using CD34 and CD31 fluorescent staining. Capillary area density (CAD) and capillary number density (CND) were quantified in the fetal cotyledon (COT) and maternal caruncle (CAR). Data were analyzed using the GLM procedure in SAS, with significance set at $P \leq 0.05$. At d 161, CAD did not differ between COT and CAR (7.96±0.65 vs. 7.35±0.65; P=0.36), and CND was also similar between regions (0.23± .02 vs. 0.27±0.02; P=0.28), indicating balanced vascular development at mid-gestation. By d 260, both CAD and CND were greater in COT compared with CAR ($P < 0.0001$), demonstrating increased fetal vascularization in late gestation. These results indicate that maternal gain and OCM supplementation influence placental vascularization, with important implications for placental function and fetal development.

Supported by the Agriculture, Food, and Resource Initiative [no. 2018-07055- 2009] the USDA National Institute of Food and Agriculture. NDSU Explore Program.

Other Contributors: Chutikun Kanjanaruch, Lawrence Reynolds, Joel Caton

Engineering isogenic rhizobial strains that exhibit varied levels of nitrogen fixation in legumes

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Microbiology; CHANGE Research and Mentoring for Post-Baccalaureates
Project Mentor: Barney Geddes, Ph.D.

Legumes such as peas, beans, and alfalfa form a symbiosis with bacteria called rhizobia, which are housed in nodules on roots. Rhizobia convert atmospheric N_2 into biologically available forms of nitrogen (NH_3 or NH_4+) through the process of nitrogen fixation in exchange for carbon from the plant. We are interested in looking at the response of plant phenotype to varied levels of nitrogen fixation in isogenic rhizobial strains (strains with identical genomes). These strains were engineered by replacing the native ribosomal binding site of either *nifH* or *dctA* with four bicistronic designs of synthetic ribosomal binding sites in the rhizobium species *Sinorhizobium meliloti*. The two target genes were chosen for their strong association with the nitrogen fixation process. The gene nifH encodes for the nitrogenase reductase protein which converts N_2 into NH_3, and *dctA* encodes for the dicarboxylate transportase which transports carbon molecules across the rhizobia bacteroid membrane – where the carbon is used for nitrogen fixation. When these *S. meliloti* strains are inoculated into our model legume, *Medicago truncatula*, we expect to see contrasting plant phenotypes between the *nifH* and *dctA* rhizobial strains, particularly the size and number of nodules. This expectation is based on knowledge that there are diverse inefficient strains in nature, but each strain behaves differently based on how they intake carbon or fix nitrogen. With decreasing nitrogen fixation, plant biomass is predicted to decrease across both the *nifH* and *dctA* strains. These results will improve understanding of how responses differ between the *nifH* and *dctA* genes. Future research will be able to investigate if lower quality rhizobia undergo sanctioning where nodules receive fewer resources from the plant host through co-inoculation of these isogenic strains.

Effect of a GLP-1 receptor agonist on food intake and mass gain in red-winged blackbirds in a migratory and non-migratory state

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Project Mentors: Timothy Greives, Ph.D.
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Preparation for migration requires deposition of large fat stores, which serve as the primary energy source during migratory flight. The mechanisms that enable birds to alter energy balance and accumulate fat stores, however, are still not fully understood. Galanin-like peptide-1 (GLP-1) in mammals decreases food intake and induces weight loss. However, the half-life of GLP-1 is short, so semaglutide, a long-lasting GLP-1 receptor agonist, is more suitable for experimental assessment of GLP-1 signaling on energy balance and fat accumulation during migratory preparation. We asked if semaglutide would decrease food intake and body mass in birds that were photoperiodically-induced into a migratory state and compared these effects with birds in a non-migratory overwintering state. We induced the pre-migratory state by decreasing daylength incrementally from 12L:12D to 8L:16D, then held birds at 8L:16D daylength for the remainder of the migratory trial. For the overwintering trial, daylength continued at 8L:16D. Birds were randomly assigned to three treatment groups and injected into the pectoral muscle with either a control (PBS, n=6), low dose (0.04 mg/kg, n= 7), or high dose (0.2 mg/kg, n= 6). Food intake and body mass were measured regularly. We found body mass of migratory-induced birds were not affected by semaglutide treatment. However, birds receiving the low dose during the overwintering state lost greater body mass than control or high dose birds, suggesting a dose-dependent physiological response. Interestingly, we did not observe effects of treatment on food intake in either trial. This may possibly be due to measurement error or the inability to collect all uneaten food. Together, these findings suggest that photoperiod-induced pre-migratory preparation supersedes the effects of semaglutide, preserving fat accumulation to fuel migration. Future work should confirm these findings and address the mechanisms that prevent semaglutide effects during migratory preparation.

Evaluating the Role of Toxin–Antitoxin Systems in Plasmid Stability of NGR234 Rhizobia Using Serial Subculturing

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Biotechnology
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Ahmad Al-Amad

Rhizobia are soil-dwelling bacteria that form symbiotic relationships with legumes, they convert atmospheric nitrogen into forms that assist with plant growth. Rhizobia NGR234 is notable for its broad range of available host plants and is promoted by symbiotic genes located on the large plasmid pNGR234a. This project investigates whether toxin–antitoxin gene pairs on the plasmid contribute to the stable inheritance of pNGR234a.

To test this hypothesis, a minimized version of pNGR234a will be constructed containing four toxin-antitoxin gene pairs and a red fluorescent tracker will be added to track plasmid retention. Bacterial cultures will serially subcultured in the absence of antibiotics. Plasmid stability will be assessed by measuring the proportion of fluorescent cells after multiple generations. To investigate which toxin-antitoxin pair is essential for plasmid stability knockouts will be performed to test the ability of the rhizobia to survive without the toxin-antitoxin pair.

Expected results indicate that the post gene knockout plasmid does remain stable across several generations without selection. This suggests that some plasmid genes and toxin-antitoxin systems do not contribute to plasmid maintenance as much as others. Ongoing analyses of individual toxin-antitoxin knockouts will help identify which genes are essential for stability.

These findings have important implications for microbiology as well as agriculture. Understanding the mechanisms of plasmid stability can help uncover new ideas about rhizobia and plasmids. Additionally, the development of a stable and minimized plasmid can serve as a valuable tool for engineering "designer rhizobia" with agricultural benefits.

Telomere length increases with latitude in adult House Sparrows (*Passer domesticus*)

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As environmental conditions continue to change, judging the resiliency and stress responses of wildlife is becoming increasingly important. Changing conditions are likely to have variable effects along a latitudinal gradient, and it is unknown how individual populations of widespread species will respond. One metric of measurement is through telomere length. Telomeres are the non-coding tails at the ends of chromosomes that serve to protect the coding regions of DNA from damage and prevent genomic instability during cellular division. Telomeres shorten naturally with age, and recent evidence suggests the rate of telomere erosion can be increased by high levels of oxidative stress induced by poor environmental conditions, such as increased temperatures or less precipitation. The accumulation of critically short telomeres often leads to genomic degradation and cell death, causing telomere length to be associated with longevity. Acquiring and analyzing telomere samples is relatively simple, inexpensive, and achievable across a variety of taxa, elevating telomere length into a valuable metric for judging responses to changing conditions. In this study, we measured the telomere lengths from populations of free-living adult House Sparrows (*Passer domesticus*). The distribution of House Sparrows spans across North America, making them a useful system for studying environmental effects at different latitudes. Samples were collected from twenty sites along a latitudinal gradient across the United States. Our study provides evidence of populations at higher latitudes having longer telomeres than populations at lower latitudes. The reason for this discrepancy is still unknown but may be related to resource abundance or quality. The results of this study indicate southern populations may be more vulnerable to changing environmental conditions. Early identification of at-risk populations will benefit future conservation efforts.

Modeling long-term drivers of wetland bird community assembly at a prairie pothole wetland complex

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Prairie potholes are depressional wetlands with highly variable surface water area, permanence, and vegetative structure, allowing them to act as critical breeding habitat for waterfowl and migratory birds of conservation concern. Understanding drivers of community assembly within these wetland habitats is crucial for effective land management, species conservation, and preservation of ecosystem services. While changes in environmental conditions have been documented over time, we lack information about linking such changes to shifts in wetland bird community composition. Therefore, we employed joint species distribution modeling with long-term data to estimate wetland-obligate bird species responses to environmental factors and interspecies interactions at the Cottonwood Lake wetland complex in North Dakota. The model suggests that breeding bird communities at these prairie potholes have changed over time, with wetland area being a strong predictor of species distributions, followed by vegetation heterogeneity. Additionally, we found evidence that waterfowl diversity and abundance was positively associated with macroinvertebrate biomass. Surface water dynamics in prairie pothole wetlands have been altered by land use changes over time, affecting wetland size and heterogeneity, which the model suggests are key determinants of species composition. This hierarchical modeling of species communities can be utilized to predict wetland bird community responses broadly across the region, which serve to inform future management strategies.

Eliminating Manual Assessment: An Automated Framework for ML Model Validation

GEORGINA SIEH
Computer Science
Project Mentor: Ahmed Rabia, Ph.D.

Evaluating machine learning student submissions presents significant challenges for educators. Professors and teaching assistants currently spend days manually processing diverse file formats such as MarkDown, Python, CSV, JSON, masks, and various file outputs. These outputs consume substantial cloud storage, computational resources, and physical energy. This manual workflow creates bottlenecks: large files slow local machines; metric calculations are error-prone, and tracking individual student progress becomes cumbersome. The process is extremely inefficient and compromises grading reliability and timeliness, in all courses but especially in courses with high enrollment. To address this gap, we developed a web application that streamlines the evaluation process with Google Workspace tools. Students submit predictions via a Google Form embedded in their customized Google Site, which accepts CSV or JSON files. Upon submission, a Google Colab notebook that utilizes Python libraries including Pandas and NumPy to automatically process files, compute evaluation metrics (F1 score, IoU, bounding box accuracy, segmentation metrics, and object counts), and compare predictions against previously linked ground truth data. Results are then sent to a dedicated Google Sheets tab for each student, which automatically generates charts that visualize their evaluations. These charts are embedded on each student's personalized site, where they can access their results. Instructors have direct access to all submissions through a centralized dashboard. To achieve these results, we tested our developed application at NDSU's 2026 AgTech Hackathon, where participants were evaluated with our web application. This architecture eliminates local computational burden and cloud storage overhead. Our system reduced evaluation time from hours per student to minutes for an entire class, maintaining accuracy while removing manual calculation errors. Although this system was developed for computer vision and segmentation tasks, we are expanding the platform to support its use in other specialized fields. We also propose standardizing our submission format, since there is currently no standardized form among Machine Learning educators. This work provided an accessible solution that automates ML evaluations, minimizes physical strain on educators, and ensures consistent, transparent feedback for students within minutes.

Night Sky Cooling - Data Center Application

ETHAN SKOTT
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Project Mentor: Adam Gladen, Ph.D.

As the demand for computational power and AI increases, data centers are becoming increasingly prevalent in today's age. These centers, however, have high cooling demands and have large amounts of excess waste heat that need to be dissipated. This study examines the concept of night sky cooling for this specific purpose. Night sky cooling, also known as radiative sky cooling, enables certain wavelengths (8 –13 μm) of infrared radiation to pass through the atmosphere. By passing through the atmosphere, space is essentially being used as a cold sink of extremely low temperatures (roughly 3 K or −273 °C), resulting in improved cooling due to the large temperature change.

This work models how a night sky radiator would behave, based on what is typical for a data center. The model is based on an energy balance equation and the heat transfer resistance network of a radiator system and was modeled using MATLAB. The Berdahl & Martin approach was used for estimating the atmospheric emissivity, which has a significant impact on the effectiveness of the radiative system. An experiment was conducted as well, measuring the inlet and outlet temperatures of two different panels, to gauge the amount of heat dissipated, validating the model against the experimental results. A brief conclusion and assessment of the energy and cost benefits that this application can provide to data centers is also discussed.

Development of a positive reinforcement training regimen for minimally invasive sample collection from gilts used for agricultural and biomedical application

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Animal Science
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The aim of this pilot study is to utilize a three-part positive reinforcement training (PRT) regimen to train adult swine to voluntarily participate in minimally invasive sample collection, thereby improving the feasibility and accuracy of repeated physiological assessments by avoiding stressful restraint techniques such as snaring. Six mature gilts (adult female swine that have not yet given birth), housed with their conspecifics, were selected to undergo the PRT regimen, consisting of three phases: (1) habituation, (2) target training, and (3) mock sampling. Each phase is expected to require approximately two to three daily sessions lasting 8-15 minutes each. During phase one, gilts are accustomed to the training stall and personnel, and the association between the primary reinforcer (frozen pumpkin purée treats) and the bridge (vocal cue "Yay!") is established by feeding and immediately using the vocal cue. During phase two, a target (spatula) is presented in front of the gilt's nose; after successful contact, a treat and vocal cue are immediately presented to enforce the behavior. During phase three, gilts will continue the target training as a second trainer begins to mimic sample collection with gentle restraint and touch. The training regimen is completed when the gilt can reliably remain stationary and engaged in successful target training during mock sampling. At this point, blood collection from the ear vein using topical anesthetic and PRT methods occurs on days +0, +2, +4, +6, +8, and +10 days post-completion, with brief (2-3 minute) daily target training on non-collection days. Behavioral data and latency times were collected throughout the PRT period in order to determine training success and will be presented.

Other Contributors: Jennifer Young, Ph.D.; Rachel Layton, CSIRO, Australian Center for Disease Preparedness

Examining Study Strategies for Introductory STEM Courses

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Students in STEM majors at undergraduate programs are often enrolled in multiple introductory STEM courses across different disciplines early on in their academic career. Assessment structures can differ across these courses based on disciplinary norms and values, however, students may use study strategies based on their prior successful experiences in high school or previous courses, rather than adapting to different course contexts or disciplines. To determine if students use study strategies that vary across introductory STEM courses, we examined how students' study in Intro Biology 1, Intro Human Anatomy & Physiology 1, Intro Chemistry 1, and Intro Physics 1 courses. We surveyed students in these courses in the FA25 semester asking them about the strategies they used when studying for exams. We compare frequencies of reported strategies and how those strategy distributions compare across different STEM courses. We report on distinctions in study strategies between disciplines and speculate on potential reasons for these differences. We encourage instructors to introduce and re-emphasize what study strategies are effective for classes in their discipline and for the focus of a given exam.

Making and using a GFP-tagged anti-ALFA-tag nanobody to study RAGE endocytosis

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Estelle Leclerc, Ph.D.

Objectives: The receptor for advanced glycation end products (RAGE) is actively studied as a drug target in neurodegenerative diseases, cancer and diabetes related complications. Besides developing RAGE antagonists, our laboratory is also interested in using RAGE for the targeted delivery of cytotoxic drugs utilizing antibody drug conjugates (ADCs). To further explore this approach, we studied the internalization of anti-RAGE antibodies and RAGE itself. The goal was to define RAGE internalization kinetics and to identify anti-RAGE antibodies as promising ADCs for cancer therapy.

Approach: We engineered and expressed in HEK293 cell the RAGE receptor tagged at its N-terminus with a short (15 residues) ALFA tag. We recombinantly expressed and purified an anti-ALFA tag nanobody fused to a fluorescent protein (sf2GFP). The hypothesis was that the anti-ALFA nanobody will bind to the ALFA tag of the engineered RAGE receptor and that the localization can be visualized using fluorescence microscopy. Further, because the sf2GFP-nanobody construct is unable to diffuse into HEK293 cells, we can use the appearance for GFP fluorescence inside the cell over time to monitor endocytotic internalization of the GFP protein and thus indirectly the RAGE receptor.

Results: The ALFA-tagged RAGE receptor was successfully expressed using transient transfection inHEK293 cells. The sf2GFP-anti-ALFA-tag nanobody was expressed in *E.coli* and purified. Incubation of the purified sf2GFP-anti-ALFA-tag nanobody with HEK293 cells transiently transfect with ALFA-tagged RAGE was performed and analyzed by confocal fluorescence imaging. Time course experiments to characterize endocytosis kinetics under a variety of conditions were performed in 96 well plate format. Results of these experiments are compared to a complementary approach measuring anti-RAGE antibody uptake by HEK293-RAGE expressing cells. Data from both experiments are used to screen a small library anti-RAGE antibodies to identify possible candidates for RAGE targeting antibody-drug conjugate development.

Role of Templates in Asymmetric Catalysis

STELLA STRONG
Chemistry
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Rebecca Huss

The formation of carbon-carbon bonds remains a crucial area of organic chemistry. When forming these bonds, chiral centers are established. The different stereochemistry may result in vastly different chemical properties, making it attractive for pharmaceutical research and natural product synthesis. To help control the selectivity of these compounds, this research tested five different achiral templates: 3,5-dimethylpyrazole, oxazolidinone, thiazole, *N*-methyl imidazole, and benzyloxy imidazole. These templates allow for bidentate coordination between the substrate and the catalyst, which facilitates the addition of the nucleophile. Results from the addition of carbon nucleophiles, Friedel Crafts alkylation reactions, will be presented.

Examining the role of Replication Factor A3 (Rfa3) modification in regulating the cell cycle in response to irreparable DNA damage of the genome

MIRIAM SULLIVAN
Biochemistry and Molecular Biology
Project Mentor: Stuart Haring, Ph.D.

Replication Factor A (RFA) is an essential complex in all eukaryotic cells from yeast to human. Composed of three subunits, RFA plays critical roles in DNA replication, repair/recombination, and cell cycle regulation. Multiple labs, including our own, have made the determination that modification of lysine residues within the Rfa1 and Rfa2 subunits of the RFA complex play complementary roles in activating and maintaining a cell cycle checkpoint in response to DNA damage. It is strongly indicated that the modification(s) responsible for checkpoint function is the attachment of a SUMO group at particular lysines within these two subunits. Our lab has previously mutated all lysine residues within Rfa1 (39 total lysines) and Rfa2 (15 total lysines), and we have shown that lysineless Rfa1 is defective in checkpoint activation while lysineless Rfa2 is defective in checkpoint maintenance. RFA is a three subunit complex, and as such, it is currently unknown if lysine residues on the Rfa3 (smallest) subunit are (1) post-translationally modified, and if so, (2) which one(s) is important.

To address this problem, I am using CRISPR-Cas9 gene editing to generate and express one of two different forms of Rfa3 in cells. One form is the replacement of the chromosomal copy of the gene with an Rfa3 lysineless (all 7 lysines mutated to arginines) form. The other form to be examined will be an Rfa3 form where only one lysine is mutated to an arginine at amino acid position 46. This particular residue has been indicated to be sumoylated in a large-scale screen; however, its role in the response to irreparable DNA damage has not yet been investigated. I generated CRISPR-Cas9 constructs to make the Rfa3 mutations in cells using Golden Gate Assembly cloning. Once verified, these constructs were introduced into yeast cells to generate the appropriate Rfa3 gene edit. These Rfa3 mutant yeast cells will subsequently be assayed for checkpoint activation and maintenance and will provide the first evidence for whether Rfa3 modification contributes to the prevention of DNA mutations, which are the leading cause of cellular disease.

Using Thresher Teeth to Explore Bonanza Farming in North Dakota

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The 4e Farmstead Historical Archaeology project examines the transition from Bonanza Farms to tenant farms. Bonanza Farms (approximately 1870s-1890s) were tens of thousands of acres large but were eventually divided into a tenant farming system that is still in practice today. Cultivation of these large farms was only possible because of innovations in technology. Artifacts recovered from the 2024 and 2025 field seasons include thresher teeth and other machinery related items. An in-depth examination of this equipment demonstrates the investment required for setting up these large farms. Moreover, advertisements demonstrate the economic networks and role the Bonanza Farms had in recruiting white settlers to the region. Early farming in North Dakota was at the forefront of agricultural technology innovation as well as proving the viability of settlement in this rather harsh environment.

Acoustic Monitoring of Overwinter Activity and Spring Emergence of Bats in the North Dakota Badlands

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Project Mentor: Mandy Guinn, Ph.D., United Tribes Technical College, Department of Environmental Science

While bat species richness is greatest in tropical regions, many insectivorous bats live at higher latitudes with harsh winter conditions. At greater latitudes, prolonged exposure to colder temperatures and reduced insect availability increases energy costs and limits survival during winter. To survive, bats may adopt one of two strategies: migrate to warmer areas with greater abundance in food or hibernate by reducing their metabolic rate and utilizing fat reserves built up during the weeks prior. In 2010-2013, a study conducted by Barnhart & Gillam (2017) monitored winter bat activity in Theodore Roosevelt National Park (TRNP) using passive acoustic monitoring, challenging the hypothesis that bats migrate out of the state during winter months. However, since 2019, *Pseudogymnoascus destructans*, the fungal pathogen responsible for White-Nose Syndrome (WNS), has affected bat populations across the state. Effective management requires a detailed understanding of bat presence and activity across seasons. The purpose of this project is to serve as a follow-up to the Barnhart &

Gillam study (2017), with more advanced acoustic devices to provide critical information about bat presence in North Dakota. Five Song Meter SM4BAF FS acoustic detectors were deployed at sites used in the 2017 study to record nightly bat calls in TRNP. Environmental variables (temperature, humidity, and barometric pressure) are being monitored to assess their relationship to winter activity. Acoustic data is run through Kaleidoscope Pro and manually vetted using SonoBat 30. Calls have been detected from *Corynorhinus townsendii, Eptesicus fuscus, Lasionycteris noctivagans*, and various *Myotis* species from October 2025 through February 2026. Preliminary findings suggest warmer temperatures increase the likelihood of winter activity, while wind generally decreases the likelihood of activity. Activity also cannot be generalized across taxa, as species exhibit distinct responses to temperature and wind. Findings from this study may aid in controlling the spread of WNS and conserving threatened or endangered bat populations by providing information on migration patterns and hibernation sites.

This project is funded by the National Science Foundation (award # 216605).

Blood Sample Handling Effects on Serum Separation and Gel Formation

EVA TASTAD
Animal Science
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Blood sampling is a routine procedure in beef cattle research and veterinary diagnostics. Factors such as temperature and time before centrifugation can influence the separation of blood components and the quality of serum obtained for analysis. We conducted two experiments to evaluate the influence of blood sample handling methods on serum separation and gel formation. In Exp. 1, two blood samples were collected from ten yearling beef bulls: sample 1 was directly placed on ice (ICE) and sample 2 was held at room temperature for 30 minutes (ROOM), followed by placement directly onto ice. In Exp. 2, two blood samples were obtained from 13 bulls. All samples were held at room temperature for 30 minutes, then sample 1 was placed directly onto ice (DIRECT), whereas sample 2 was placed in a rack in the cooler (INDIRECT). After centrifugation (1500 x g at 4 °C for 20 minutes), measurements recorded included: height of total sample, red blood cell (RBC), and serum fractions, as well as amount of gel formation in serum (scale of 0 to 1, with 0 being fully liquid and 1 being fully gelatinized). In Exp. 1, samples with gel formation had the gel portion disrupted with a wooden stick and were subjected to re-centrifugation. Data were analyzed using the GLM procedure of SAS with treatment as fixed effect. In Exp. 1, ICE samples had greater ($P = 0.003$) gel formation compared with ROOM samples (1.00 vs. 0.55 ± 0.094). After gel breakroom, though both treatments improved, ICE still had more ($P = 0.003$) gel formation than ROOM samples (0.78 vs. 0.33 ± 0.093). In Exp. 2, gel formation was less frequent overall. There was no difference ($P = 0.68$) in gel formation between DIRECT and INDIRECT samples (0.34 vs. 0.27 ± 0.118). In both experiments, there were no differences ($P \geq 0.13$) in total, serum, and RBC heights. Based on our findings, blood collection vials should remain at room temperature for 30 minutes to aid clotting at which point they can either be placed on a rack or directly into ice in the cooler.

VEXAS Syndrome: A Recently Discovered Disorder Characterized by Multisystem Inflammation

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VEXAS syndrome (Vacuoles, E1 enzyme, X-linked, Autoinflammatory, Somatic) is a recently identified adult-onset autoinflammatory disorder caused by somatic mutations in the UBA1 gene within hematopoietic stem cells. This disease is marked by systemic inflammation, hematologic abnormalities, and refractory treatments. This often leads to diagnoses that are delayed due to its overlap with more prevalent rheumatologic and dermatologic disorders. Highlighting awareness is critical especially in older males who present with multisystem inflammation.

We present the case of a Caucasian male in his seventies with a history of macrocytic anemia, recurrently severe dermatologic inflammation, inflammatory arthritis, and the unintentional weight loss of around 40 pounds over several years. Despite being treated with multiple disease-modifying antirheumatic drugs (DMARDs) and biologic agents, his skin and joint manifestations remained refractory. Upon physical examination, persistent synovitis of multiple peripheral joints and recurrent erythematous, indurated plaques with violaceous borders on the trunk and extremities were noted. Laboratory evaluation also demonstrated macrocytic anemia, thrombocytopenia, and elevated inflammatory markers. Autoimmune serologies were unremarkable. Bone marrow biopsy findings were also consistent with myelodysplastic syndrome with multilineage dysplasia without increased blasts. Given persistent inflammation as well as hematologic abnormalities, genetic testing was pursued and confirmed a pathogenic UBA1 mutation was detected consistent with VEXAS syndrome.

This case highlights the challenges associated with the diagnostics of VEXAS syndrome and brings to light the importance of considering this condition in older male patients with refractory inflammatory disease as well as macrocytic anemia. Early recognition, including the application of tools such as the SWIM score (Skin involvement, Weight loss, Inflammation, Macrocytic anemia) may facilitate more timely genetic testing as well as multidisciplinary management. By having greater clinical awareness, it may reduce misdiagnosis as well as prevent prolonged ineffective therapies and improve patient outcomes.

Variation in Sunflower Bud Morphology: Potential Predictor of Damage by Insect Pests

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In cultivated sunflower, early reproductive morphology varies among lines and may influence susceptibility to insect damage. Sunflower lines whose involucral bracts do not cover the immature disc florets ('open bud' type) 2–3 weeks before flowering allow insect pests easy

access to reproductive disc florets. Insect injury to florets from open buds potentially reduces yield at the individual head level.
We evaluated bud morphology across 180 lines of public inbred sunflower lines using replicated plants under controlled (greenhouse) conditions. Developing buds were photographed twice weekly after entering the reproductive stage and were scored using both qualitative (open or closed) and quantitative (% open) measures. The results were compared to a prior attempt to evaluate this trait in field-grown plants. Scores from the greenhouse trial were also used to test whether quantitative trait loci (QTL) mapping could map one or more locations controlling the open bud trait.

Preliminary results indicate that the open bud type is common and heritable. However, infrequent observations (1–2 dates per line) as used in prior field research can result in false negatives (incorrectly scoring an open line as closed). If QTL associated with open buds can be validated, selection for closed buds in breeding programs would be simplified, and sunflower yields protected without a need for insecticide applications prior to bloom.

2026 Childcare Regulations Index

SAMUEL TIPKA
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Project Mentor: Ricky Feir, Ph.D.

Childcare availability and quality remain significant policy challenges in the United States, with regulations playing a key role in shaping both access and standards of care. This study evaluates childcare regulations across all U.S. states by constructing a regulatory index based on 17 variables. Each variable was standardized on a scale from 0 to 10, and the average of these values was used to calculate an overall regulatory index for each state.

With each state terminology varying from state to state, we defined a teacher as the position requiring the lowest level of education for an individual to assume sole responsibility for a group of children. We used a coding scheme to find each state's respected variable ranging from 1 (less than high school diploma or equivalent) to 8 (bachelor's degree in ECE or related field). With our coding scheme, we were able to calculate the value for each state's minimum education requirement and then used our formula to calculate the coefficient variable. To visualize these results, our research mapped the respected coefficients across states. These visualizations highlight key metrics including child-to-staff ratios, maximum group size limits, training hour requirements, and education standards for childcare providers. Our analysis finds that states in the Northeast region in the United States tend to have lower index scores, indicating more stringent childcare regulations compared to other regions.

The findings suggest that policymakers may improve childcare availability and affordability by relaxing regulations related to child-to-staff ratios and maximum group sizes while strengthening requirements for provider training and educational qualifications. Such policy adjustments could help address ongoing challenges in childcare supply, quality, and cost, while potentially supporting increased workforce participation and broader economic growth.

Cubital Tunnel Syndrome and the Potential Benefits of Vibration Therapy

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Cubital tunnel syndrome is the second most common peripheral nerve entrapment in the upper extremity and occurs when the ulnar nerve is compressed at the elbow, often due to prolonged flexion or repetitive mechanical stress. This compression can reduce blood flow to the nerve and lead to numbness, tingling in the ring and little fingers, weakness, and in severe cases muscle atrophy. Treatment options include both conservative approaches, such as splinting and nerve gliding exercises, and surgical treatment for more advanced cases; however, conservative treatments may have limitations related to comfort, cost, and patient compliance. This study investigates the feasibility of a wearable vibration device designed to provide mechanical stimulation to the flexor-pronator muscle group near the cubital tunnel. Planned preliminary testing will involve testing several types of flexible piezo polymers that will be activated using low voltages, not more than 9 volts.

Exploring Waterlogging Tolerance in Common Bean (*Phaseolus vulgaris L.*) to Enhance Climate Resilience

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Increasing precipitation variability associated with climate change is intensifying flooding events that threaten crop production worldwide. Common bean (*Phaseolus vulgaris L.*), the most important grain legume for human consumption worldwide, is particularly susceptible to excess soil moisture, especially during early growth stages. In 2024 alone, excess rainfall and flooding resulted in an estimated $6.7 billion in agricultural losses across the United States, with $1.6 billion of losses in North Dakota and Minnesota. Despite the agronomic importance of this challenge, most breeding efforts are focused on drought tolerance, and the physiological and genetic mechanisms underlying waterlogging tolerance in common beans remain poorly understood. In this study, we are investigating variation in waterlogging tolerance among breeding lines from North Dakota State University's dry bean breeding program. A panel of 324 genotypes is being evaluated under controlled greenhouse conditions using flooded and non-flooded treatments arranged in a randomized incomplete block design with three replications per treatment. Flooding is imposed at the V1 seedling stage to simulate conditions commonly experienced in northern dry bean-producing regions. Plants are evaluated for chlorophyll content (SPAD); survival and adventitious root development; and for root, shoot, and total biomass after drying for 2 weeks. Trait responses are analyzed using analysis of variance and linear mixed models to quantify tolerance and identify resilient genotypes that maintain growth and physiological function under hypoxic stress. A genome-wide association study will also be conducted to identify genomic regions associated with waterlogging tolerance. Together, these results will support breeding efforts to improve dry bean performance and yield stability under increasingly variable precipitation conditions.

Other Contributors: Nusrat Khan, José Figueroa Cerna, Carly George and Maria de Oliveira

Using auditory priming to increase risk perception of blackbirds to approaching drones

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Blackbird predation of sunflower seeds results in millions of dollars in damages annually in North Dakota. To mitigate damage by blackbird flocks in agricultural fields, many producers and researchers have turned to using drones as pest management tools. Evaluating what added or modified features make drones appear riskier to blackbirds is paramount to increasing the effectiveness of this method in future use. Here, we tested the impacts of auditory priming with threatening bird calls on the subsequent risk perception towards an approaching drone by mixed-species blackbird flocks in sunflower fields across North Dakota. We assessed risk perception to a priming broadcast by observing behavioral changes to restlessness (i.e. liftoffs) and to subsequent drone approaches by measuring flight initiation distance (FID). A greater FID indicates a greater perceived risk. We analyzed effects of priming and approach broadcasts, along with flock size and environmental factors (e.g. ambient light, temperature, or day of year) using linear mixed-effect models to understand which factors influence blackbird risk perception of drones. We found that flocks primed with Red-winged Blackbird alarm calls – which normally alert others when an aerial predator is detected – flushed significantly sooner when approached with a drone compared to control approaches with no auditory priming. Our results suggest that exploiting innate antipredator behavior of blackbirds can increase the effectiveness of drones in pest management strategies.

Mining Beta Testing Posts from GitHub to Understand Practices and Challenges.

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Beta testing is an important pre-release activity that allows software to be evaluated by selected users under realistic conditions before official release. Despite its practical importance, beta testing has received limited research attention compared with other software testing activities. In this study, we investigate how beta testing is discussed in developer communities by analyzing beta testing-related posts from Stack Overflow. Our goal is to explore the types of questions developers raise, the contexts in which beta testing is performed, and the challenges reflected in these discussions. By examining practitioner conversations, we aim to identify recurring themes that can improve understanding of beta testing practices and inform future research on tool support and guidance for pre-release testing.

Behavioral Response of the Fall Field Cricket (*Gryllus pennsylvanicus*) to Predator and Non-predator Acoustic Stimuli

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The ability of prey to eavesdrop on acoustic signals produced by predators allows for the preemptive employment of antipredator behaviors, reducing the risk of detection and capture, and increasing the chance of survival. Multiple vertebrate prey species have been shown to respond to the vocalizations of their predators with antipredator behaviors including increased vigilance, freezing, and fleeing. Little is known, however, about the ability of invertebrates to eavesdrop on vertebrate predator vocalizations. Here we show that cricket behavioral responses differ when exposed to predator and non-predator acoustic stimuli compared to a control treatment. We measured latency to emerge, overall activity, and shelter visits in 30 wild-caught fall field crickets (*Gryllus pennsylvanicus*) following the introduction of acoustic stimuli. Acoustic stimuli included both ultrasonic and avian predator vocalizations representing varying levels of predation risk, an avian non-predator vocalization, white noise, and control treatment. In accordance with previous studies, we predicted that crickets would have reduced overall distance travelled, spend less time moving, spend more time in shelter, and take less time to stop moving following exposure to acoustic stimuli representing greater risk levels. Contrary to our predictions, our results showed that crickets spent significantly less time moving and more time in shelter when exposed to the control treatment compared to other stimuli. Additionally, crickets were quicker to stop moving following exposure to the control treatment than to a predator treatment. We did not, however, find clear differences in responses between other treatments. In conclusion, fall field crickets did not respond to predator vocalizations as predicted. Our results also suggest that crickets may not differentiate between the vocalizations of predators and non-predators and other abrupt sounds. These results indicate that eavesdropping may not be a viable method of assessing predation risk for this species. Future research should further explore the ability of the fall field cricket to eavesdrop on predators using acoustic, visual, chemical, and vibrational stimuli.

Comparing stress, anxiety, and depression as predictors of Insomnia

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Psychology
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Introduction: Our objective is to better understand factors that influence insomnia in college students, particularly those related to mental health. Students frequently experience high stress alongside other mental health challenges; we examined how these factors relate to insomnia symptoms. This study compares perceived stress as well as depression and anxiety symptomology to determine which better predicts sleep difficulties. We evaluated these variables together to identify the strongest predictors of insomnia and help inform better support and resources for students.

Methods: Participants consisted of undergraduate students (n = 203) who provided self-reported related measures using the Perceived Stress Scale (PSS), Center for Epidemiological Study Depression scale (CES-D), PROMIS Anxiety-Short Form, Insomnia Severity Index (ISI). These scores were compiled, cleaned, and prepared for quantitative analysis. To evaluate the predictive relationships among variables, predictors were entered into independent regression models followed by an additive regression model, allowing examination of how psychological and sleep indices contributed to the outcomes of interest. This analytical approach supported estimation of effect sizes and identification of significant predictors within understanding of insomnia.

Results: We found that depression was the strongest predictor of insomnia ($\beta=0.62$, $p<.0001$) followed by anxiety ($\beta=0.54$, $p<.0001$) and then stress ($\beta=0.28$, $p<.0001$). However, once entered into an additive model, stress was no longer a significant predictor ($\beta=-0.08$, $p=0.40$). Depression ($\beta=0.50$, $p<.0001$) remained the stronger predictor of insomnia symptoms over anxiety ($\beta=0.19$, $p=0.04$). These results teach us that mental health concerns are more important for sleep than daily stress.

Conclusion: Our study indicates that higher depressive symptoms increase the risk for insomnia symptoms. Even though the vast majority of the participants reported high levels of stress, they reported little to no issues with sleeping. High stress may not be as detrimental to sleep as was predicted. This leads us to believe that factors such as depression and anxiety can cause sleep-related issues such as insomnia. These results suggest sleep interventions should focus on mental health such as anxiety or depression to be impactful for sleep. More research could be done to differentiate different kinds of stress and its other physical repercussions apart from sleep.

Exploring resuscitation-promoting factors (Rpfs) in environmental bacteria and their potential effects on plant growth

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Resuscitation-promoting factors (Rpfs) are secreted bacterial proteins known to stimulate the growth and revival of dormant cells, but their ecological roles in environmental systems and plant-associated microbiomes are relatively unknown. The objective of this study is to research the effects of Rpfs on soil bacterial microbes and evaluate their potential to enhance growth through microbiome related mechanisms. Environmental bacterial isolates capable of producing Rpfs, specifically *Micrococcus luteus*, were cultured, and supernatants containing Rpf activity were applied to dormant/low activity soil microbial communities. Changes in microbial abundance and diversity were assessed using dilution series and 16S rRNA sequencing to determine whether Rpf exposure increases the resuscitation of previously unculturable or dormant taxa. Also, plant growth assays were performed using model plant species grown in treated and untreated soils to evaluate the downstream effects of microbial activation. Key growth metrics like biomass accumulation and root development were measured to assess plant responses. Previous studies have suggested that Rpf-containing supernatants stimulated microbial activity and altered community composition, potentially enriching for taxa involved in nutrient cycling and plant growth promotion. These shifts were also associated with measurable improvements in plant growth parameters, indicating a possible link between microbial resuscitation and enhanced plant performance. Overall, further research is needed to identify other microbial taxa and mechanisms responsible for the observed plant growth effects, and to evaluate the scalability of Rpf-based interventions in field settings.

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gamma sigma delta

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POSTER PRESENTATIONS

Histopathological analysis of the early stages of infection of canola flowers by *Sclerotinia sclerotiorum* using confocal microscopy

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Sclerotinia sclerotiorum causes Sclerotinia stem rot (SSR) on canola (*Brassica napus*). Genetic resistance to this disease is quantitative and controlled by many genes. The development of SSR-resistant canola breeding lines provides an opportunity to study the morphological changes that occur at the microscopic level in the host and the pathogen during the initial stages of infection. Consequently, a study was conducted to characterize the initial stages of SSR development on flowers, leaves and stems of a resistant and susceptible canola breeding line using confocal microscopy. Here, we report the results of the inoculations of canola flowers. For the study, *S. sclerotiorum* ascospores were produced and harvested in the laboratory. A suspension of 3 x 105 ascospores was drop-inoculated on the petals of open canola flowers. Inoculated plants were incubated for 24 h in mist chambers at 22oC and 16 hours of white fluorescent light. This experiment was conducted twice. Each time, samples were collected at 4, 8, 12, and 24 h after inoculation and immediately immersed in 96% ethanol. After 24-48 h, the petals were briefly immersed in KOH, rinsed in PBS, and stained. Stained samples were mounted on microscope slides for observation using a confocal microscope. Six technical replications per sample were prepared. Software Imaris v. 10.0.0 was used to measure fungal biomass. The results indicate that almost 50% of ascospores germinated within 4 hours post inoculation (hpi). Penetration started 8 hpi without formation of specialized structures on flowers independently of them being from resistant or susceptible lines. Cell collapse started 12 hpi. During the first 24 hpi, fungal biomass developed at the same rate (P= 0.05) on susceptible and resistant flowers. These observations suggest genetic resistance is not expressed in flowers. The information generated by this study will help enhance our understanding of the events that transpire during the early stages of infection and would complement ongoing efforts to elucidate gene activity during that interaction.

Identifying Genetic Loci for Cercospora Leaf Spot Resistance in Sugar Beet and Wild Sea Beet Through Genome-Wide Association Mapping

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Cercospora leaf spot (CLS) is a severe foliar disease of sugar beet (*Beta vulgaris* ssp. *vulgaris* L.) caused by the pathogen *Cercospora beticola* Sacc, and it poses a major threat to global sugar beet production by reducing both root yield and sugar content. Genetic resistance is considered the most sustainable strategy for managing CLS, however, only four to five major quantitative trait loci (QTL) associated with CLS resistance have been reported in sugar beet to date, highlighting the need to explore additional genetic sources of resistance. Wild relatives such as sea beet (*Beta vulgaris* ssp. *maritima*), the progenitor of cultivated sugar beet, represent an important source of novel resistance alleles for crop improvement. Therefore, this study aims to identify genomic regions and candidate genes associated with CLS resistance in both sugar beet and sea beet. A diverse panel of sugar beet and sea beet accessions was evaluated under field conditions for CLS resistance. Based on disease severity ratings, extreme phenotypes were selected, including 96 highly resistant and 96 highly susceptible *maritima* accessions, and 145 resistant and 145 susceptible sugar beet accessions. Genotyping-by-sequencing (GBS) is ongoing to generate SNP marker data, and genome-wide association studies (GWAS) will be conducted to identify genomic regions associated with CLS resistance, which will further to identify candidate genes, and diagnostic SNPs for resistance introgression. Resistance gene identification in both cultivated sugar beet and wild sea beet will allow comparison of resistance loci to detect novel resistant QTL in sea beet, and adding novel QTL into sugar beet will provide long-lasting protection to CLS. Information from this research will not only elucidate genetic control of CLS resistance, but also is the necessary tool for introgression of CLS resistance from sea beet into sugar beet.

Understanding the Reproductive Barriers for Improved Hybrid Breeding in Sugar Beet (*Beta vulgaris* ssp. *vulgaris* L.)

BARKAN BOSTAN
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Advisor: Xuehui Li, Ph.D.

Sugar beet (*Beta vulgaris* ssp. *vulgaris* L.) is predominantly an outcrossing species that exhibits strict self-incompatibility, preventing fertilization by pollen from the same plant. Meanwhile, cytoplasmic male sterility (CMS) is present in sugar beet and plays an important role in hybrid variety development. Genetic mechanisms underlying cytoplasmic male sterility and fertility restoration have been extensively characterized, but the genetic basis of self-incompatibility and the relationship between CMS and self-incompatibility in sugar beet remains poorly understood. The objective of this research is to investigate the genetic basis of self-incompatibility and identify genomic regions associated with self-incompatibility and CMS in sugar beet. From a sugar beet population segregating for CMS and self-incompatibility, we evaluated 267 sugar beet plants for pollen production and the success of self-fertilization, and the results were further confirmed through a seed germination test. All plants are being genotyped using SNP markers from GBS (Genotype-by-Sequencing), and genome-wide association analyses will be conducted to identify genomic regions associated with CMS and self-incompatibility, which will then be used to determine whether the two traits are related. Understanding the genetic architecture of the two traits will advance our knowledge of sugar beet reproductive biology and contribute to the development of molecular tools that enhance both inbred line and hybrid variety development in sugar beet breeding programs.

How Non-coding Regulatory Regions Provide Disease Resistance in Polyploid Plants

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Polyploid plants contain complex genomes derived from multiple ancestral species that offer unique opportunities to study disease resistance mechanisms. Different subgenomes of polyploids can show dominant/recessive expression making one subgenome contribute more towards the gene expression that others; creating intricate regulatory networks and hierarchies that pathogens need to navigate to establish successful infections. In this study, we investigated triticale (×*Triticosecale* Wittmack) (2n=6x=42, AABBRR), a synthetic hexaploid hybrid derived from wheat & rye that shows natural resistance to bacterial leaf streak (BLS). The main causal bacteria *Xanthomonus translucens* pv. *undulosa* (Xtu) employs a sophisticated molecular mechanism- transcription activator-like (TAL) effector that functions as an exogenous regulator. Each TAL-effector is programmed to recognize precise DNA sequences & exploit subtle nucleotide differences within the host & modulate the gene expression, leading to distinct infection outcomes between strain infections. We identified the molecular basis for the difference between TAL-effector proteins; employing two different distinct phenotypes in identical triticale genotypes- chlorosis (resistance) for LB10, water-soaking (susceptibility) for P3. This demonstrates how TAL-effectors exploit the plant's own gene expression system to achieve strain-specific virulence outcomes. Understanding how non-coding regulatory variations in polyploid genomes can be leveraged to develop improved disease resistance & better crop protection for triticale & other polyploid plants.

From Ground to Air: The Precision Agriculture Evolution - Why Spray Drones Are Outpacing Traditional Application Methods

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Global food production must increase by 35-56% by 2050 to meet rising demand, while simultaneously addressing environmental sustainability and labor shortage challenges. Traditional ground-based spraying methods face critical limitations including operator health risks, soil compaction, crop damage, and increasing herbicide resistance. This research examines how unmanned aerial vehicles (UAVs) are revolutionizing agricultural spraying through precision application technologies that outperform conventional methods. Our comprehensive analysis reveals that UAV-based spray systems deliver superior operational efficiency compared to traditional sprayers. While conventional ground sprayers require 225-450 L/ha carrier volumes, UAVs achieve effective control with significantly reduced application rates (0.5-2 L/ha), enabling up to 90% reduction in chemical usage. Advanced flight control systems maintain precise altitude (1-3m) and speed (3-6 m/s), ensuring consistent droplet distribution impossible with manual applications affected by operator fatigue and variable walking speeds. Precision calibration protocols demonstrate UAVs' ability to adapt spray characteristics to specific crop requirements through real-time parameter adjustment. Integration of GPS guidance, variable rate technology, and AI-powered weed detection enables site-specific applications with accuracy levels unattainable by conventional boom sprayers. Field evaluations across multiple cropping systems show 15-25% improved spray deposition uniformity and 60-80% reduction in off-target drift. Economic analysis reveals UAV systems reduce operational costs by 40-50% compared to traditional methods through decreased chemical consumption, elimination of soil compaction damage, and enhanced field accessibility during critical application windows. Labor requirements drop significantly as single operators can manage multiple autonomous units simultaneously. Future developments focus on swarm technology for large-scale operations, enhanced AI integration for real-time pest identification, and improved battery technologies extending operational ranges. Machine learning algorithms continuously optimize spray parameters based on environmental conditions, crop stage, and target pest pressure. This technology transition represents Agriculture 4.0's practical implementation, where data-driven precision replaces broadcast applications. UAV spray systems demonstrate measurable advantages in environmental sustainability, operator safety, application precision, and economic efficiency. As herbicide resistance continues spreading and environmental regulations tighten, UAV-based precision spraying emerges as the essential technology for sustainable crop protection, positioning itself as the dominant application method for future agricultural systems.

Companion Cropping Kernza with Barley, Oat, and Spring Wheat Improves Forage and Maintains Small Grain Yield

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Kernza® is a cool-season perennial grain crop developed from intermediate wheatgrass (*Thinopyrum intermedium*). Spring planting Kernza results in no grain production because it requires vernalization, which means there is no revenue from Kernza grain during the establishment year. However, companion cropping Kernza with small grains can help improve income for producers. The aim of this study was to evaluate the effects of companion cropping Kernza with barley, oat, and spring wheat (annual small grains) on forage and grain yield in Prosper and Fargo, ND. Kernza monoculture produced significantly higher dry forage biomass yield, averaging 700 kg ha^{-1} compared with companion-cropped Kernza (Kernza averaged only 76 kg ha^{-}1 in companion cropping treatments). Total dry forage biomass yields were highest when Kernza was grown with barley (8599 kg ha^{-}1) or oat (8264 kg ha^{-}1). In the seeding year 2024, companion cropping did not reduce the grain yield of the small grains, which ranged from 2100 kg ha^{-}1 to 4600 kg ha^{-}1 across locations. Kernza grain yield in 2025 was similar between monoculture Kernza (1343 kg ha^{-}1) and Kernza that had been companion-cropped with spring wheat (1195 kg ha^{-}1), while companion cropping with oat appeared to reduce Kernza grain yield (961 kg ha^{-}1). These findings suggest that barley and oat may be the best companions for increasing total forage yield during Kernza establishment. Furthermore, the study indicates that companion cropping does not negatively impact the grain yield of the small grains. This suggests producers can establish Kernza with small grains without compromising the grain yield of the small grains to increase revenue opportunities in the establishment year.

Host Status and Root Penetration of *Pratylenchus penetrans* on Selected Cover Crops and Potato Cultivars

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The root-lesion nematode, *Pratylenchus penetrans*, is a significant pest of potato, reducing both yield and tuber quality. This study evaluated the host status and root penetration of *P. penetrans* on selected cover crops and potato cultivars under greenhouse conditions. Three experiments were conducted using eleven cultivars of cover crops (alfalfa, annual ryegrass, and winter rye) and two cultivars (Castle Russet and Red Norland) of potato, with initial nematode populations of 2,125, 1,670, and 1,200 *P. penetrans* kg^{-1} soil in trials 1, 2, and 3, respectively. Root samples from two selected cover crop cultivars and the two potato cultivars were stained to assess nematode penetration at 20, 40, 60, and 80 days after planting (DAP). Data collected included final nematode population densities, reproductive factor (RF), and numbers of nematodes within roots. Nine cover crop cultivars significantly reduced P. penetrans populations, with RF values ≤ 1, indicating poor host status. In contrast, Red Norland consistently exhibited the highest RF values (3, 3, and 2 across the three trials), confirming it as a good host. Castle Russet was a poor host, with RF values of 0.2, 0.3, and 0.6, respectively. Root staining revealed substantially greater nematode penetration in Red Norland at all sampling times, with 3, 5, 25, and 33 nematodes g^{-1} roots at 20, 40, 60, and 80 DAP, respectively. In Castle Russet, nematodes were detected only at 60 and 80 DAP, with 4 and 6 nematodes g^{-1} roots, respectively. No nematode penetration was observed in the roots of the two selected cover crops, alfalfa (FSG 527) and annual ryegrass (*Tetilia*), throughout the study. Overall, these results indicate that poor-host cover crops and the resistant potato cultivar Castle Russet can effectively suppress *P. penetrans* populations and represent promising components of integrated nematode management strategies.

Improving Fusarium Head Blight Resistance in Durum Wheat Using Recurrent Phenotypic Selection and Genomic Selection

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Breeding for Fusarium head blight (FHB) resistance in durum wheat (*Triticum turgidum* L. subsp. *durum*) is particularly challenging due to the limited availability of resistant germplasm. Several durum wheat lines with moderate resistance, carrying different resistance genes, have been developed using resistant sources identified in tetraploid wheat relatives and hexaploid bread wheat. Given the complex genetic architecture of FHB resistance, recurrent selection provides an effective approach to improve resistance by integrating multiple resistance genes and increasing the frequency of favorable alleles. This strategy also enhances the likelihood of developing FHB-resistant inbred lines from the improved populations. A base population was developed by crossing ten moderately FHB-resistant lines with five elite durum wheat cultivars. Five cycles of phenotypic selection for FHB severity were conducted from 2019 to 2024, one cycle per year. The mean FHB severity decreased from 82.5% in Cycle 0 to 59.3% in Cycle 5. A genomic prediction model was developed using 318 breeding lines from the NDSU durum program and 438 S0:1 lines from recurrent selection Cycle 3–5 populations. Prediction accuracies were 0.51 for FHB severity, 0.53 for plant height, and 0.79 for days to flowering. Two cycles of genomic selection (GS), initiated with the top 15 S0:1 lines from the Cycle 5 population, were conducted from September 2024 to April 2025. Field evaluations in 2025 showed progressive improvement in FHB severity across GS cycles at both locations. The top 24 lines selected from GS-Cycle 0–2 were genotyped using the KASP marker for Fhb1, revealing that over 65% of lines carried the resistant allele. Several of these top lines also exhibited significantly lower FHB severity and deoxynivalenol (DON) content compared with the check cultivar ND Riveland at both Fargo and Prosper, ND. These results demonstrate the effectiveness of recurrent phenotypic selection and genomic selection in enhancing FHB resistance in durum wheat, providing a strong foundation for developing resistant cultivars adapted to the Northern Great Plains.

Chlorophyll Fluorescence Imaging for Quantifying Temperature Responses in Dry Bean

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Rising temperatures pose one of abiotic stress to crop species, including dry bean (*P. vulgaris*). Increased temperature affects photosynthetic processes by disrupting the balance between photochemical energy conversion and photodamage in the photosystems. The chlorophyll fluorescence imaging provides the tool to quantify these changes and direct measure the changes when plants exposed to elevated temperature. In this study, three dry bean varieties -- ND Redbarn, ND Galaxy, and ND Rodeo -- were used in a pilot experiment to evaluate their responses to elevated temperature relative to control conditions. Plants were subjected to different durations of heat exposure, and their photosynthetic responses were quantified using more than ten photosynthetic indices derived from chlorophyll fluorescence imaging. These indices collectively provide a comprehensive assessment of photosynthetic performance and stress responses. Our results reveal distinct genotype-dependent differences in temperature sensitivity, with XX exhibiting the most robust tolerance to elevated temperature compared with the other varieties. These findings highlight the potential of chlorophyll fluorescence imaging as a rapid phenotyping tool and provide a foundation for identifying heat-resilient genotypes that may support the development of stress-tolerant dry bean cultivars.

Characterising the role of accessory genes within the *Mesorhizobium japonicum* Integrative Conjugative Element (ICE) in mediating competitive symbiosis with *Lotus japonicus*

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Agricultural nitrogen fertilizer production relies heavily on the Haber–Bosch process, which requires substantial energy input and contributes to environmental degradation. Symbiotic nitrogen-fixing bacteria associated with legumes offer a sustainable alternative; however, the efficiency of this system is often limited by competition among rhizobial strains. Highly competitive yet poorly nitrogen-fixing strains can outcompete more efficient strains for nodule occupancy, ultimately reducing overall nitrogen fixation. *Lotus japonicus*, a model legume, provides an ideal system to study symbiotic interactions with its natural partner, *Mesorhizobium japonicum* strain R7A. In R7A, symbiosis related functions are encoded on a 502 kb chromosomally integrated element known as the Integrative Conjugative Element (ICE-Sym). While approximately half of this element contains well characterized genes essential for nodulation (nod), nitrogen fixation (nif and fix), and horizontal transfer, the rest of the genetic content remains largely unexplored. We hypothesize that many of these accessory genes contribute to competitive fitness during root nodule colonization. To investigate this, we generated 16 large deletions across the ICE-Sym region using FLP-FRT-based site-directed mutagenesis. A fluorescent bioreporter system expressed under synthetic consensus *nifH* promoter for *Mesorhizobium*, Meso_PsnifH utilizing three fluorescent proteins (mScarlet-I, sfYFP and sfCFP), developed in-house was employed to assess competitive colonization and root entry. Our results identified deletions 3 and 4 as key regions influencing competitive symbiosis. Notably, these regions encode components of a Type IV secretion system. Targeted disruption of genes associated with this system will further clarify its role in mediating rhizobial competitiveness and host interaction.This work provides new insights into the genetic basis of competitive symbiosis and highlights previously uncharacterized accessory genes as important determinants of rhizobial competition in legume hosts.

Quantification and Isolates Characterization of Microbial Contaminants in Pressed Water from Sugar Beet Processing Factories in the Red River Valley

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Effective monitoring of microbial activity during sugar beet extraction process is important in ensuring the quality of the end product and minimize economic losses. Pressed water is obtained when wet pulp is pressed mechanically after the extraction process. This water is typically recycled back into the diffuser, making it a potential processing point for microbial proliferation. Therefore, this study focused on the quantification of microbial populations in pressed water during sugar beet processing across different factories in the Red River Valley. Samples were collected from four processing factories at different periods throughout the 2024/2025 processing campaign. Total aerobic mesophilic bacteria, facultative anaerobic thermophilic bacteria and yeasts were quantified using plate count methods. Physical parameters like pH and water activity (Aw), were also measured to support interpretation of microbial viability. Results showed that the differences in microbial contamination among processing periods for the pressed water samples were statistically significant (P value ≤ 0 .05). A greater microbial diversity was observed at the start and end of the processing period. The bacterial community shifted significantly over processing period, with *Bacillus cereus* dominating mid–period. Also, the fungal populations were primarily driven by *Pichia fermentans* (yeast),whilst *Penicillium paneum* (mold) and *Candida parapsilosis* (yeast) appeared intermittently across the processing period. The presence of these microorganisms is of major concern in sugar production due to their potential to promote sucrose degradation, organic acid production, biofilm formation, and processing inefficiencies.

Optimizing Nitrogen Inputs in Malting Barley Production

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Nitrogen (N) management plays a critical role in balancing yield and malting quality of two-row spring barley (*Hordeum vulgare* L.) grown in the Northern Plains. A field experiment was conducted at three locations in North Dakota to evaluate the effect of N fertilizer source on grain yield, protein, and kernel plump. Treatments included eight commercially available N sources including urea, enhanced efficiency urea, urea ammonium nitrate, calcium ammonium nitrate, sulfur enriched granular urea and a non-fertilized check. Treatments were arranged in a randomized complete block design. All fertilized treatments received 150 lb N ac-1, corresponding to 80% of the regional agronomic optimum N rate for malting barley production. Results showed N fertilization significantly increased grain yield and protein concentration compared with the unfertilized check, while kernel plump remained unaffected by N source. Despite small differences among sources, all fertilized treatments produced protein concentrations within the AMBA-recommended range (10-13%), indicating acceptable malting quality. The non-fertilized check exhibited the most desirable protein level (10%), demonstrating the typical trade-off between yield and quality. These findings highlight that applying uniform nitrogen rates while varying fertilizer source can sustain yield gains without exceeding protein thresholds critical for malting quality in North Dakota barley production systems.

Metribuzin Tolerance Identification and Characterization within North Dakota State University Soybean Germplasm

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Weed management in soybean production has become increasingly difficult in the United States due to evolving herbicide resistances and the limited number of effective post-emergence chemical options available to growers. In addition, some widely used herbicides can injure sensitive soybean varieties and rotational crops due to the extended winter chemical carryover and high pH soils in North Dakota. An important pre-emergence herbicide, metribuzin, provides valuable early-season weed control but must be applied at reduced rates in North Dakota due to metribuzin sensitivity associated with unknown genetics. Increasing herbicide tolerance in commercial soybean varieties will provide growers with greater flexibility in selecting effective and economical weed control programs. Metribuzin tolerance has been identified within the North Dakota State University soybean breeding program, but the genetic control associated remains unknown. This research aims to identify loci associated with metribuzin tolerance and develop molecular markers to accelerate breeding for this trait. A genome-wide association study (GWAS) will be conducted in a greenhouse setting using 400 PI lines. Field trails will be performed for characterization of yield and crop safety in North Dakota cultivars and advanced breeding lines. Results from this research are expected to provide further insights into the mechanisms controlling metribuzin tolerance in soybean and may be utilized by breeding programs in North Dakota and throughout the country to expedite the development of cultivars tolerant to metribuzin and improve crop safety.

Identification of two QTLs for leaf rust resistance in durum wheat using bulk segregant RNA sequencing (BSR-seq)

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Leaf rust, caused by *Puccinia triticina* is an important fungal disease in durum wheat. This study aimed to investigate the inheritance pattern and identify underlying resistant genes (Lr) against race BBBQD in two durum wheat accessions, PI244061 and PI 209274. Two biparental populations were developed by crossing PI 244061 and PI 209274 with the susceptible genotypes Divide and Rusty, respectively. About 250 F2 plants form each population were phenotyped at the seedling stage for leaf rust resistance. Phenotypic evaluations indicated that leaf rust resistance is controlled by a single dominant gene in each of these accessions. A subset of highly resistant and highly susceptible F2 plants were pooled for RNA isolation and subjected to Bulked Segregant–RNA sequencing (BSR-seq) analysis. BSR-seq analysis identified two distinct resistance loci on chromosome 6BS, one derived from PI 244061 spanning 14.5 Mb and another from PI 209274 spanning 5.04 Mb. For validation and fine mapping, six accession-specific KASP markers were developed for PI 244061 and five for PI 209274. Genotyping of the F2 populations identified the QTLs to a 2.07 Mb of distal end for each of the F2 populations. A total of three candidate genes from three reference genomes (Svevo.v1, PI 192051, and Langdon) have been identified. Two of them are structurally different but functionally similar which encode RGA5 defense protein whereas another candidate gene encodes defense related WAK (wall-associate kinase) protein. Our future studies will focus on functional validation of these genes for their effective deployment in both tetraploid and hexaploid wheat breeding programs.

Looking ahead: What can 37 years of management practices do for soil health?

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Soil health management strategies are essential for building agricultural resilience to withstand extreme weather events. However, the duration and consistency with which these practices are applied strongly influence the soil response. For example, the adoption of conventional tillage instead of no tillage mixes the soil, breaking down soil structure and organic matter, which are essential for conserving plant, microbial, and human life. The objective of this research was to evaluate the long-term effects of crop rotations, tillage systems, and nitrogen management on soil health indicators. This study was conducted in a 37-year cropping systems trial at the NDSU Carrington Research Extension Center. Soil samples were collected in Fall 2024 from 0–5 and 5–15 cm depths to compare two crop rotations (R1: Hard Red Spring Wheat (HRSW)-Soybean-Corn-Field Pea, R2: HRSW-Corn-Soybean-HRSW), two tillage systems (NT: no-till, CT: conventional-till), and two nitrogen sources (mineral fertilizer, organic fertilizer), with a grassland reference from Glenfield, ND with the same soil type. Soil health indicators analyzed included pH, soil organic carbon (SOC), total nitrogen (TN), permanganate-oxidizable compounds (POXC), and water-stable macroaggregates, where higher values of these soil properties indicate better health of the production system. Results indicated that mineral fertilizer application acidified the soil, whereas organic fertilizer maintained a neutral pH. Under NT management, organic fertilizer application increased SOC, TN, and POXC above the grassland mean at the 0–5 cm depth. At 5–15 cm, organic fertilizer application was the only management capable of increasing these indicators. Macroaggregate stability was highest in the grassland, suggesting greater soil structure, followed by NT, which promoted significantly greater aggregation than CT. Crop rotations did not influence the analyzed soil health indicators. In conclusion, the long-term integration of conservation practices, particularly no-till combined with organic fertilizer application, significantly improved overall soil physical and chemical health, achieving levels that surpassed those of minimally managed soils.

Beneath the Surface: Microbiome Dynamics Driving Soil and Water Quality

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Agricultural intensification has dramatically increased global food production, but at a significant environmental cost, particularly through nonpoint source (NPS) pollution driven by nitrogen and phosphorus losses. In the USA alone, ~12 million tons of nitrogen and 4 million tons of phosphorus fertilizers are applied annually, yet only 40–58% is utilized by crops, leaving substantial residual nutrients vulnerable to leaching. This challenge is especially pronounced in agricultural states such as North Dakota, where almost 89% of land is under farming and over half of the perennial streams are impaired by nutrient runoffs. Here, we conducted a regional-scale, longitudinal study investigating how soil microbiomes mediate nutrient dynamics across the soil-vadose zone-groundwater continuum. By integrating 16S and ITS amplicon sequencing with shotgun metagenomics across long-term experimental plots in Carrington Research and Extension Center, NDSU and farmer-managed fields, over 10 timepoints spanning three calendar years (2022-2024), we assessed how tillage and fertilization regimes shape microbial communities, soil health, and shallow groundwater quality. Our results reveal a clear management fingerprint on both soil chemistry and microbiome structure. Microbial communities were significantly structured by tillage and fertilization (PERMANOVA, $p = 0.01$), with soil pH and organic carbon emerging as dominant drivers. Reduced tillage consistently enhanced soil organic matter and soil health scores, while excessive fertilization reduced soil health, highlighting a nonlinear "sweet spot" – of moderate levels of nutrient inputs. Linking soils to groundwater, we observed depth-dependent nutrient patterns: nitrate concentrations declined with depth (p<0.01 over 5 timepoints), while orthophosphate showed increasing trends, suggesting differential mobility and potential leaching pathways. Notably, soil-groundwater coupling differed by nutrient, with a positive association for phosphorus ($p = 0.031$) but weak coupling for nitrogen. Metagenomic analyses further revealed enrichment of amino acid biosynthesis and transcription-related pathways, indicating active microbial processing for building nucleic acids. Together, our ongoing study demonstrates that integrating microbiome-derived indices and information into soil health frameworks can improve prediction of nutrient leaching risks and inform management strategies. As sequencing technologies become more accessible, microbiome-enabled decision tools offer a promising frontier for sustainable agriculture and water quality stewardship.

Understanding photosynthetic stress responses to improve crop resilience in barley

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Rising temperatures and increasing atmospheric dryness have dealt massive drops in global crop production over the past five decades. These abiotic stresses disrupt photosynthesis, the plant's engine for growth. Non-photochemical quenching (NPQ), a photoprotection process that helps plants safely dissipate excess absorbed light energy as heat, plays a critical role in protecting the photosynthetic machinery during environmental stress. Recent studies have shown that optimizing NPQ dynamics can improve photosynthesis and thus enhance crop performance under fluctuating environmental conditions. In this study, we leveraged a chlorophyll fluorescence (ChlF) imaging pipeline to investigate photosynthetic stress responses in barley. This platform enables large-scale quantification of photosynthetic performance across thousands of plants and computes 18 image-derived fluorescence indices. Barley serves as a major cool-season cereal crop and an informative system for studying heat and drought-stress physiology because of its sensitivity to these abiotic stresses. Using diverse barley panels exposed to both heat and drought, we captured multiple fluorescence-derived traits associated with both photoprotection and photosynthetic performance. ChlF imaging provides a rapid, non-invasive, and non-destructive way to monitor NPQ dynamics and photosystem activity, making it well suited for semi-high-throughput phenotyping across large plant populations. To investigate the genetic basis of these responses, our generated fluorescence phenotyping data were integrated with genomic analyses. Genome-wide association analyses identified genomic regions associated with variation in NPQ dynamics across barley genotypes. Additionally, spatially-resolved chlorophyll fluorescence data revealed consistent differences in photoprotective responses along the barley leaf axis, suggesting that photosynthetic stress responses vary across different regions of the same leaf. These findings highlight how integrating physiological phenotyping with genomic analysis allow us to better understand how crops respond to their environment. This framework provides a scalable strategy for identifying physiological traits and genetic factors that can support the development of crop varieties better adapted to increasingly challenging growing conditions.

Evaluating Genomic Prediction Models for Protein Improvement in Dry Bean Breeding

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As an important crop in global food systems, dry bean (*Phaseolus vulgaris* L.) plays a crucial role in food security, making the improvement of its nutritional profile essential for maximizing its benefits to consumers. Known for being a rich source of plant-based protein, dry beans are widely recognized as a nutritious food source. However, combining key agronomic, seed quality, and nutritional traits into a single dry bean cultivar remains challenging. To address this, genomic prediction has emerged as a promising tool which leverages genetic information to predict traits of economic importance. Genomic prediction uses genome-wide molecular markers and statistical models to estimate the genetic potential of breeding lines before they are tested in the field, hence having potential savings in time and resources. This approach has been successfully applied in other legume crop species-such as lentils (*Lens culinaris* M.) and peas (*Pisum sativum* L.) and has shown improved selection efficiency by 1.9- and 2.4-fold for seed yield and two-fold for protein content. This study evaluates the protein content of approximately 530 breeding lines within the North Dakota State University (NDSU) dry bean breeding program, along with check cultivars, to assess the effectiveness of genomic prediction models for improving protein content. Protein was measured using Near Infrared Reflectance (NIR), while genotyping was conducted using a custom single nucleotide polymorphism (SNP) chip containing 4K SNP markers. Among the models tested, the highest predictive ability achieved was $R^2 = 0.56$, which indicates a moderate prediction accuracy for protein content. When identifying lines within the lowest 20% of protein concentration, the model achieved an accuracy of 37%. This suggests that genomic prediction could effectively eliminate low-protein lines early in the breeding process. These findings may support a more efficient selection of nutritionally improved cultivars.

Microbial Immunity in Action: Discovery of Phage Resistance Genes in Rhizobia

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Bacteria have evolved diverse mechanisms to defend against bacteriophages, including receptor modification, degradation of phage DNA, and abortive infection systems that eliminate infected cells. However, these defenses remain poorly characterized in agriculturally important nitrogen-fixing rhizobia. To address this gap, we investigated phage resistance in wild *Sinorhizobium meliloti*, a nitrogen-fixing symbiont of alfalfa. Studying phage resistance in rhizobia is important because phage pressure alters rhizobial community composition, which can influence nodulation success and nitrogen-fixation efficiency. Understanding these systems will allow the development of inoculants that are both phage-resistant and highly effective nitrogen fixers. We isolated, sequenced, and screened 185 wild strains for susceptibility to phage ΦM12 and performed a pan-GWAS analysis that identified 64 candidate resistance genes. Based on genomic context and predicted function, 22 candidates were selected for gain-of-function testing by assembling them into four multi-gene clusters (Clusters 1–4) and expressing them in a susceptible *S. meliloti* background. Cluster 2 conferred the strongest resistance. Subdividing this cluster into four subclusters (2.1–2.4) showed that Subcluster 2.1 retained partial activity. Deleting a helicase-annotated gene reduced resistance by ~100-fold, indicating an essential role, although the helicase alone was insufficient to confer protection. Additional deletion and complementation analyses narrowed the resistance phenotype to two methyltransferase-annotated genes within Subcluster 2.1. Together, these findings suggest that Cluster 2 encodes a previously uncharacterized Type I restriction–modification system involved in phage resistance in *S. meliloti.* This work provides new insight into defense mechanisms in nitrogen-fixing rhizobia and lays the foundation for understanding how phage pressure shapes the evolution and stability of legume symbioses.

Alfalfa and diversified cropping systems improve arthropod biodiversity and ecosystem services

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Crop biodiversity has declined since the Industrial Revolution and has been exacerbated by traditional annual monocropping systems. Currently, research efforts are focused on enhancing biodiversity in agricultural cropping systems to protect key environmental areas, including human health, ecotoxicity, and natural resources. Therefore, the objective of this study is to assess the environmental impacts of perennial crops integrated into annual cropping systems. The SimaPro software was used to assess ten cropping sequences that include alfalfa (*Medicago sativa* L.), camelina (*Camelina sativa* L. Crantz.), wheat (*Triticum* aestivum L.), sunflower (*Helianthus annuus* L.), and soybean (*Glycine max* (L.) Merr.), during 2022–2023 in two locations (Hickson and Prosper, ND). Additionally, arthropod community composition, family abundance, and biodiversity indices were assessed in six treatments (crops and cropping sequences) using the Permutation Multivariate Analysis of Variance (PARMANOVA), Generalized Linear Mixed Model (GLMM), and Rényi biodiversity profile respectively, in R software (version 4.5.2). Cropping sequences that include alfalfa decreased environmental impacts related to human health and ecotoxicity compared with annual cropping systems. However, both alfalfa integrated annual cropping sequences and traditional annual cropping sequences had similar impacts in terms of resource depletion. The Rényi biodiversity profile also showed alfalfa with the highest arthropod family richness. Out of the six crops and cropping sequences sampled for arthropod biodiversity, alfalfa showed the highest overall diversity of species with dominance patterns, except the sunflower–camelina sequence at higher alpha values. Information from this study highlights the importance of using perennial crops in improving cropping system arthropod biodiversity and ecosystem services in a sustainable manner. Acknowledgements: Funded by USDA-NIFA-SAS R-CAP Award #2021-68012-35917.

Evaluation of Commercial Biocontrol Products Performance for Managing Soilborne Pathogens in North Dakota Soybean Fields

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Root rot diseases caused by soilborne pathogens significantly threaten soybean production, requiring effective management strategies. This study evaluated nine commercial biocontrol products across three North Dakota locations, Oakes, Mohall, and Fargo, in 2024 and 2025. Using a randomized complete block design with four replication of 20’ x 10’ plots, we evaluated Avodigen (*Bacillus licheniformis* FMCH001, 1.02 fl oz/cwt), F4034-5 (*Bacillus subtilis* RTI477, 0.64 fl oz/cwt), RootShield Plus Granule (Trichoderma harzianum Rifai T-22, 24 lb/cwt), RootShield Plus seed treatment (*Trichoderma virens* G-41, 4 lb/cwt), Howler (*Pseudomonas chlororaphis* AFS009, 5 lb/cwt), Heads Up (*Chenopodium quinoa* saponins, 8 fl oz/cwt), Rhizotrop seed treatment (*Bacillus* spp, 300 ml/100,000 seeds), and RootShield (*Trichoderma harzianum* (KRL-AG2), 5 oz/cwt), non-treated control and fungicide CruiserMaxx APX (3.9 fl oz/cwt) as a positive control. Stand count (plants/ac), root rot severity, and yield (bu/ac) were recorded and data showed potential effects on measured traits, though these effects were not significant (P>0.05). In 2024, Avodigen yielded (44.7 bu/ac) compared to CruiserMaxx APX (44.3 bu/ac) and non-treated control (39.8 bu/ac). In 2025, Rhizotrop and RootShield yielded (53.6 bu/ac each). In 2024, CruiserMaxx APX showed highest stand count (45700 plants/ac and lowest root rot severity (22.35%), followed by RootShield Plus Granule and Heads Up. In 2025, Heads Up showed highest stand count (47700 plants/ac, while CruiserMaxx APX showed lowest root rot severity (19.9%). These findings provide valuable insights into the potential of these products for root rot management in soybeans. Further multi-year trials are necessary to validate the efficacy of these commercial biocontrol products for managing soilborne pathogens in soybean fields. The findings will be distributed to agriculture professionals and soybean growers and will impact input decisions.

Sunflower Intercropping Reprograms Gene Expression in Alfalfa Roots

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Intercropping can improve agricultural sustainability by increasing resource-use efficiency and crop productivity. Alfalfa (*Medicago sativa* L.) is an important perennial forage crop owing to its nutritive value. However, its relatively low productivity during the establishment year often discourages farmers from including it in crop rotations. Intercropping alfalfa with sunflower (*Helianthus annuus* L.) has been proposed as a strategy to offset establishment costs while maintaining productivity. Although the agronomic benefits of this system are well known, the molecular mechanisms underlying crop-crop interactions in field environments remain poorly understood. In this study, we investigated how alfalfa roots respond at the gene expression level when grown alone or intercropped with sunflower across multiple field environments in the northern Great Plains. Root samples were collected from field trials conducted in Hickson, North Dakota, in 2021 and 2022; Prosper, North Dakota, in 2021; and Red Lake Falls, Minnesota, in 2022, and analyzed using RNA sequencing. A total of 49,095 Medicago sativa genes were quantified in the RNA-seq dataset. Among these, 45,686 genes showed detectable expression. After removing low-expression genes (≥10 counts in at least three samples), 31,028 genes were retained for differential expression analysis. Of the annotated genes, 33,296 had identifiable *Arabidopsis thaliana* orthologs that were used for functional annotation and Gene Ontology enrichment analyses. Intercropping resulted in significant transcriptional changes in alfalfa roots. Most differentially expressed genes were environment-specific, indicating that local field conditions strongly influence plant responses to neighboring crops. However, a subset of genes responded consistently across locations, including 43 genes for ALIC76 vs AL, 67 genes for ALIC152 vs AL, and 2 genes for ALIC152 vs ALIC76 at the first sampling timepoint. Gene Ontology enrichment analysis indicated that these genes are involved in stress responses, chemical signaling, cell wall organization, and metabolic pathways. These findings demonstrate that alfalfa roots undergo substantial transcriptional reprogramming when grown with sunflower and provide new insight into plant-plant interactions in intercropping systems that may guide the development of more sustainable cropping strategies.

Companion crops suppress weeds during pollinator plant species establishment

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Amid ongoing ecological decline and species loss, perennial pollinator plants have emerged as a strategy to restore natural habitats within farmlands, however, their establishment often faces challenges of early-season weed competition. This study evaluates whether companion crops, barley (*Hordeum vulgare* L.), oat (*Avena sativa* L.), and flax (*Linum usitatissimum* L.) can suppress weed growth to improve early establishment of pollinator plants while also providing forage for livestock. Six treatments were evaluated at two North Dakota locations (Fargo and Prosper) under field conditions. A perennial plant species mix was used in all treatments; alone, with companion crops, mowing, and manual weeding. Weed biomass and species counts were evaluated for each treatment while companion crop biomass was harvested and analyzed for forage nutritive value. Two sampling (harvest) times were conducted, before mowing and then two months later. From the results, there was a significant difference in weed biomass among treatments ($P \leq 0.05$). Less weed biomass was observed in the species with manual weeding, while the species mix alone (no weeding) had the highest biomass. Companion crops provided intermediate suppression, with barley and oat reducing weeds similarly to mowing. Companion crops forage yield for barley, oat, and flax were 2.71, 2.38, and 1.87 Mg ha-1, respectively. Relative forage quality values were 102.9, 92.0, and 98.6 for barley, oat and flax, respectively, which meet the forage nutritive value required for beef cows. These results indicate that companion crops can reduce weed competition during the establishment period of perennial species while providing forage.

Mapping Rz1: Advancing Durable Resistance to Rhizomania in Sugarbeet

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Beet necrotic yellow vein virus (BNYVV) is a devastating soil-borne pathogen that causes major losses in sugarbeet production worldwide. BNYVV causes rhizomania disease, which can persist in soil for decades. Because there is no effective chemical control, long-term management depends entirely on genetic resistance. For more than 30 years, the Rz1 resistance gene has been the foundation of rhizomania control in commercial sugarbeet production. However, despite its importance, the exact genetic identity of Rz1 remains unknown. At the same time, emerging virus strains are beginning to overcome Rz1, threatening its long-term effectiveness. Without a deeper genetic understanding, current resistance strategies may not be sustainable. My research focuses on identifying the precise location and molecular identity of the Rz1 gene. To achieve this, we used genotyping-by-sequencing and genome-wide analyses to identify genomic regions associated with resistance. Our results place Rz1 on chromosome 3, narrowing the search from a broad genomic region to a specific target area. This represents a key step toward identifying the gene itself. By refining the genetic location of Rz1, this work provides a clear target for breeding programs. Ultimately, it will accelerate the development of next-generation resistant sugarbeet varieties and strengthen sustainable crop protection in the United States.

Understanding the Different types of the Clubroot Pathogen in North Dakota

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Plasmodiophora brassicae is a soil-borne protist that causes clubroot disease in Brassicaceae crops, including canola (*Brassica napus* L.). The virulence of P. brassicae populations is highly dynamic and evolves over time. Clubroot was first detected in canola in Cavalier County, North Dakota, in 2013 and has since continued to spread across the region. Among available management strategies, the use of clubroot-resistant cultivars is the most practical and widely adopted. However, variability among pathogen pathotypes and the presence of pathotype-specific resistance genes can lead to resistance breakdown, highlighting the importance of pathotype characterization for effective disease management. This study aimed to characterize four isolates of *P. brassicae* collected from canola fields in North Dakota using the Canadian Clubroot Differential (CCD) set to determine their pathotypes. Resting spores were isolated from infected root galls, quantified and used to inoculate 10 differential hosts of CCD set for pathotype characterization. Plants were maintained under controlled greenhouse conditions at 22 ± 2°C which are conducive to disease development. Disease severity was assessed six weeks after inoculation using the 0-3 rating scale described by Kuginuki et al. (1999). The experiment was conducted twice under greenhouse conditions in a completely randomized design. The four isolates exhibited distinct virulence patterns across the differential hosts, indicating variability among *P. brassicae* populations in North Dakota. Notably, two isolates were virulent on the first-generation resistant cultivar 'Mendel', indicating the emergence of new pathotypes capable of overcoming clubroot resistance in canola. These findings highlight the need for continued pathotype surveillance and responsible stewardship of resistance cultivars.

Reproductive Potential of Root-lesion Nematodes (*Pratylenchus scribneri* and *P. neglectus*) on Corn Cultivars

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Root-lesion nematodes (*Pratylenchus* spp.) are widely distributed plant-parasitic nematodes associated with many crops, including corn. Among them, *Pratylenchus neglectus* and *P. scribneri* are frequently detected in corn-growing regions, where they infect root tissues, cause root damage, reduce plant performance, and interact with other soil-borne pathogens to increase disease risk. Their reproduction abilities can vary among species and is influenced by corn cultivars. However, limited information is available on the reproductive potential of these nematode species in commercially grown corn cultivars and their capability for population increase. Therefore, this study aimed to evaluate reproduction ability of *P. neglectus* and *P. scribneri* on eleven commercial corn cultivars. Four independent greenhouse experiments (two per nematode species) were conducted to quantify nematode multiplication using a reproductive factor (RF = final population/initial population), where RF represents the extent of nematode reproduction on a host, with values greater than 1 indicating population increase. Reproductive ability varied among cultivars, with approximately half of the cultivars supporting similar levels of multiplication for both nematode species, whereas the remaining cultivars showed variation in reproduction levels between *P. scribneri* and *P. neglectus*. For *P. scribneri*, RF values for experiment 1 ranged from 4.0–14.2 and 4.6–12.3 for experiment 2. For P. neglectus, RF values for experiment 1 ranged from 2.0–7.3 and 2.4–6.7 for experiment 2. These results demonstrate the strong and variable reproduction abilities of root-lesion nematodes on corn cultivars, underscoring their potential to increase populations and threaten corn productivity. The findings highlight the critical need to identify and screen additional corn cultivars that reduce nematode reproduction as part of integrated nematode management strategies.

Determining QoI fungicide resistance in *Diaporthe* spp. using the cytochrome b gene sequencing

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Diaporthe species cause diseases of soybean (*Glycine max* L.) such as seed decay, pod and stem blight, and stem canker worldwide. In 2024, yield losses associated with *Diaporthe* species in the United States were estimated at 1.06 million metric tons. Quinone outside inhibitor (QoI; FRAC Group 11) fungicides are labeled against *Diaporthe* species causing pod and stem blight, with applications typically recommended at reproductive growth stages (R3–R5). Soybean plots treated with QoI fungicides such as pyraclostrobin showed increased prevalence of *Diaporthe* spp. in stems, leaves, and seeds compared to non-treated controls, and led to speculation of possible QoI resistance within fungal populations. In this study, a cytochrome b (cyt b) gene-based Polymerase Chain Reaction (PCR) assay was developed to identify QoI-resistant *Diaporthe* strains. Forward and reverse primers were designed based on the cyt b sequence of *Diaporthe longicoll*a. A total of 50 isolates of *D. aspalathi, D. caulivora*, and *D. longicolla*, collected from 15 U.S. states, were cultured in potato broth for 14 to 21 days at 23–25 °C under 12 h light and 12 h dark conditions, after which genomic DNA was extracted. The cyt b gene fragments from the isolates were amplified, sequenced, and analyzed for mutations. Sequence analysis of the 50 isolates, aligned with reference cyt b sequences of *D. longicolla* revealed no mutations associated with QoI resistance, including G143A, F129L, or G137R substitutions in the cyt b gene. This research suggests that the tested *Diaporthe* isolates are sensitive to QoI fungicides.

Phosphorus Up! Beneficial Fungi Still Holding Strong?

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Arbuscular mycorrhizal fungi (AMF) can aid many crop plants in nutrient uptake, including phosphorus (P) in soybean. With decreasing phosphate rock reservoirs and increase in P-fertilizer prices, reliance on beneficial symbiotic organisms such as AMF is becoming increasingly important. Thus, we investigated whether levels of P fertilizer affected the colonization of AMF in soybean roots and AMF biomass in the soil, estimated with PLFA 16:1ω5 biomarker. Five field trials were sampled, one in 2023 and four in 2024. All trials had five different P fertilizer application rates (0, 26, 52, 77, 103 kg ha-1) replicated four times. Arbuscular mycorrhizae fungi colonized soybean roots at all sites, with the highest colonization (33% - 35%) at our only true no-tillage site, Dickinson, ND. Across all trials, P additions did not impact either AMF root colonization or biomass in soil. These findings suggest that fertilizing soybean with P doesn't negatively affect AMF, at least in the short term. When combining data across locations, AMF biomass was not correlated with soil P availability, but there was a significant but weak negative correlation between subsequent root colonization and spring soil test P (r = -0.35). Soybean relative yield was also weakly negatively correlated with AMF root colonization (r = -0.34). However, there were weak positive correlations between relative yield and Olsen spring P (r = 0.41), as well as midseason Mehlich-3 P (r = 0.45). These results suggest an indirect interaction and highlight the complexity of AMF interactions with soil P.

Enhancing Northern Great Plains Integrated Crop Livestock Systems with Grazing Technologies

JOSHUA WIANECKI
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Advisor: Miranda Meehan, Ph.D.

Intensive grazing practices are a valuable strategy with the potential to enhance livestock production within grazing systems. One intensive grazing practice is strip grazing, where a pasture or field is divided into multiple strips and grazed sequentially. Strip grazing can increase forage utilization and total livestock gain compared to continuous grazing. However, strip grazing requires greater labor and infrastructure to achieve these benefits. Various technologies such as virtual fencing (VF) and automated gate openers could reduce labor while implementing intensive grazing practices. Virtual fencing utilizes GPS enabled devices worn by livestock which uses stimuli to manage livestock movement. Automated gate openers modify existing infrastructure to open grazing strips at timed intervals. The objective of this study is to determine the livestock containment efficacy of VF and automated gate openers compared to conventional fencing within strip grazing systems; and identify the impacts of intensive strip grazing on forage utilization and stocking rates compared to continuous grazing. Three 8.1-to-14.2-hectare fields were established with an annual forage and divided into four equal paddocks. Strip grazing with VF, automated gate openers, manual poly-wire gates; or continuous grazing treatments were randomly assigned to each paddock. Strip grazed paddocks were divided into eight strips and grazed sequentially using the assigned technology. All cattle were fitted with VF collars for GPS tracking and trained to VF cues. Only the VF grazing treatment was managed with VF. Utilization was determined by biomass removed and stocking rates calculated following grazing. Containment efficacy was determined by the proportion of GPS points within the allocated strip. Livestock containment did not differ (P = 0.23) by grazing technology. Forage utilization (P = 0.48) and stocking rates (P = 0.46) did not differ between treatments. Mean grazing duration was greater (P = 0.02) in strip grazed paddocks with 52 days compared to 45 days grazed in continuously grazed paddocks. Grazing technologies have demonstrated to be effective at containing grazing livestock and can be useful for implementing strip grazing, increasing the duration of grazing.

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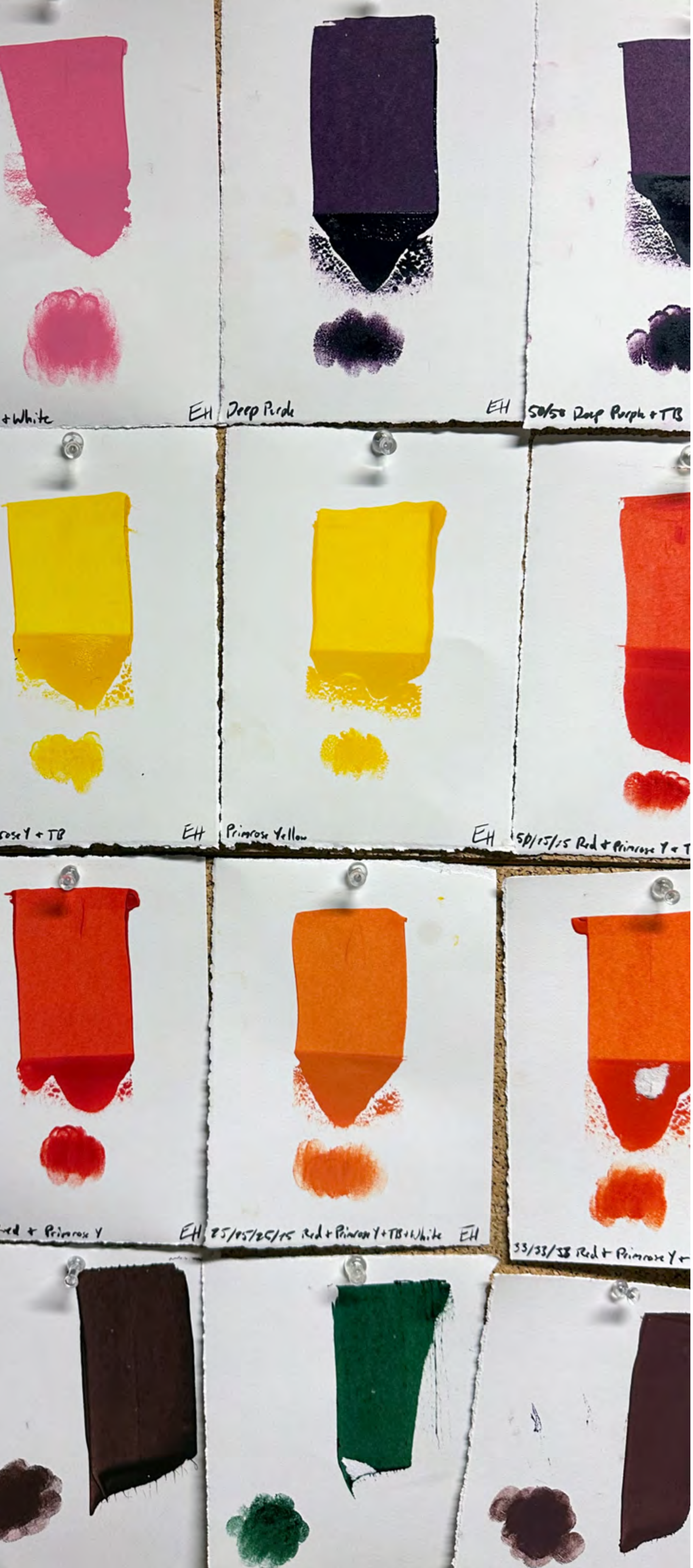

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Class-Aware Cooperative Perception for Multi-Class LiDAR-based 3D Object Detection in V2X Systems

BLESSING AGYEI KYEM
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Advisor: Armstrong Aboah, Ph.D.

Cooperative perception can extend the sensing range and scene awareness of autonomous driving systems by allowing vehicles and roadside infrastructure to share LiDAR observations. However, most existing Vehicle-to-Everything (V2X) 3D object detection methods use a uniform fusion strategy for all object classes, even though pedestrians, cars, and trucks differ substantially in size, point density, and localization requirements. This study proposes a class-aware cooperative perception framework for multi-class LiDAR-based 3D object detection in V2X systems. The framework combines multi-scale window attention to adapt receptive fields to object scale, a class-specific fusion block that routes features through separate pathways for small and large objects, a multi-scale bird's-eye-view enhancement module to capture richer contextual information, and a class-balanced loss to reduce the effect of class imbalance during training. The method is evaluated on V2X-Real, a large-scale real-world benchmark for cooperative perception in autonomous driving, across five collaboration settings: vehicle-centric, infrastructure-centric, vehicle-to-vehicle, infrastructure-to-infrastructure, and vehicle-to-infrastructure. Results show consistent improvements in mean average precision across all cooperation modes, with gains ranging from 1.5 to 6.2 points over strong intermediate-fusion baselines. The proposed framework delivers especially strong improvements for underrepresented and scale-sensitive classes. It achieves a 4.5-point gain in pedestrian AP under infrastructure-to-infrastructure cooperation and a 12.7-point gain in truck AP under vehicle-to-vehicle cooperation, while maintaining competitive vehicle detection performance. These findings show that class-aware fusion offers a practical and effective way to address scale variation and class imbalance in cooperative 3D perception. The study demonstrates that tailoring feature fusion to class-specific characteristics can improve robust multi-class detection in real-world V2X environments.

MSMT: A Memory-Augmented Transformer with Multi-Scale Spatio-Temporal Modeling for Network-Wide Traffic Flow Prediction

JOSHUA KOFI ASAMOAH
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Traffic forecasting plays a vital role in building smarter, safer, and more responsive transportation systems. However, existing models often struggle to generalize across diverse traffic settings due to limited temporal adaptability, rigid spatial structures, and insufficient handling of prediction uncertainty. These limitations are especially critical when forecasting traffic in both highway and complex urban environments, where temporal rhythms and spatial dependencies vary widely across time and location. To address these challenges, we propose a Memory-augmented Spatio-temporal Multi-scale Transformer designed to extract richer traffic dynamics through a modular and memory-aware architecture. The model introduces an Adaptive Temporal Embedding module that encodes contextual time features such as time-of-day and day-of-week. Our Multi-scale Temporal Convolution module, developed as part of this study, captures short, mid, and long-term dependencies in parallel, while a Memory-Augmented Spatial Attention module dynamically attends to spatial patterns using soft graph reasoning and memory-guided attention. Finally, an Uncertainty-Aware Output Head integrates multi-resolution predictions through confidence-based fusion to improve robustness. MSMT is extensively evaluated on eight real-world datasets at 3, 6 and 12 prediction steps. The results demonstrate consistent performance gains across all settings. Notably, across 12-step horizons, MSMT maintains superior accuracy with an average 8.2% improvement in MAE and 11.8% in RMSE over the next best model. In addition to its predictive performance, MSMT achieves strong computational efficiency, requiring only 58.06s (on PEMS04) per training epoch and 12.06 ms per inference step on an NVIDIA A40 GPU.

Western Snowberry Encroachment Constraints on Rangeland Biomass Production

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Woody plant encroachment into grasslands has increased dramatically in recent years, altering ecosystem functions and services. Reductions in herbaceous biomass mediated by woody encroachment have been shown to lower livestock production, particularly in cattle grazing systems. In the Northern Great Plains, the native shrub western snowberry (Symphoricarpos occidentalis) has become a dominant component of many grasslands due to altered disturbance regimes and climate change. However, the proposed link between western snowberry encroachment and reduced forage production has yet to be demonstrated. This study sought to quantify the relationship between variation in western snowberry cover and herbaceous biomass in a North Dakota mixed-grass prairie. We estimated western snowberry foliar cover and clipped current-year vegetative biomass in 0.25 m2 frames along transects spanning a gradient of snowberry cover. Biomass samples were dried and weighed by functional group (graminoids, forbs, and woody-stemmed plants). Preliminary results indicate a shrub encroachment threshold at approximately 45% western snowberry foliar cover, above which graminoid biomass declines. In contrast, total annual aboveground production increased with western snowberry cover, driven by increases in western snowberry biomass. These findings demonstrate that western snowberry encroachment decreases forage production at high densities and provide a benchmark for implementation of brush management strategies before forage losses occur.

Fragmented Market Attention to Fiscal Policy

LOUIS BENTIL
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Fiscal policies are often employed for managing economic stability, promoting growth, and addressing socio-economic challenges through government spending and taxation. As a fiscal policy, the CHIPS Act involves direct government intervention in the economy through spending and tax incentives aimed at achieving strategic economic and national security goals via semiconductor production.1 As of June 2, 2025, the United States federal government had allocated $50 billion to the Department of Commerce to support semiconductor research, development, innovation, and manufacturing along with authorization for up to $75 billion in direct loans and loan guarantees.2 However, these types of policies may have unintended consequences in several sectors including the financial markets (Pástor & Veronesi, 2013; Albulescu et al., 2019, Goldberg et al., 2024). As a key driver of the global economy, the semiconductor industry, according to Goldberg et al. (2024), may inadvertently divert resources toward less efficient firms. This article examines the implications of the CHIPS Act on extreme downside risk among a selected group of stocks. Recent literature has established that investors are typically concerned with downside risk (Huang et al., 2012; Ergun, 2023; Dobrynskaya, 2024). To achieve the objective of this study, we adopt two downside risk measures (Ergun, 2023; Dobrynskaya, 2024). Preliminary results show that the relative downside risk and extreme downside risk declined across the categories of stocks after the implementation of the CHIPS Act. The results reveal the importance of fiscal policies for risk mitigation.

Violence Exposure and Suicidal Ideation Among U.S. Adolescents: The Roles of Persistent Sadness and School Connectedness

ENOCH BOATENG
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Adolescent mental and behavioral health continues to pose a serious public health challenge, with suicide remaining one of the leading causes of death among youth. Experiences such as bullying, cyberbullying, threats at school, and neighborhood violence may contribute to emotional distress and increase the risk of suicidal ideation. This study examines whether exposure to these forms of violence predicts persistent sadness and suicidal ideation among U.S. adolescents, and whether school connectedness reduces this risk. Data were drawn from the 2023 Youth Risk Behavior Survey (YRBS), a nationally representative sample of U.S. high school students (N = 20,103). After listwise deletion for missing data, the analytic sample ranged from 10,016 to 10,086 participants. Hierarchical logistic regression models were used to assess predictors of persistent sadness and suicidal ideation. This study provides a comparative model of multiple violence-related risk factors and protective influences on adolescent suicidal ideation within a nationally representative sample. Adolescents who experienced bullying, cyberbullying, school threats, or neighborhood violence were more likely to report persistent sadness. Persistent sadness was the strongest predictor of suicidal ideation. In contrast, students who reported higher levels of school connectedness had significantly lower odds of suicidal ideation, even after accounting for violence exposure and emotional distress. These findings suggest that violence exposure is strongly associated with increased emotional distress, which in turn is closely linked to suicidal ideation, while school connectedness is associated with lower odds of suicidal ideation. By examining multiple forms of violence within a single model, this study provides a more integrated understanding of how these experiences shape adolescent mental health. These results highlight the need for school-based interventions that both reduce exposure to violence and strengthen students' sense of connection within the school environment. Future research should examine these relationships longitudinally and assess whether strengthening school connectedness can buffer the long-term effects of cumulative violence exposure.

Attitude & Effort: Student Perceptions of Feedback in Introductory Biology Courses

SAVANNAH CHRISTENSON
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Self-regulated learners, those who can engage in metacognitive processes and increase self-efficacy, often use feedback as a tool for identifying areas of misunderstanding (Yan & Carless, 2021). Effective feedback must be seen by students as useful, comprehendible, and actionable (Wiltbank et al, 2021). However, students' emotional and personal responses often impact how they process feedback (Lipnevich, 2009). This exploratory study investigated students' responses to receiving feedback from instructors on written exams in an introductory biology course that used standards-based grading with retesting. Specifically, our research questions were: How do students feel about getting feedback? Does feedback confuse them in any way? Do students use feedback in the learning process, and if so, how? We recruited students to participate in semi-structured interviews where they were asked to review their exam feedback from a recent assessment with the interviewer (a graduate student). Students were given prompts to explain their initial reactions to feedback, areas of confusion, and ultimately how the feedback either solidified or altered their understanding of course material. Interview transcripts were reviewed using thematic analysis. We found students struggled to decode instructor feedback – shorthand notation and symbols can compound students' confusion; in some cases, students sought clarification. Through the coding process, we also discovered the importance of the instructor-student relationship in how students framed, interpreted, and ultimately used (or did not use) instructor feedback. Positive rapport increases student engagement with content and course material (Mattanah, 2024). Students who viewed the instructor as a learning ally were more likely to discuss feedback and seek clarifying resources; in contrast, students who articulated a negative relationship with the instructor tended to avoid course resources, and were less likely to engage in the feedback process in ways that meaningfully impacted learning (i.e., they didn't retest). We suggest instructors can create keys for their feedback, avoid complicated abbreviations, and allow space for clarifying questions. There is also value in developing trust and rapport in a classroom, as it potentially helps remove barriers in the feedback process. Helping students correctly interpret the feedback makes the feedback useful and worthwhile.

Cognitive Reserve and Self-perceptions of Aging: Psychosocial Pathways to Dementia Risk Reduction

BET-INI CHRISTIAN
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Advisor: Heather Fuller, Ph.D.

As global populations age, it is important to understand factors that promote cognitive resilience and reduce dementia risk. Cognitive reserve (CR) and self-perceptions of aging (SPA) are both linked to cognitive and health outcomes, yet they are typically studied independently, limiting understanding of how psychosocial beliefs influence CR and cognitive outcomes in later life. This integrative review synthesized evidence on the relationship between SPA and CR and examined how their interaction may influence cognitive aging and dementia risk in later life. Following Whittemore & Knafl's (2005) methodology, structured searches were conducted in PubMed, Web of Science, and MEDLINE using terms across three domains: SPA, CR, and cognitive outcomes. The search yielded 2,224 records. After multiple screening steps and deduplication, 20 full articles were selected for review. Initial synthesis revealed consistent associations between negative SPA and poor cognitive outcomes, including accelerated cognitive decline and increased dementia risk. Evidence suggested SPA may influence cognitive trajectories by influencing engagement in cognitively stimulating social and lifestyle behaviors that build CR, as well as through stress-related processes and physiological pathways. Further, CR buffered clinical expression of neuropathology through more efficient and flexible neural networks that delay dementia symptom onset despite underlying brain changes. Findings also indicate that SPA may influence the development and mobilization of CR across the life course. Integrating SPA and CR within a single framework could advance understanding of psychosocial contributions to cognitive resilience and highlight the modifiable targets for life-course interventions to strengthen CR and reduce dementia risk in later life.

PowerLiteNet: A Lightweight Anomaly Detection Model for Powerline Transmission Infrastructure

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Anomaly detection in power transmission infrastructure prevents failures and ensures grid reliability. Recent methods have demonstrated excellent accuracy but struggle with computational efficiency when deployed on resource-constrained devices such as UAVs. Memory-based approaches with dominant performance like PatchCore require external memory banks that significantly increase execution time, while heavyweight normalizing flow models demand substantial computational resources. This paper introduces PowerLiteNet, a lightweight anomaly detection framework that maintains high detection performance while drastically reducing computational requirements. By integrating Squeeze-and-Excitation (SENet) attention with our lightweight architecture, our approach achieves a 57% reduction in computational demands and sub-millisecond inference times (0.6ms versus 179ms). Evaluated on the Inspection Power Line Asset Dataset (InsPLAD), our SENet-enhanced lightweight model achieved significantly better performance (81.99% mean AUROC) compared to their non-enhanced models (76.69%). This research bridges the gap between advanced deep learning techniques and real-world deployability by balancing computational efficiency with detection accuracy. Our approach offers a scalable automated powerline asset monitoring solution on UAV platforms with limited computational resources.

The Effects of Putrescine on Diapause Incidence in The Alfalfa Leafcutting Bee, *Megachile rotundata*

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Diapause is a halt in development in insects to avoid undesirable environmental conditions. It is unknown what is responsible for controlling diapause in many species. In the solitary bee widely reared for use in alfalfa crop production, *Megachile rotundata*, maternal effects are thought to play a role. In diapausing *M. rotundata*, the amine putrescine was found to be highly upregulated when compared to non-diapausing individuals. Putrescine is a biogenic amine in the spermine pathway that is found in all organisms. The aim of this study is to determine the role of putrescine in *M. rotundata* diapause. We hypothesized that higher putrescine levels in larval *M. rotundata* provisions cause a hormonal cascade resulting in higher diapause incidence. We tested this using in vitro rearing and adding putrescine to the larval diet, as well as measuring putrescine content of natural larval provisions. The treatment groups are as follows: unchanged diet (0.0% putrescine added to diet), low putrescine (0.01% putrescine solution added to diet), and high putrescine (0.1% putrescine solution added to diet). It was predicted that putrescine presence in larval diet will increase diapause incidence in first cohort *M. rotundata*. Putrescine addition the larval diet was not found to influence diapause incidence or larval development time. The high putrescine treatment group had a significantly higher mortality rate than the control group. Determining mechanisms influencing diapause may lead to ways of controlling diapause incidence, which could be helpful for farmers to increase yields and decrease bee losses.

Learning-Based Drift Mitigation in GNSS–IMU Fusion for Worker Localization in Highway Work Zones

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Real-time localization is fundamental to improving safety and operational efficiency in highway work zones, where reliable worker tracking must be maintained under dynamic and infrastructure-limited conditions. Multi-sensor fusion, particularly the integration of the Global Navigation Satellite System (GNSS) and Inertial Measurement Units (IMUs), is widely adopted to combine absolute positioning with short-term motion continuity; however, under intermittent GNSS availability, inertial propagation accumulates drift rapidly, leading to substantial errors during prolonged outages. This study presents a GNSS–IMU fusion framework with learning-based drift mitigation tailored to such environments. Orientation is estimated using a Mahony filter, and position and velocity states are computed through an Extended Kalman Filter (EKF) that integrates GNSS and IMU measurements. To constrain long-term drift during GNSS-denied intervals, a step-based pedestrian dead reckoning (PDR) formulation is enhanced using a lightweight Temporal Convolutional Network (TCN) for step-length estimation. The framework was evaluated in Webots simulation and controlled field experiments across L-shaped, curved, and zigzag trajectories. In simulation, GNSS–IMU fusion reduced positioning error by approximately 51% relative to raw GNSS. In field testing, fusion reduced root mean square error (RMSE) by 7.7% on average, while the TCN-based correction reduced outage error by 90.1% compared to inertial propagation alone. These results demonstrate that learning-enhanced drift mitigation substantially improves trajectory continuity in temporary highway work zones where standalone GNSS performance is insufficient.

AI-Driven Risks and Mitigation in Quality Assurance and Quality Control for Highway Construction

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The integration of artificial intelligence (AI) in highway construction has significantly transformed construction processes. It has enabled automation, predictive analytics, and data-driven decision-making. However, alongside these advancements, emerging risks associated with AI, particularly data manipulation, falsification, and misuse, pose critical challenges to the integrity of Quality Assurance and Quality Control (QA/QC) systems. Existing literature predominantly focuses on the application of AI for inspection and defect detection, with limited attention given to the risks introduced by AI-driven technologies in construction workflows. Furthermore, there is currently limited availability of standardized frameworks or software tools to support Departments of Transportation (DOT) auditors in detecting synthetic or manipulated patterns in construction data. The most critical gap is the lack of federal and state guidance on managing this specific risk. To address this gap, this research aims to develop an intelligent software capable of detecting, assessing, and mitigating AI-induced risks in highway construction QA/QC processes. The study adopts a Bibliometric-Systematic Literature Review (B-SLR) to analyze the application and advancement of AI in highway construction. This approach combines quantitative bibliometric mapping with qualitative thematic analysis to identify key research clusters, technological trends, and knowledge gaps. In addition, a survey of ten U.S. State DOTs will be conducted to assess current industry practices, including the AI techniques, models, and data sources used in QA/QC processes. The findings will inform the development of a prototype decision-support software/program designed to detect AI-induced data manipulation, evaluate associated risks, and support QA/QC decision-making in highway construction projects. This research contributes to bridging the gap between AI applications and AI risk governance, enabling the development of more resilient, transparent, and trustworthy QA/QC systems for infrastructure projects.

Test-Retest Reliability and Least Significant Change of Bioelectrical Impedance Metrics

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Methods of body composition measurement vary largely in affordability and reliability. The Tanita is a relatively cost effective and convenient method of body composition analysis via bioelectrical impedance analysis (BIA). The purpose of this study is to assess the test-retest reliability of the Tanita DC-430U bioelectric impedance scale (Tanita Corporation, Tokyo, Japan). A total of 50 participants (n= 25 male, n= 25 female) aged 18-39 years completed two BIA assessments in a single session. Participants reported to the lab after a 12-hour fast, and measurements were completed approximately 15 minutes apart. Reliability was assessed using intraclass correlation coefficient (ICC) and the coefficient of correlation obtained from paired samples t-tests. Additionally, least significant change (LSC) was calculated for each variable. Intraclass correlation coefficients were excellent for all variables. Paired samples t-tests indicated that there were no significant differences between the two timepoints for any variable. Least significant change values are reported as root mean square standard deviation (RMSSD) with a confidence level of 95%. Body Mass= 0.123 kg, BF%= 1.31%, Fat Mass (FM)= 1.069 kg, Fat-free Mass (FFM)= 1.039 kg, Skeletal Muscle Mass (SMM) = 0.981 kg, Total Body Water (TBW)= 0.334 kg, TBW%= 0.429%, Metabolic Age= 3.04 yrs, Bone Mass= .08 kg, BMR= 25.718 kcals. The Tanita DC-430U floor scale presents high intra-subject reliability under identical conditions.

Watching Ice Freeze: A Methodology for Insect larvae

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Insects utilize many physiological processes to survive harsh environmental conditions, including freezing temperatures. Some insects have evolved the ability to survive internal ice formation, leading to freeze tolerance. Internal ice formation comes with many challenges, including cellular dehydration, oxidative stress, and physical damage from ice crystals. To limit damage, some species induce ice formation in specific internal regions. The timing of ice formation, both location and timing, is considered a key factor to successfully surviving freezing. However, the location of ice nucleation within freeze-tolerant organisms is an understudied area. This poster shows how infrared (IR) imaging can be used to determine where ice formation occurs within a freeze-tolerant insect. The freeze-tolerant, sugarbeet root maggot, Tetanops myopaeformis, which is a crop pest found in North America, was used for this experiment. Insects were placed on a chilling plate and cooled from 4°C at 1°C/min to -20°C. The exotherm; the increase in temperature that occurs during a phase change during freezing, can be visualized using a thermal camera. This poster focuses on the protocol that allows for the accurate determination of the location of ice nucleation in an insect by recording the exothermic heat released during freezing.

Floral Resource and Bee Response Following Woody Encroachment Reduction Strategies in Northern Great Plains Grasslands

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Grassland pollinators and the goods and services they provide are threatened by a number of global change drivers including invasive plant species, climate change, habitat loss and degradation, and simplified disturbance regimes. Habitat degradation due to woody encroachment occurs when shrubs and trees begin displacing native grasses and forbs. Western snowberry (*Symphoricarpos occidentalis* Hook.) is a shrub native to the Northern Great Plains but has become a major encroacher, often dominating communities where it was once in low abundance. Research on controlling western snowberry, hereafter snowberry, has been limited, and no studies assessing the potential trade-offs between snowberry removal and bee and floral resources currently exist. We investigated how floral resources and bee populations differ between snowberry patches treated with prescribed fire (spring or fall treatments), high intensity short duration (HISD) grazing, herbicide (2,4-D), and mowing (spring or spring and fall treatments). Visual encounter surveys identified bees actively pollinating and all accessible flowers along four line transects within the 25x25m snowberry patches three times throughout the growing season (June, July, August). Preliminary results show that time after treatment greatly affected bee and floral abundance, with herbicide and both mowing treatments having the lowest average abundance of both bees and floral resources, and HISD having the highest average of both. Additional years of data collection will provide more detailed insights into the tradeoffs between controlling snowberry and bee and floral abundance within grassland ecosystems. Applying our findings could increase the efficacy of future conservation actions intended to restore diversity to snowberry-encroached grasslands.

Spotted Elk's Flight from Sitting Bull's Camp to Wounded Knee

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A U.S. Congressional map of Spotted Elk ("Big Foot") and his journey was published in 1891. All the English from this map has been removed and replaced with Lakota placenames. View this reconstruction of a long-occupied Ocheti Shakowin ("Great Sioux Nation") and chain of events following the tragic death of Sitting Bull.

Gluten Synergy in Wheat Blends: Cooperative Protein Interactions Enhance Dough Strength and Bread Functionality

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Blending wheat classes in different proportions is widely practiced to optimize dough functionality, yet whether such blending produces true synergistic rather than just additive effects remain unclear. This study aimed to determine whether incorporation of Hard Red Spring (HRS) wheat into Hard Red Winter (HRW) base flour produced any synergistic enhancements in dough rheology and bread quality. Two HRS flours differing in protein content (high protein, HP; low protein, LP) were blended at 40% and 60% with two HRW base flours of contrasting protein levels in a completely randomized design with three replications. Protein content increased proportionally with HRS inclusion accompanied by higher wet gluten yields, reaching 33.33% in HP-HRW and 30.33% in LP-HRW blends containing 60% HP-HRS. Gluten aggregation behavior produced clear rheological synergy where 60% HP-HRS blend significantly increased aggregation energy by 1.17-fold in HP-HRW (16.8%) and 1.21-fold in LP-HRW system (20.7%) with reduced peak maximum time (37.5% with HP-HRW and 28.5% with LP-HRW) indicating faster and more efficient gluten network formation. In contrast, blending effects in strong HP-HRW system were largely additive. Synergy was most pronounced in low-protein HRW system. Incorporation of 60% HP-HRS increased dough development time by 264.7% (3.65-fold), farinograph stability by 84.1% (1.84-fold), and farinograph quality number by 98% (1.98-fold), alongside 18.9% reduction (1.23-fold) in mixing tolerance index, reflecting enhanced resistance to mechanical breakdown. Rheological synergy translated into improved baking performance in LP-HRW blends, with loaf volume increasing 6.2% (1.06-fold), resilience 3.4% (1.03-fold), cohesion 4.9% (1.05-fold), and hardness decreasing 22.2% (1.28-fold reduction). These results demonstrated that high-protein HRS acted not only as a protein supplement but as a structural synergist, where gluten quality and matrix compatibility governed cooperative network reinforcement and improved bread functionality.

Influence of Variable Nitrogen Rates on Dough Rheology, Bread Structure and Shelf-life of Hard Red Spring Wheat

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Hard Red Spring (HRS) wheat is widely valued for high protein content that make it suitable for wide range of baking applications. While nitrogen (N) is an essential macronutrient for protein synthesis how its variable application influences the flour functionality and bread quality through starch-protein interactions is not fully understood in HRS wheat. This study evaluated the effects of four N fertilization rate (0, 56, 112 and 168 kg ha^{-1}) on dough rheology, bread structure, texture, shelf life and sensory quality of HRS wheat three cultivars grown across four locations. Increasing N rate significantly altered starch pasting behavior by increasing peak viscosity (2467.5-2681.7 cP) and pasting temperature (68.45-71.39 °C), while reducing breakdown and setback viscosities ($p < 0.05$), indicating stronger starch–protein interactions and a lower retrogradation tendency. Dough mixing and extensibility properties improved with higher N, as reflected by longer development time and stability, reduced mixing tolerance index, and greater resistance to extension. These rheological changes translated into higher loaf volume, increased from 928.3 cc at N0 to 1027.7 cc at the highest N rate, along with a more uniform crumb structure. This also demonstrated slower crumb firmness while storing at room temperature indicating better shelf life. Bread hardness was negatively correlated with specific volume ($r = -0.63$), confirming the relationship between loaf expansion and textural softness. Sensory evaluation showed higher consumer preference for breads produced under moderate to high N rates, driven primarily by improvements in texture and appearance rather than color or aroma. For most quality attributes, responses plateaued beyond moderate N levels, indicating limited additional benefits from excessive fertilization. Overall, optimized nitrogen management improves breadmaking performance and shelf-life quality of HRS wheat while supporting economically efficient fertilizer use across diverse growing environments.

Metamorphosis and its Impact on Cellular Age in Specific Tissues

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Cellular aging is a complex process that affects fitness, reproduction and susceptibility to disease. Understanding the factors that regulate cellular age could provide insights into how to combat this inevitable decline. Telomere attrition is a cellular hallmark used to measure age. In most organisms, telomere length decreases with subsequent cell divisions until they reach a critically short length. However, in some insects such as the alfalfa leafcutter bee, *Megachile rotundata*, and the orchard mason bee, *Osmia lignaria*, telomere length is longer in later developmental stages as insects age. To further examine this phenomenon, we used the moth, *Manduca sexta*, to explore the impact of metamorphosis on telomere length. Metamorphosis involves intense structural remodeling using stem cell-like imaginal cells, often replacing larval tissues with comparable adult tissues. Consequently, metamorphosed adults could possess "old" larval tissues and "new" adult tissues, which calls into question the cellular age of these different tissues. We hypothesized that metamorphosis alters the cellular age of specific tissues. Using qPCR, we measured relative telomere length and telomerase activity in specific tissues of fourth and fifth instar larvae as well as adults following metamorphosis. We predicted that "new" adult tissues would possess longer telomeres than non-remodeled tissues. We also predicted that telomerase would be more abundantly expressed in late larval stages to prepare for the tissue development that occurs during metamorphosis. Understanding how cellular age is regulated in insects could clarify how developmental processes impact telomere length in different tissues and reveal cellular mechanisms that contribute to telomere maintenance.

Bees in the Trap: Pollinator Bycatch in Traps Targeting Insect Pests

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Monitoring plant pests is a foundational element of integrated pest management programs. Traps use visual and chemical cues to attract target pests. However, they can inadvertently attract non-target arthropods, including beneficial insects such as bees (Hymenoptera: Apidae). Bee bycatch has been relatively well studied for some traps, but not others, and few studies compare bycatch among traps. We surveyed the diversity and abundance of bees in three traps: green/yellow Japanese beetle pheromone traps (Coleoptera: Scarabidae, *Popillia japonica*), white/yellow Helicoverpa bucket traps with pheromone (Lepidoptera: Noctuidae), and black or green Lindgren funnel traps (Coleoptera: Curculionidae, Scolytidae). We also investigated how lure identity affected bee bycatch in Lindgren traps. Pest traps were placed in 23 locations around North Dakota near agricultural fields in May 2025. At each location, we hung one Japanese beetle trap, one Helicoverpa trap, and five Lindgren traps. Each of the latter had one of the following lures: hexanol (control), quercivorol, Ips aggregate pheromones, alpha-pinene + gelled ethanol, and alpha-pinene + gelled ethanol + monochamol. Traps were left in the field until September 2025, after which bees were removed, pinned, and identified. To date the greatest diversity and abundance of bees was in Helicoverpa traps, followed by Lindgren and Japanese beetle traps. Results for Lindgren trap lures are still being processed. This study can help inform trap design, lure selection, and placement risks to avoid harm to bees and other non-target organisms.

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Integrated Effects of Wheat Class, Flour Particle Size, and Fermentation Time on the Functional and Sensory Quality of Whole Wheat Sourdough Bread

Sourdough (SD) bread is widely valued for its distinctive flavor, improved texture, nutritional benefits, and extended shelf life. Fermentation time, wheat class, and flour particle size (PS) are key factors influencing these changes; however, their combined effects on SD bread quality remain insufficiently understood. Therefore, this study evaluated the interactive effects of wheat class, fermentation time, and flour PS on SD bread quality. Whole wheat flours (WWF) from three wheat classes; hard red spring (HRS), hard red winter (HRW), and hard white wheat (HWW) and their 50:50 blends with HRS were stone milled using three gap settings (wide, medium, and narrow). The flours were analyzed for physicochemical, functional, and rheological properties. Breads were prepared using two fermentation times (12 h and 24 h) and evaluated for loaf volume, crumb structure, texture profile, and sensory attributes. A completely randomized design with three replications was used. Data were analyzed by ANOVA followed by Tukey's test at a 5% significance level using JMP software (version 17). Among the wheat classes, HRS showed the highest dough stability (9.25 min). However, blending with HRS improved the dough stability of HRW from 5.65 to 8.25 min and that of HWW from 5.82 to 8.65 min. Rheological analysis indicated that blending HRW and HWW with HRS balanced dough viscoelastic behavior, reflected by a reduction in complex modulus (G^*) from 10,000 Pa to 8,100 Pa and 7,200 Pa, and a decrease in tan δ from 0.31 (HRW) to 0.22 and 0.19, respectively. This produced dough that was neither overly stiff nor excessively extensible. PS reduction significantly improved bread quality, increasing loaf volume by 9.4% and reducing hardness by 28.5%. Extending fermentation from 12 h to 24 h reduced loaf volume by 5% and increased hardness by 11%, although longer fermentation enhanced aroma and lower pH. Overall, bread prepared from the 50:50 HRS: HWW blend with small PS and 24 h fermentation showed the best quality, with high springiness (91.6%), cohesiveness (74.0%), resilience (35.3%), and superior sensory scores. These findings provide useful guidance for optimizing SD bread formulations based on wheat class selection.

Syrphin' USA: Surveying Adult Hoverflies (Diptera: Syrphidae) Across the Sheyenne National Grasslands

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Hoverflies (Diptera: Syrphidae) are a diverse family of flies and important members of the pollinator community. Adults are nectar- and pollen-feeders with a cosmopolitan distribution, while larvae exhibit a variable array of ecological habits, including biological control of plant pests and decomposition of organic matter. Despite their ecological importance, the distribution of *Nearctic* species is understudied. Furthermore, host-plant associations with hoverfly genera remain poorly understood. To address these knowledge gaps, we conducted a survey of adult hoverflies to: 1) identify species present across a spectrum of grassland habitats within south-eastern North Dakota; and 2) catalogue host-plant associations of hoverfly genera. We established 16 130-m transects within NDSU's Albert K. Ekre Grassland Preserve and The Nature Conservancy's Brown Ranch. These sites represent six different prairie microhabitats that occur across eastern North Dakota. We sampled insects twice a month from May to September 2025 using bee bowls (early season only) and sweep netting. Our sweeping protocols consisted of both "general" sweeps along the length of the transect, and "targeted" sweeps, wherein surveyors collected only from identified species. To date, we have identified 26 species and morphospecies, which are primarily habitat generalists and marsh specialists. This research will improve our understanding of hoverfly species diversity within North Dakota and allow us to begin defining associations between hoverfly genera and plant species. This information can help inform conservation and land management efforts and contribute to our understanding of Nearctic syrphid distributions.

Additive Manufacturing of Complex Cores in Sandwich Composites

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The additive manufacturing industry has grown considerably in the last two decades. While it is mainly consumer based, the application of additive manufacturing at a large scale is increasingly attractive and companies have investigated where AM can fit into their products. This research aims to study different core geometries for sandwich composites using a syntactic foam composed of polypropylene and glass microspheres. This foam core will be 3D printed and adhered to the face sheets, which will consist of a compression molded PET and glass fiber composite.

Detection of Violent Scenes in Cartoon Movies Using a Deep Learning Approach

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Cartoon movies are a primary source of entertainment for children. However, concerns arise when these movies inadvertently expose children to violent scenes. This paper addresses the challenge of detecting subtle instances of violence within cartoon movies. The main difficulty in this task is the sequential nature of movies, where a sequence of frames must be considered in their given order. Existing methods have not effectively addressed the issue. In this study, we tackled this challenge by employing a sequential model. The research comprises three key steps. Initially, a histogram technique was implemented to select key frames from the video sequences. Subsequently, a Convolutional Neural Network (CNN) was utilized to extract prominent features from these selected key frames. In the third phase, the acquired features were utilized to train a sequential model using sequence-based learning. The model was then refined through transfer learning, using a dataset containing scenes devoid of violence, as well as scenes depicting varying forms of violence, including bloodshed, fights, gunshots, and explosions. A significant contribution of this study is the meticulous categorization of violent scenes into four distinct types, allowing for further investigation into the diverse effects of different violence categories. Furthermore, the study introduces an innovative approach by integrating a dense layer into the sequential model to enhance final classification. The trained model's performance was comprehensively evaluated using metrics such as F1 score, precision, accuracy, and recall. To validate the effectiveness of the proposed model, it was benchmarked against state-of-the-art methods. This study presents an innovative deep-learning methodology for the identification of violent scenes in cartoon movies. Its potential applications encompass a wide range, including safeguarding children from inappropriate content.

Host Plant Resistance to Wheat Stem Sawfly: Evaluation of Bread and Durum Wheat from Different Genetic Backgrounds

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Wheat stem sawfly is a major pest of the Northern Great Plains, and host plant resistance using a solid wheat cultivar is the primary means of management. We evaluated wheat genotypes with different genetic backgrounds for stem solidity in greenhouse and field conditions. Golden Ball-derived durum wheat genotypes had higher and consistent stem solidity across growth stages and environments. Golden Ball-derived genotypes had reduced stem damage, Rescue and Conan alleles could not lower stem damage despite lower egg density. Larvae feeding on Golden Ball had reduced head capsule and body length.

Generation of Conditional Hepatic VPAC1 Deficient Mice for Glucose Metabolism Regulation Analysis

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Diabetes, the eighth leading cause of death in the United States, affects approximately 38.4 million people and incurs over 300 billion dollars in annual healthcare costs. This metabolic disorder elevates blood glucose levels, leading to widespread, systemic complications due to glucose toxicity. Vasoactive intestinal peptide (VIP) influences many biological processes, including immunology, circadian rhythm, and metabolism. Previously, our laboratory reported that VIP and VPAC1 deficient mice are lean and have gut microbiota dysbiosis; while others have observed a pre-diabetic state with elevated blood glucose and insulin in VIP deficient mice fed a regular chow diet. It is well established that continuous glucose production by the liver due to hepatic insulin resistance drives diabetes progression. In addition, VPAC1, one of two VIP receptors, is exclusively expressed on hepatocytes and its expression increases in mice fed a high-fat diet (HFD). However, the underlying mechanisms remain unclear. Given the role of VIP in metabolism and glucose homeostasis, we hypothesize that hepatic VPAC1 signaling contributes to insulin resistance on a HFD. To investigate this, a conditional hepatic VPAC1 knockout was generated using the Cre-lox system. The confirmation of this was completed through the evaluation of DNA recombination, RNA and protein to monitor the presence of GFP and Cre recombinase. Future studies with these mice will focus on elucidating the contribution of hepatic VPAC1 signaling to glucose metabolism, including mRNA and protein analysis of relevant enzymes involved in glycogen metabolism and insulin signaling.

Biophysical Characterization And Structural Insights Into The Complex Between The Extracytoplasmic Function Sigma Factor, PupI, with the Anti-Sigma Domain Of The Sigma Regulator, PupR, from *Pseudomonas capeferrum*

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Iron acquisition is essential for bacterial growth and virulence. Under conditions of low iron, Gram-negative bacteria secrete iron chelating molecules, called siderophores to scavenge iron from the environment. *Pseudomonas capeferrum* produces the siderophores, pseudobactin BN7/8, which triggers cell surface signaling (CSS) involving TonB-dependent transporters (TBDTs) (1). CSS pathways allow for rapid response to extracellular stimuli via transcriptional activation. Iron import CSS pathways consist of an outer membrane (OM) TBDT, an inner membrane sigma regulator, and an extra-cytoplasmic function sigma factor that activates transcription of target genes (1). The *P. capeferrum* sigma regulator, PupR, has an N-terminal cytoplasmic domain, known as an anti-sigma domain (ASD). The PupR ASD was previously purified as a dimer in the absence of its cognate sigma factor, PupI (2). Here we use affinity pulldown assays to qualitatively demonstrate that His6-PupIFL interacts with the PupR ASD as well as with ASD homodimer-disrupting mutants. We show that the wild-type PupR ASD and PupI bind with a dissociation constant (Kd) of 180 nM using microscale thermophoresis (MST). Circular dichroism (CD) spectroscopy confirms that each protein - as well as their complex - is well-folded, with predominantly alpha-helical structures and there is no significant change in overall secondary structure content upon complex formation. A high-confidence AlphaFold3 (3) prediction of the PupR ASD:PupI heterodimer complex indicates that the PupR ASD interacts with the C-terminal region of PupI. This model is supported by our Hydrogen-Deuterium Exchange-Mass Spectrometry data (HDX-MS), which indicate that residues that show reduced solvent exchange map to the predicted PupR ASD interface. This model of the complex was experimentally validated by showing that a truncated PupI, composed of residues 99-173, binds to the PupR ASD. Further, a PupR ASD double mutation that maps to the heterodimer interface disrupts complex formation. These findings provide insights into how a sigma regulator interacts with its sigma factor during iron import CSS.

An Approach to Develop Standard Testing Methodology to Measure Tensile Properties of Continuous Fiber Reinforced 3D Printed Thermoset Composites

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Additive manufacturing (AM), commonly known as 3D printing, has emerged as a transformative technique for producing complex geometries with high material efficiency and design flexibility. Among its advancements, the 3D printing of continuous carbon fiber reinforced (CCFR) thermoset composites has attracted significant attention due to its ability to fabricate lightweight, high-strength components with tailored mechanical properties. These composites offer superior strength-to-weight ratios, high stiffness, and excellent thermal stability, making them suitable for demanding applications in aerospace and automotive industries. In particular, ultraviolet (UV) light-assisted 3D printing has shown strong potential for improving the mechanical performance and quality of CCFR thermoset composites. This study aimed to evaluate the tensile behavior of 3D-printed CCFR thermoset composites, focusing on the influence of specimen geometry and testing speed on tensile performance. It also sought to contribute toward the development of standardized testing methodologies for additively manufactured fiber-reinforced (FR) thermoset composites. Due to the layer-by-layer fabrication process, the microstructure, bonding characteristics, and anisotropy of these materials differ significantly from conventionally manufactured composites, raising the need for AM-specific testing standards. In the experimental setup, a 3K continuous carbon fiber tow was passed through a resin-filled syringe containing a photocurable resin (Peopoly Nylon-like Tough). The syringe acted as a resin bath, enabling effective fiber impregnation before deposition. The impregnated fiber was then deposited onto the print bed and cured using a 405 nm UV laser to solidify the composite structure. Specimens with varying numbers of print lines (12, 16, and 24) and layers (3, 5, and 7) were tested at a crosshead displacement rate of 1 mm/min. The optimized configuration (12 print lines and 3 layers) was further tested at rates of 1, 3, and 5 mm/min. Results indicated that specimens with 12 print lines and 3 layers tested at 1 mm/min exhibited the highest tensile strength and lowest variability. Overall, the findings highlight that specimen architecture and testing rate significantly influence tensile performance. The study underscores the necessity of developing AM-specific tensile testing standards for fiber-reinforced thermoset composites.

Testing Hyperspectral Remote Sensing for Rapid Plant Species Identification in a Managed Mixed-Grass Prairie

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Hyperspectral imaging is an emerging technology that measures the electromagnetic reflectance of material and can be utilized to study the chemical composition of plants. It has been implemented through remote sensing to detect and measure plant health, plant functional traits, invasive species distribution, biodiversity, and other environmental management interests. Hyperspectral imaging of leaves has recently been shown to provide a viable method for species identification. However, remotely sensing individual species' identities is difficult due to the high spectral similarities between species—the result of a similar chemical composition. Identifying individual species' unique spectral signatures and applying that information in remote sensing data, could allow rapid identification of plants species using field spectrometers and even satellites. In Summer 2026, the Plant Ecology and Diversity Lab will use hyperspectral remote sensing to analyze the plant reflectance spectra in 1 by 1 m. experimental plots in an NDSU-managed prairie at the Central Grasslands Research Extension Center. Within each plot, the coverage of common plant species—Kentucky bluegrass (*Poa pratensis*), smooth brome (*Bromus inermis*), western snowberry (*Symphoricarpos occidentalis*), and an additional species of interest—will be estimated. Hyperspectral images of leaves and entire plots will be obtained in the field, creating a continuum of spectral data from the individual leaf level to plant community level. Statistical analyses will investigate relationships among the spectral signatures from the individual species to help untangle their spectral signature at various spatial scales, from the experimental plots up to satellite observations. Species identification via remote sensing will potentially allow rangeland managers to remotely detect fine scale environmental changes in an era of shifting climate and land use.

Electrochemical and DFT Investigation of Sunflower-Derived Phenolics as Corrosion Inhibitors for Carbon Steel in Acidic Solution

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Advisor: Eugene Caldona, Ph.D.

Electrochemical performance and molecular-level interfacial interactions jointly govern the effectiveness of corrosion inhibitors in acidic environments, where adsorption behavior, charge transfer, and surface coverage directly control metal dissolution kinetics and inhibitor durability. In this work, sunflower-derived phenolic compounds are investigated as sustainable corrosion inhibitors for mild steel in 1 M HCl through a combined electrochemical and ab initio modeling approach. Water-extracted sunflower head and leaf biomasses were chemically profiled using chromatographic and spectroscopic techniques, identifying oxygen-rich phenolics, including caffeic acid, quinic acid, and caffeoylquinic acid derivatives as the primary interfacial species. Corrosion behavior was evaluated using electrochemical impedance spectroscopy, potentiodynamic polarization, and relative electrochemical area (REA) analysis. Both extracts act as mixed-type inhibitors, with inhibition efficiency increasing with concentration. The head-derived phenolics exhibit superior performance, achieving a maximum inhibition efficiency of 93%. Adsorption behavior follows the Langmuir isotherm, and calculated standard free energies of adsorption (-25 to -27 kJ mol^{-1}) indicate spontaneous, physisorption-dominated surface coverage. Increasing temperature leads to reduced inhibition efficiency, consistent with partial desorption of the adsorbed layer. Surface and nanoscale characterization using SEM-EDX, AFM, KPFM, XRD, and XPS confirms that phenolic adsorption suppresses chloride incorporation, reduces surface roughness, and minimizes electronic heterogeneity, forming a compact mixed-valence interfacial layer that limits localized galvanic activity. Ab initio density functional theory calculations support these findings by identifying caffeic acid as a key active species with favorable electronic properties for adsorption on iron surfaces. These results demonstrate the viability of sunflower-derived phenolics as bio-based interfacial modifiers for corrosion protection and highlight their potential integration into aqueous pretreatments and environmentally compliant coating systems.

Detection of Insect-Damaged Sunflower Seeds Using Near-Infrared Hyperspectral Imaging

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Advisor: Xin Sun, Ph.D.

Insect damage can significantly affect seed germination rates and overall seed quality, resulting in notable economic losses. Detecting insect-damaged seeds is vital for upholding food safety standards and satisfying consumer expectations in confectionery sunflower markets. To tackle this issue, this study explores the potential of hyperspectral imaging combined with machine learning to accurately classify damaged and undamaged sunflower seeds. Spectral data were acquired and preprocessed using principal component analysis (PCA) to reduce dimensionality while retaining essential spectral information. Machine learning techniques, specifically multilayer perceptron (MLP), support vector machine (SVM), random forest (RF), light gradient boosting machine (LGBM), extreme gradient boosting (XGB), gradient boosting (GB), and partial least squares discriminant analysis (PLS-DA), were trained and evaluated based on the spectral features. The results showed that MLP achieved the highest classification performance with an accuracy of 0.91 and an F1-score of 0.91, followed by SVM with an accuracy of 0.89 and an F1-score of 0.89. LGBM and RF also performed well, both achieving an accuracy of 0.88 and an F1-score of 0.88, while XGB and GB recorded accuracies of 0.85 and 0.86, respectively. In contrast, PLS-DA demonstrated the lowest performance, with accuracy falling to 0.65 and an F1-score of 0.64. These findings underscore the effectiveness of machine learning in utilizing hyperspectral data for precise seed quality assessment. Its integration into the seed sorting process can enhance seed inspections, food safety, damage scoring for scientific investigations, and ensure that only high-quality seeds are chosen for planting.

Surface Self-Segregation in Moisture-Curable Hybrid Urea-Siloxane Coatings for Durable Large-Scale Ice Shedding properties.

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Ice accumulation on infrastructure, transportation systems, and energy networks disrupts their operation and leads to significant economic and safety concerns, emphasizing the need for effective ice-shedding surfaces. Conventional ice-shedding coatings often rely on non-reactive, unbound siloxane oils, which reduce ice adhesion due to their low surface free energy. However, their performance typically degrades over repeated icing de-icing cycles as the unbound oil is gradually depleted. In this work, a self-segregating, moisture curable urea-siloxane coating system was developed to overcome this limitation. Functional siloxanes were chemically grafted onto isocyanate in the presence of a catalyst to form a siloxane-modified isocyanate prepolymer. This prepolymer was subsequently reacted with a silane, followed by incorporation of a moisture curable silicone resin to enhance the overall coating properties. The influence of siloxane molecular weight on ice-shedding behavior was systematically examined. Ice adhesion measurements revealed that coatings containing high molecular weight functional siloxanes exhibited superior ice-release performance. Surface topography analysis further confirmed the formation of distinct domains on coating surfaces with high molecular weight, which are believed to play a critical role in promoting ice shedding properties. To better understand how domain size and distribution contribute to ice-shedding properties and promote low interfacial toughness, an essential requirement for large-scale ice removal, siloxanes of varying molecular weights were incorporated. According to fracture mechanics principles, differences in elastic modulus between soft and hard surface segments (domains and bulk matrix) facilitate crack initiation and propagation, enabling the design of materials with low interfacial toughness below the theoretical limit of 1 J/m^2. This low interfacial toughness design strategy represents a new direction in ice-shedding coating development. The optimized formulation achieved an interfacial toughness of 0.4 J/m^2 and maintained its ice-shedding capability after 30 icing de-icing cycles, attributable to its exceptionally smooth surface and presence of well-defined siloxane domains on surface, indicating its superior mechanical durability, and large scale ice-shedding application.

Living Shorelines: A Regenerative Landscape Approach to Coastal Protection and Community Resilience in Bhasan Char, Bangladesh

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Bhasan Char, a precarious silt island in Bangladesh, currently hosts over one million Rohingya refugees—an ethnic Muslim minority from Myanmar fleeing decades of systemic persecution (Human Rights Watch, 2021). This community faces extreme vulnerability to cyclones and sea-level rise on a landscape of profound precarity (Biswas et al., 2024). This research addresses the inadequacy of traditional, hard-engineered coastal defenses, which are ecologically damaging, prohibitively expensive, and fundamentally unsuitable for the island's dynamic geomorphology (Sutton-Grier et al., 2018). It argues that such static infrastructure fails to address the Rohingya community's extreme social vulnerability (Adger et al., 2005). This study forwards a regenerative model for shoreline protection that is affordable, adaptable, and socially just. This work contributes to the knowledge base by specifically applying principles of Blue-Green Infrastructure to a humanitarian crisis (Hansen et al., 2015), creating a model that intersects coastal resilience with refugee empowerment. Drawing on the work of practitioners like Kate Orff/SCAPE (Orff, 2016) and the "Sponge City" concept (Yu, 2021), the analysis finds that nature-based coastal systems create landscapes that are more resilient, biodiverse, and liveable than traditional engineered solutions. Using a qualitative case study methodology guided by the frameworks of Mark Francis (1999) and Robert K. Yin (2018), this research analyzes three international precedents: the habitat-centric Living Shorelines Project (USA), the Can Gio Biosphere Reserve (Vietnam), and the Cobble Bell (USA). The primary finding is a design method for protective living shorelines that prioritizes embracing natural processes, layering ecological and bio-engineered systems, and integrating community stewardship. The resulting proposal, "Island as a System," synthesizes a protective mangrove buffer with a community-based management framework known as the "Shoreline Stewardship Cooperative." The study concludes by showing how social factors shape resilience, emphasizing that empowering displaced communities through landscape design is the most profound way to achieve observable ecological, economic, and social benefits (Cohen-Shacham et al., 2016).

Designing Earth-Abundant W(0) Complexes via Ligand Optimization for Near-Infrared Emission

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This research focuses on developing new earth-abundant metal complexes as efficient near-infrared (NIR) emitters and photosensitizers for applications in photocatalysis, bioimaging, and photodynamic therapy. By modifying ligand types coordinated to a metal center, W(0) in our case, we aim to enhance NIR absorption and emission, increase quantum yields, and reduce nonradiative decay pathways. We synthesized twelve new W(0) complexes coordinated with four carbonyl and one 2-(pyrid-2-yl)(benz)imidazole ligands. These complexes exhibit strong absorption at 580-600 nm and emission at 650- 700 nm spectral range in solvent dichloromethane, though their emission is relatively weak. Our calculations based on time dependent density functional theory (TDDFT) predict that employing diamine-based ligands with enhanced conjugated length or pyridocarbazole-type ligands, can significantly redshift both absorption and emission bands into the NIR region up to 800 nm range. Furthermore, replacing 1-2 carbonyl groups with pyridines or bipyridines in W(0)-diamine complexes extends the spectra from 600–650 nm up to 800–1100 nm and significantly enhances the optical activity of the lowest-energy transitions, indicating promising avenues for efficient emission. Our results demonstrate a promising pathway toward the rational design of W(0) complexes with optical responses in the NIR range, advancing the development of cost-effective, earth-abundant NIR emitters for applications in photocatalysis, bioimaging and photodynamic therapy

An Analysis of Sales and Online Review Data for a Sample of 10,000 ETSY Stores

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ETSY is a well-known large e-commerce platform that offers an opportunity to small businesses to sell different types of niche products including jewelry, clothing, home décor and craft supplies. It acts as a community driven alternative to mainstream e-commerce platforms. In this research, we conduct data visualization and exploratory analysis of a sample to 10,000 ETSY stores. Our variables of interest include sales volumes, favorite counts by users of the stores, average ratings, rating counts, level of free shipping and customization offered by the stores and the type of brand names used by the stores. As part of our data visualization, we find evidence of long tail type of distribution of sales and review counts among the stores consistent with theories on long tail phenomenon observed in sales of niche products. Average rating of products on the platform are overwhelmingly positive with mean average rating of 4.9, suggesting that the platform and its sellers are patronized by customers who are very favorable towards them. Our analysis also shows that stores offering both additional customization and free shipping tend to have higher sales, and stores with impersonal brand names as opposed to personal brand names tend to have higher average sales. Taken together these findings enable us to better understand the nature of stores on the ETSY platform.

Characterizing Chrononutrition Patterns and Sleep in West African Adults

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Chrononutrition, the timing, frequency, and distribution of eating, is associated with metabolic health, weight regulation, cardiovascular disease risk, and sleep outcomes. However, studies examining chrononutrition patterns and their effects on sleep and circadian health in African adults are sparse. Given that chrononutrition may differ substantially from Western settings due to cultural and socioeconomic contexts, this study sought to characterize chrononutrition and sleep behaviors among West African adults to identify patterns that may inform culturally relevant interventions. West African adults (N=273; M age=25.5 years, SD=6.0, 42.1% females) from Ghana, Sierra Leone, Ivory Coast, The Gambia, and Liberia completed an online survey including the validated Chrononutrition Profile-Questionnaire (CP-Q). Key chrononutrition behaviors and nocturnal sleep duration were assessed via self-report. Eating window, the daily duration between first and last meals, averaged 10.1 hours (SD=4.0), with over one-quarter (27.2%) exceeding 12 hours, a threshold associated with increased metabolic risk. Morning latency (time from waking to first meal) was prolonged, averaging 3.2 hours; notably, 57.9% of participants delayed breakfast beyond 2 hours, and 21.0% were habitual breakfast skippers (≤2 days/week). However, a beneficial pattern emerged where 54.9% identified lunch as their largest meal, reflecting front-loading of caloric intake earlier in the day. Evening eating patterns showed adequate meal-sleep spacing, with last eating event averaging 7:25 PM and a 3.5-hour gap before bedtime, meeting sleep hygiene recommendations. Night eating (eating after sleep onset) occurred on average 1.2 days/week, with 62.6% reporting never waking to eat. Sleep duration averaged 6.1 hours (SD=2.0), with 59.2% reporting habitual short sleep (≤ 7 hours). Despite widespread sleep restriction, sleep timing was consistent between weekdays and weekends (71.7% reported ≤ 30 minutes social jetlag), contrasting with typical Western patterns. West African adults demonstrate a chrononutrition profile characterized by prolonged morning fasting, lunch-predominant eating, and adequate evening meal-sleep spacing, alongside widespread sleep restriction but minimal social jetlag. Extended eating windows in over one-quarter of participants represent a modifiable risk factor for metabolic dysfunction. Future research should examine whether preserved chrononutrition patterns (consistent timing, lunch front-loading) moderate metabolic consequences of chronic sleep restriction in this population.

Trauma-Informed Interventions for Nicotine Cessation: A Scoping Review

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Background and Aims: Nicotine use remains one of the most preventable causes of death worldwide, yet trauma-informed approaches (TIA) to cessation remain underdeveloped. Evidence shows that trauma exposure, including adverse childhood experiences (ACEs), interpersonal violence, and systemic discrimination, is associated with earlier tobacco initiation, heavier nicotine use, and reduced cessation success. Trauma can also shape coping behaviors and engagement with healthcare. This scoping review synthesizes the evidence on trauma-informed nicotine interventions to identify promising practices and inform more equitable cessation strategies for trauma-affected populations. Methods: Following Arksey and O'Malley's scoping review framework and PRISMA-ScR guidelines, we searched four databases (CINAHL, PsycINFO, PubMed, and Web of Science) in July 2025 for peer-reviewed studies published between 2014 and 2025. Eligible studies described trauma-informed, trauma-sensitive, trauma-focused, or trauma-responsive interventions addressing nicotine use or cessation. Three reviewers conducted a three-phase screening process: title/abstract review, brief full-text screening, and in-depth synthesis. Data were extracted on intervention characteristics, target populations, study designs, and outcomes. Results: Sixteen studies met inclusion criteria, most from the United States and primarily pilot studies or program evaluations. Interventions commonly targeted vulnerable populations, including pregnant or parenting women, individuals with co-occurring substance use disorders or PTSD, and adolescents with high ACE exposure. Four themes emerged: (1) integrated care combining nicotine cessation with trauma and mental health services; (2) harm reduction approaches emphasizing gradual reduction and safer alternatives; (3) tailored interventions for trauma-affected populations; and (4) diverse strategies including trauma-focused therapies, trauma-informed care programs, prevention initiatives, and provider training. Conclusions: Trauma-informed nicotine cessation is widely endorsed but remains limited in practice. Early evidence suggests integrated care and harm-reduction models are feasible and promising, though most interventions lack standardized frameworks and rigorous evaluation. Expanding this field will require pragmatic research, workforce training, and system-level integration of trauma-informed principles to support more equitable and effective nicotine cessation.

Food Insecurity and SNAP Participation in the United States

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Food insecurity remains a significant public health concern in the United States despite the availability of federal nutrition assistance programs such as the Supplemental Nutrition Assistance Program (SNAP). Using data from the 2023 National Health Interview Survey (NHIS), this study examines demographic, socioeconomic, and health characteristics associated with SNAP participation and food insecurity among U.S. adults. Two analyses were conducted: (1) profiling adults who received SNAP benefits and comparing them to the overall U.S. adult population, and (2) examining adults who met federal SNAP income eligibility criteria (<131% of the federal poverty level) to compare SNAP recipients with eligible non-recipients. SNAP participants were more likely than the overall adult population to experience socioeconomic disadvantage, including lower educational attainment, unemployment, limited workplace benefits, and higher levels of financial strain. They also exhibited higher prevalence of chronic health conditions and mental health disorders, including diabetes, anxiety, and depression. Despite program participation, SNAP recipients reported significantly higher rates of food insecurity than the general population. Among adults who met income eligibility criteria, nearly half were not receiving SNAP benefits. Eligible non-recipients were more likely to be male, married, White or Asian, and to have higher educational attainment, employment, and private insurance coverage compared with eligible recipients. Eligible SNAP recipients, in contrast, experienced greater health limitations, financial strain, housing instability, and food insecurity. These findings highlight substantial disparities in both SNAP participation and food security that are shaped by broader social determinants of health. While SNAP plays a critical role in mitigating food insecurity, the program alone cannot fully address structural economic and health inequities. Policy strategies aimed at improving benefit adequacy, reducing administrative barriers, and expanding outreach to eligible populations may help improve participation and reduce persistent food insecurity among vulnerable groups.

Microbial Remediation of Arsenic

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Arsenic (As) is a naturally occurring toxic and carcinogenic metalloid that exists primarily in two inorganic forms: arsenite, As (III) and arsenate, As(V). Globally, over 200 million people are exposed to arsenic contamination, mainly through drinking water and crops cultivated in contaminated soils. Microorganisms play a critical role in controlling the mobility, transformation, and bioavailability of arsenic in soil and aquatic environments. This review highlights microbial-based remediation strategies for arsenic-contaminated systems. Key biochemical mechanisms involved in arsenic transformation include arsenite oxidation, arsenate reduction, methylation, biosorption, bioprecipitation, and intracellular bioaccumulation. These processes significantly influence arsenic speciation and its uptake by plants. The role of arsenic-resistant microorganisms in mitigating toxicity is discussed, with emphasis on their interactions with plant and soil systems. Additionally, environmental factors and stimulants that influence microbial activity and remediation efficiency are examined to identify opportunities for enhancing bioremediation performance. Challenges and future research directions in developing and applying microbes for arsenic remediation are addressed, emphasizing the importance of genetic engineering and technological innovation to address this pressing environmental and public health concern.

High-Fat Diet–Induced Modulation of Renal epithelial cell Cubilin and Matrix Receptors

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Obesity is a major risk factor for chronic kidney diseases (CKD). One of the hall marks of CKD is podocyte dysfunction and proteinuria. Increased urinary protein levels trigger inflammatory responses in proximal tubular epithelial cells and promote basement membrane remodeling during CKD progression. Filtered proteins are reabsorbed by the cubilin–megalin complex, which plays a critical role in maintaining protein homeostasis. However, the impact of obesity-induced changes in the basement membrane and associated signaling pathways on renal epithelial cell functions and protein handling remains unclear. Integrin β1, a key extracellular matrix (ECM) adhesion receptor, anchors renal cells to the basement membrane and regulates cell–ECM signaling, while cubilin mediates albumin reabsorption in proximal tubules. To investigate the effect of obesity on these pathways, mice were fed a normal diet or high-fat diet (HFD) 60% fat for 6 months, followed by kidney collection and analysis. Quantitative immunoblotting normalized to α-tubulin showed that integrin β1 expression was significantly increased under HFD in both females ($P = 0.0349$) and males ($P = 0.0476$). In contrast, integrin α subunits (α1, α2, α3, α5, αV) were unchanged, indicating a selective increase in β1 that may reflect enhanced ECM anchoring and signaling. Analysis of cubilin expression revealed a significant increase in female HFD mice ($P = 0.0033$), while no significant change was observed in males, indicating a sex-specific response in tubular protein handling. This divergence suggests that, despite a common increase in integrin β1, downstream effects on albumin reabsorption may differ between sexes. Overall, these findings suggest that obesity induces early ECM remodeling through upregulation of integrin β1. Functionally, obesity enhanced cubilin-mediated albumin reabsorption in females. This highlights a potential sex-specific mechanism in obesity-associated CKD. Future studies will investigate the interplay between ECM signaling and cubilin mediated functions.

Acute effects of Thai yoga (Ruesi Dadton) on Cardiovascular and Metabolic Responses in Healthy Adults

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Thai yoga, also known as Ruesi Dadton, improves physical fitness including flexibility, muscular strength, and balance, yet its acute physiological effects remain largely unexplored. The purpose of this study was to examine the acute effects of a single 30-minute Thai yoga session on cardiovascular, metabolic, and postural control responses. Twenty healthy adults (10 males, 10 females; aged 18–35 years) participated in a 30-minute Thai yoga session consisting of 13 postures. Before and immediately after the session, we measured heart rate, capillary blood glucose, blood pressure, hydration-related metrics (via bioelectrical impedance), and balance (center of gravity [COG] sway velocities across four visual and surface conditions). We also continuously tracked oxygen consumption (VO_2) and metabolic equivalents (METs) during the practice to quantify exercise intensity. Data were analyzed using Wilcoxon signed-rank tests, Mann-Whitney U tests, and Spearman's rank-order correlations. The session elicited light-intensity physical activity (2.17 ± 0.33 METs) with no significant intensity differences between sexes. Post-intervention, participants showed a distinct drop in fasting blood glucose ($p = 0.012$, $r = 0.40$). Regarding hydration-related aspects, total body water decreased ($p \leq .05$), reflecting expected exercise-induced fluid loss, while blood pressure remained stable. Postural control improved remarkably. Sway velocities dropped significantly during eyes-closed conditions on both firm and foam surfaces ($p = 0.008$), driving better overall composite balance scores ($p = 0.010$). Interestingly, participants with higher baseline glucose levels experienced the sharpest glucose reductions ($rs= - 0.71$, $p \leq .0001$). The 30-minute Thai yoga practice offers an accessible, light-intensity workout that immediately engages glucose metabolism and sharpens proprioceptive balance. These acute physiological benefits suggest Thai yoga could be a potentially effective, low-barrier functional intervention for both metabolic health management and fall prevention programs.

You are What You Eat, Uses for Insects Fed on Waste Products

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The use of insects for cost effective bioremediation of waste products is of interest for the creation of a circular economy. However, safety concerns regarding insect-based feed continue to hinder the adoption of these practices. While the FDA mandates that human-grade insects be reared under strict sanitary conditions, livestock feed guidelines remain less defined. This regulatory gap has raised concerns over microbial contamination, heavy metal accumulation, and toxins, prompting a re-evaluation of safety standards for the entire industry.

Understanding the Differences Between Hydrosilylation VS Moisture-Cured Fluid-Containing Silicone Elastomers for Fouling and Ice-Release Applications

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The adhesion of foulants and contaminants to surfaces is a persistent challenge, particularly in marine environments, and can be mitigated using appropriately designed coatings. Over the years, poly(siloxane)-based elastomers have demonstrated outstanding fouling and ice-release performance due to their inherently low elastic modulus and low surface energy, which enable removal under relatively low applied stresses. To further enhance release performance, non-reactive silicone fluids are often incorporated into these elastomeric networks. However, the mechanisms by which oils interact with the elastomer and control release performance remain poorly understood. This study thus attempts to investigate oil-elastomer interactions using model silicone elastomers in which fluid interactions occur exclusively within the elastomer network. Moisture-cured and hydrosilylation-cured silicone elastomer coatings were prepared as model ice-release systems. Moisture-cured networks (1K/2K) were formed via ambient-moisture condensation using a tin catalyst and alkoxysilane crosslinkers, whereas hydrosilylation-cured networks were synthesized through Pt-catalyzed addition between vinyl- and hydride-functional siloxanes. In both systems, catalyst optimization yielded elastomers with gel content exceeding 95% across a controlled range of crosslink densities. From these complementary curing chemistries, representative silicone elastomer models were selected to assess fluid-elastomer compatibility. Different fluids were examined and the fluids and elastomers' solubility parameters (δ) were estimated through energy/tension measurements. Elastomers' crosslink density, as well as elastomers and fluids' calculated δ values, were injected into the Harper and Liu model to predict maximum swelling capability. This work highlighted a sharp difference in predictions capabilities as a function of the elastomers' curing mechanism. To explain this difference, we investigated the curing capabilities of each elastomer through crosslink-density monitoring in presence of fluid and highlighted a fluid-induced cure inhibition for one of these curing chemistries. When present on the surface, we investigated the link between fluid's surface coverage and curing extend, as well as surface oil composition. Finally, we investigated the impact of fluid addition on ice-release properties for both curing mechanisms. This work provides fundamental insights onto the effect of fluids on different elastomers and onto the mechanisms governing the release performances for these elastomers.

Deep Learning-Based in Situ Estimation of Surface Roughness in Light-Assisted 3D Printed Continuous Carbon Fiber Reinforced Composites

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Additive manufacturing of continuous carbon fiber–reinforced composites enables lightweight, high-stiffness, high-strength components that are difficult to fabricate conventionally. However, layer-by-layer deposition of resin and fiber makes the process vulnerable to resin flow disruptions, incomplete wet out, and filament misalignment, which generate interlayer roughness, disturb interlaminar stress distribution, and may propagate if unmitigated. Conventional roughness assessment is costly and slow because the specimen must be removed from the print bed and scanned with a surface profiler. Consequently, in situ roughness monitoring is essential for improving process efficiency, verifying layer to layer print quality, and ensuring void-free parts for optimal performance. This study develops a deep learning based model to predict surface defects in printed parts from laser scans of the specimen. The approach allows in situ monitoring of surface roughness during printing, providing real-time information without removing the specimen or performing post-printing profiling. To train the model, a custom three-axis printer is used to print continuous carbon fiber reinforced composite specimens with UV curable resin. Beads extruded through a nozzle positioned at a 90 degrees angle to the print bed are cured with the ultraviolet light. A scanner module is employed to scan the specimen after printing. A profiler is used to determine the actual surface roughness values of the printed layer that are then scaled and linked to the corresponding scanner-derived surface roughness data. A convolutional neural network based on ResNet-50 architecture is used as the base for extraction of the scanned surface data, and the final classifier layers of the ResNet-50 architecture are replaced with a regression head to output linear numerical sur-

Allium Vegetables: Sources of Antioxidants and Potential Antidiabetic Compounds

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Dietary phenolics contribute to the prevention of chronic diseases due to their antioxidant and antihyperglycemic properties. This study evaluated four cultivars within each of four *Allium* species (onion, shallot, green onion, and leek) to determine total soluble phenolic (TSP) content, antioxidant activity (DPPH and ABTS), and inhibition of carbohydrate-hydrolyzing enzymes (α-amylase and α-glucosidase), and to assess the effects of traditional cooking compared with raw consumption. TSP content did not differ significantly among cultivars or between raw and cooked samples in onion, shallot, and leek, whereas cooked green onion exhibited higher TSP than raw samples. Antioxidant activity varied among species and cultivars. In onion cultivars differed in DPPH and ABTS activity, with cooking having limited effect on DPPH but increased ABTS inhibition. In shallot, cultivar × cooking interactions influenced both DPPH and ABTS activities. Green onion cultivars differed in both assays, and cooking increased DPPH activity, but had limited effect on ABTS inhibition. In leek, cooking increased DPPH inhibition, while ABTS activity remained consistent among cultivars and treatments. Enzyme inhibition responses also varied. In onion, α-amylase inhibition increased significantly after cooking, whereas α-glucosidase inhibition differed among cultivars but was not affected by cooking. Shallot α-amylase inhibition showed no cultivar or cooking effects, while α-glucosidase inhibition was influenced by cultivar × cooking interactions. In green onion, α-amylase inhibition increased with cooking, whereas α-glucosidase inhibition remained consistent across cultivars and cooking. In leek, α-amylase inhibition was influenced by cultivar and cooking interaction, while cooked samples exhibited higher α-glucosidase inhibition than raw samples. Antioxidant activity showed a moderately strong positive correlation with TSP across most species, whereas associations between TSP and enzyme inhibition were generally weak, except for a moderate correlation with α-glucosidase inhibition in onion and green onion. Overall, these results demonstrate that both cultivar selection and cooking influence the functional properties of Allium vegetables. The observed antioxidant capacity and inhibition of carbohydrate-hydrolyzing enzymes support the potential role of Allium vegetables as dietary components contributing to the modulation of postprandial hyperglycemia and the prevention of chronic metabolic diseases.

Reducing the Data Bottleneck: Real-Time Annotation for Precision Agriculture

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Timely and accurate dataset annotation remains a critical bottleneck in deploying object detection models for precision agriculture, where rapid decision-making depends on large volumes of well-labeled field data. Conventional annotation workflows rely on offline, labor-intensive labeling of crop and weed images, slowing down experimentation and limiting responsiveness to dynamic field conditions such as weed emergence, pest outbreaks, or crop growth stages. To address this challenge, we introduce a real-time annotation framework that integrates YOLO-based detectors directly on agricultural edge devices, enabling immediate labeling during UAV or UGV scouting missions. The system is released as an open-source software package with both command-line and REST interfaces, supporting single- and multi-class mappings relevant to agricultural targets (e.g., weeds, pests, fruits, or diseases). It allows either automated or human-in-the-loop acceptance of detections and generates YOLO-format annotations, metadata logs, and training-ready datasets in real time, significantly reducing dataset preparation overhead in the field. To evaluate performance, we conducted a comparative study across three YOLO architectures (v5, v8, v12) under pretrained and scratch-based initializations, and in single- versus multi-class annotation settings. Statistical analysis of learning dynamics and accuracy metrics shows that pretrained and single-class configurations achieve faster convergence, higher robustness, and improved annotation throughput. The results validate real-time annotation as a practical strategy for accelerating dataset development in precision agriculture, enabling more adaptive, scalable, and high-quality model deployment for tasks such as weed detection, disease monitoring, and crop yield estimation.

Structure-Guided PROTAC Design Targeting COPZ1 in PDAC

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Proteolysis-targeting chimeras (PROTACs) are heterobifunctional molecules that induce selective protein degradation by recruiting an E3 ubiquitin ligase are highlighted. PROTACs form a ternary complex among the protein of interest bound to a ligand on one end, a middle linker, and an ER ligase at the other end, where the latter will trigger ubiquitination and proteasomal degradation when brought to proximity to a target protein. Once degradation is accomplished, the complex is released and can initiate additional catalytic cycles. This approach is a novel therapeutic strategy for multiple scenarios, most importantly for treatment-resistant malignant cells, as in pancreatic ductal adenocarcinoma (PDAC). COPZ1 is a protein involved in tumor cell survival and intracellular trafficking. Small-molecule inhibitors of COPZ1 were prepared and will be used as ligands for PROTAC design. These will be linked to E3 ligase binders, including CRBN and TRIM-59, an E3 ligase overexpressed in pancreatic cancer, to increase selectivity. To initiate this approach, in silico studies were performed such as the analysis of biomedical and genomic databases (PubMed, MDPI, GTEx Portal, and ELiAH), leading to the identification of TRIM59 as a promising E3 ligase candidate for PDAC-targeted PROTAC design. Thus far, this work has achieved several major in silico milestones. First, structural analysis of TRIM59 enabled the mapping and characterization of potential ligand-binding pockets, providing insight into its suitability as a recruitment scaffold in PROTAC systems. Second, molecular docking simulations between CRBN and COPZ1 were conducted to determine the spatial orientation and intermolecular distance required for effective ternary complex formation. These structural parameters informed the rational design of the chemical linker, a crucial component that ensures the stability and functionality of the COPZ1–PROTAC–E3 ligase complex. Additionally, the identification and characterization of TRIM59 binding pockets pave the way for subsequent virtual screening campaigns aimed at discovering novel ligands. Therefore, these computational findings establish a robust structural framework for the future chemical synthesis of CRBN-based PROTACs targeting COPZ1. This research contributes to the development of a new generation of highly selective therapeutic strategies designed to disrupt tumor survival mechanisms in pancreatic cancer.

Machine Learning-Based Prediction of NADES Anti-icing Properties for Advanced Coating Applications

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Ice formation and frost on solid surfaces pose significant challenges in both industrial and daily situations. Natural deep eutectic solvents (NADES) have recently come to attention as potential eco-friendly anti-icing agents in coatings. Herein, we present a method to predict the melting temperature of NADES to expedite the identification of acceptable NADES. In this regard, data-driven machine learning techniques have been employed to evaluate the melting temperatures (*Tm*) of NADES. This study analyzed an in-house dataset comprising 164 NADES compounds with measured *Tm* to develop a predictive model highlighting the structure-property relationships. The resulting dataset was refined through the incorporation of descriptor-based feature engineering. The combination of components and their mixing ratios for NADES was employed to provide customized mixture descriptors for machine learning modeling. A collection of mixture-based descriptors was generated from the initial descriptors of chemically different components of NADES. To identify the optimal model, various machine learning algorithms, including multiple linear regression (MLR), decision trees (DT), random forests (RF), and gradient boosting regression (GBR), were examined. As a result, a model containing a subset of six descriptors was built to accurately predict melting temperatures. The percentage of oxygen atoms and leverage-weighted autocorrelation were identified as significant features influencing the *Tm* values. The resulting ML/QSPR model demonstrated strong predictive capability, achieving correlation coefficients of $R2$=0.96 for the training set, $R2$=0.92 for the test set, and $R2$=0.81 for the calibration set, with an RMSE of 0.006 and MAE of 0.004 for the training set. In addition, the developed structure-property model was implemented to build a virtual library for further identifying suitable NADES with desired *Tm* values for anti-icing purposes.

Flower Microclimates and the Foraging Preference of a Solitary Bee

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Bee pollinators are influenced by multiple interacting factors when choosing flowers to forage on, such as flower color, shape, and odor. Differences in floral morphology can also alter the microclimates of flowers, potentially affecting insect behavior. Alfalfa (*Medicago sativa*) produces flowers of various colors including blue, purple, green, yellow, and white. While some bees prefer darker-colored alfalfa flowers, the underlying mechanisms remain unclear. We hypothesize that the alfalfa leafcutting bee, *Megachile rotundata*, may select flower microclimates associated with color and morphology. In field conditions, we measured internal temperature and humidity of alfalfa flowers. We subsequently conducted a foraging preference test using flower cuttings from the field. Our results revealed no differences between flower color and floral temperature or humidity but did find that overall, alfalfa flowers are 2.73 ± 0.14 °C cooler than ambient temperatures, while having a floral humidity 2.9% ± 0.44% higher than ambient humidity. In laboratory tests, bees visited intermediate-colored (yellow and green) flowers more frequently but spent more time foraging on darker-colored (blue and purple) flowers. This preference for longer visits to darker flowers may aid in thermal balance during flight. Future tests should investigate whether higher ambient temperatures might shift pollinator preference towards lighter-colored (green, yellow and white) flowers to further facilitate thermoregulation.

Impact of Tempering and Milling Method on Pigment Retention and Color of Durum Wheat Pasta

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Pasta color is a critical quality attribute that influences consumer perception and acceptance. Durum wheat contains a natural yellow pigment, carotenoids, which contribute to the yellow color of pasta. These pigments can degrade during processing due to enzymatic activity such as polyphenol oxidase (PPO) and peroxidase (POD) and can significantly affect the final color of pasta. Grain tempering and milling method plays a critical role in determining the end-product quality. Stone milling is a traditional method of grinding wheat that preserves the grain's nutrients and flavors by retaining the original proportions of the bran, germ, and endosperm. In contrast, roller milling removes the bran and germ and grinds the endosperm into a refined flour. The objective of this study was to evaluate the effects of grain tempering (12%, 14%, and 16% moisture) and milling method on pasta color characteristics and quality. Pasta was produced from stone-milled semi-refined flour (SRF), whole wheat flour (WWF), and roller-milled semolina, and analyzed for yellow pigment content, polyphenol oxidase (PPO) and peroxidase (POD) activity, as well as color parameters, including brightness(L*) and yellowness (b*) were measured using the CIE Lab* and Hunter color systems. Results showed that yellow pigment content decreased with increasing tempering moisture in both SRF and WWF, with SRF consistently exhibiting higher pigment levels than WWF. However, pasta pigment levels were substantially reduced compared to flour, indicating pigment degradation during processing. Brown pigment concentration consistently decreased as tempering moisture increased, remaining significantly more concentrated in whole wheat flour relative to the SRF and semolina samples. Enzymatic activity differed significantly by flour type. WWF showed higher PPO and POD activity compared to SRF, contributing to increased browning. In contrast, semolina showed the lowest enzyme activity. Color analysis showed that stone-milled WWF pasta had lower brightness (L*) and yellowness (b*) compared to SRF and semolina. Increasing tempering slightly reduced yellowness in WWF, while SRF showed improved brightness with higher tempering. Overall, higher tempering reduced pigment retention but also lowered enzymatic activity. These findings demonstrate the importance of optimizing tempering conditions and flour refinement to balance pigment retention for improved pasta color quality.

Brain-Targeted Delivery of Plasmid VGF Using Multifunctionalized Liposomes for Alzheimer's Disease

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Alzheimer's disease (AD) is a neurodegenerative disorder characterized by progressive cognitive decline and synaptic dysfunction. VGF, a neurotrophin-responsive protein involved in synaptic plasticity, is significantly reduced in AD brains, highlighting its potential as a therapeutic target. However, effective delivery of VGF across the blood–brain barrier (BBB) remains a major challenge. This study investigates triple-functionalized liposomes incorporating two targeting ligands (mannose and transferrin) and a cell-penetrating peptide (penetratin or tetanus toxin fragment C) to enhance BBB penetration and neuronal uptake. Nanoparticles were synthesized and characterized for particle size, polydispersity index (PDI), zeta potential, and plasmid encapsulation efficiency. Their in vitro biocompatibility, hemocompatibility, cellular uptake, and transfection efficiency were evaluated across multiple brain-derived cell lines. The therapeutic potential of nanoparticles encapsulating plasmid VGF was assessed in SH-SY5Y cells stably expressing APP-Swedish and MAPT (P301L) by measuring amyloid-beta (Aβ) and phosphorylated tau levels following treatment. Furthermore, biodistribution and transfection efficiency of triple-functionalized nanoparticles were evaluated in 3-month-old wild-type mice. The synthesized nanoparticles were below 200 nm in size, with PDIs under 0.3, positive zeta potentials, and plasmid VGF encapsulation efficiencies ranging from 85–95%. Triple-functionalized nanoparticles demonstrated enhanced cellular uptake and increased VGF expression in brain endothelial cells, primary astrocytes, and primary neurons, while remaining biocompatible at therapeutic concentrations. In SH-SY5Y APP-Swedish and SH-SY5Y MAPT (P301L) cells, treatment with triple-functionalized nanoparticles significantly reduced Aβ42 and phosphorylated tau levels. Ex vivo imaging revealed enhanced brain accumulation of these nanoparticles, and intravenous administration in 3-month-old mice resulted in significantly increased VGF expression compared with control formulations. Future studies will evaluate in vivo biocompatibility, organ toxicity, and VGF expression in both young (3-month-old) and aged (24-month-old) mice following intravenous and intranasal administration. Additionally, the therapeutic effects of nanoparticle-mediated VGF delivery on cognitive function and AD-related pathology, including Aβ and tau accumulation, will be investigated in Alzheimer's disease mouse models.

Weaving the Intangible

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Weaving the Intangible begins with the understanding that culture is both carried and transformed when people move. It can create a sense of grounding in new places, yet it may also fade into memory when shared spaces to sustain it are absent. In diaspora, the difference between traditions that are still practiced and those that exist mainly in memory influences how younger generations understand and carry their cultural identity. This project explores how architecture can act as a medium for cultural continuity by giving spatial form to intangible heritage. Using the Ethiopian community in Alexandria, VA as the primary focus, the research examines how everyday cultural practices can inform spatial experience. The aim is to create a cultural center where cultural practices can be experienced and shared in ways that help people remain connected to their identity.

Effect of Crystal Structure and Surface Stoichiometry on the Electronic Structure of CdSe

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Cadmium Selenide (CdSe), a II–VI semiconductor, has attracted broad interest for its potential in chemical and biochemical sensing, as well as photocatalytic reactions. In both applications, the activity and efficiency of these materials strongly depend on the properties of its exposed crystal facets, which control charge separation, carrier transport, catalytic reactivity, and the interaction with molecular adducts and environment. A detailed atomistic understanding of these properties is therefore essential for designing CdSe-based materials that combine sensitivity with stability. We computationally investigated the structural and electronic properties of the CdSe surfaces, focusing on two main questions. First, we compared the electronic properties of the two main polymorphs, Wurtzite and Zinc Blende, to clarify how surface structure influences electronic and optical responses, and thereby affects their photo-reactivity. Secondly, the influence of quantum confinement was explored by systematically varying the slab model thickness, ranging from a single monolayer to ten monolayers. This study systematically explores the relationship of the work function and band structure to the exposed miller indicies crystal faces cut through a variety of crystal planes, and crystal structure morphology. We investigate wurtzite and zinc blende surfaces with max miller indicies of one (100) (110) (111) terminated with both cadmium and selenium. Our study focuses particularly on the work function, a property that governs electron transfer at surfaces and is directly linked to sensing efficiency and photocatalytic activity. We have found that non-polar, stoichiometric surfaces indicate a diminishing effect of slab thickness on the work function, saturating at approximately ten monolayers. For polar surfaces, significant surface reconstruction effects were observed, particularly for structures of a few layers thick. Importantly, the calculated values of work functions fall within the experimental range, validating the modeling approach and strengthening the link between atomic-level structure and functional performance.

How Does RAGE in Melanoma Cells Affect the Population of T Cells in the Tumor Microenvironment?

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The receptor for advanced glycation end-products (RAGE) is a cell surface receptor that promotes melanoma cell proliferation, migration, and invasion as well as tumor growth, chemoresistance, and metastasis. The tumor microenvironment (TME) consists of blood vessels, signaling molecules, and immune cells (T cells, B cells, and macrophages), which surround cancerous tumors and promote growth and metastasis. The goal of this study was to determine if RAGE expression in melanoma cells affects the population of T cells in the TME. To reach our goal, we use a melanoma spheroid/immune cells co-culture model, which mimics the TME in melanoma cells. Two cell lines deriving from B16F10 murine melanoma cells were used to form the spheroids: the parental B16F10 RAGE (+), and the B16F10 RAGE (-), which was engineered using the CRISPR/Cas9 gene editing tool and lacks RAGE expression. Spheroids were formed from the melanoma cells in Nunclon Sphera 96U-bottom wells plates, using 250 cells/well in media supplemented with methylcellulose to promote cell aggregation. The spheroids were imaged daily and their diameters estimated using ImageJ analysis from brightfield microscopic images. The immune cells were obtained from spleens of immune competent C57BL6 mice. Immune cell staining for T cells (CD3+, CD4+, and CD8+) was performed before co-culturing with melanoma spheroids to obtain a baseline population of the T cells. Flow cytometry and data analysis were conducted using the Beckman Coulter CytoFlex S flow cytometer at the NDSU Biotech Innovation Core Lab. We initially investigated if the presence of splenocytes in the co-cultures affected the growth of RAGE expressing or RAGE knocked-out melanoma spheroids. Our current data shows no difference in spheroid growth rates in the presence or absence of splenocytes. We are currently investigating if the presence of RAGE in spheroids affects the population of T cells.

Joint Nonparametric Tests for Location and Scale Differences in Multiple Populations

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Nonparametric methods are useful when data do not meet parametric assumptions such as normality and equal variances. However, most existing tests examine location or scale differences separately, which may reduce effectiveness when both vary simultaneously. This study proposes new combined nonparametric tests to jointly assess location and scale differences across multiple populations. The methods integrate the Kruskal–Wallis test with scale components from Moses and Levene-type procedures, using mean, median, and trimmed mean measures for robustness. Simulation results show that the proposed tests maintain appropriate Type I error rates and achieve higher power when detecting scale or joint differences. Moses-based methods perform better for heavy-tailed data, while Levene-based methods are more stable across different distributions. Overall, these tests provide effective tools for joint nonparametric analysis.

Microbial Delivery and Timing Enhances Phyllosphere Colonization and Biocontrol Potential in Barley

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Harnessing beneficial microbes to protect crops requires more than selecting the right strains, it depends on understanding how, when, and where those microbes successfully establish on the plant. In this study, we developed a controlled barley system to test how different inoculation strategies influence the establishment of a defined synthetic microbial community. Barley seeds were sterilized and grown under controlled conditions, and microbes were introduced using three delivery approaches: seed soaking, leaf spraying, and head dipping. We also evaluated how the duration of leaf spraying affected colonization over time, with appropriate non-living and buffer controls to confirm microbial viability. Across all experiments, leaf spraying consistently resulted in the strongest microbial establishment, particularly in aerial tissues. Leaves and heads showed substantially higher colonization (40–60%) compared with roots. Extending leaf spray applications through the soft dough stage significantly improved colonization success. Importantly, live microbial communities consistently outperformed heat-killed controls, confirming active biological establishment rather than residual DNA detection. Prolonged leaf spraying enriched several genera commonly associated with plant health, including *Massilia*, *Sphingomonas*, *Pantoea*, and *Pseudomonas*, particularly in the grain head. Notably, this colonization strategy coincides with the critical susceptibility window for Fusarium Head Blight, suggesting strong potential for disease management. Together, our findings provide a reproducible framework for optimizing microbiome delivery strategies in cereal crops and advancing microbiome-based approaches for sustainable agriculture.

A Computer Vision Framework for Temporal Segmentation of Traffic Congestion Events

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Traffic congestion imposes substantial economic and environmental costs on urban areas world- wide, and its effective management requires not only recognizing that congestion is occurring but also identifying when it begins, how long it persists, and when it clears. This paper presents a comprehensive review of computer vision and deep learning methods relevant to the temporal segmentation of traffic congestion events from video. The review progresses from the visual feature extraction methods that underpin congestion analysis from image classification, vehicle detection and tracking, motion estimation, and density mapping to the temporal modeling architectures that operate on these features, including recurrent networks, temporal convolutional networks, and transformers. It then evaluates how techniques from adjacent fields, namely temporal action seg- mentation, video anomaly detection, spatio-temporal graph neural networks, and vision-language models, can be adapted to the congestion domain, while also addressing edge deployment con- straints and available datasets. A central finding is that while the individual components of a congestion segmentation pipeline have reached maturity, no unified framework exists for seg- menting continuous video into temporally bounded congestion events with well-defined onset and clearance boundaries, and no dedicated benchmark dataset supports this task. The review identifies this integration gap as an important direction for future research and outlines the methodological and data requirements for addressing it.

The Butterfly Effect: Cattle Grazing's Influence on Butterfly Populations

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Grazing, both domestic and wildlife, is the most dominant land use in grasslands and shapes plant community composition, including floral resources that pollinators depend on. Strategies that promote heterogenous landscapes are hypothesized to promote floral resources and associated pollinator populations, as opposed to traditional grazing strategies, which emphasize livestock production which is created using homogenous landscapes. In this study we compare the response of butterfly populations and floral resources to grazing strategies that aim to restore heterogeneity to rangelands. Our study included two treatments designed to restore heterogeneity, patch grazing with virtual fence technology (PG-VF) and patch-burn grazing (PBG) with early-season fire (late April-early May), and compared these approaches to season-long grazing (SLG), which acted as a reference for traditional grazing management. Our first year of data showed that community composition of butterflies ($p < 0.05$) and floral resources ($p < 0.05$) varied among grazing strategies but strategies that focused on increasing heterogeneity (PG-VF, PBG) promoted the highest species richness and abundance. We found increased richness for both PG-VF and PBG ($p < 0.001$) compared to SLG, and abundance was greater in PG-VF ($p < 0.001$) compared to PBG and SLG. Additionally, both floral species richness ($p < 0.001$) and abundance ($p < 0.01$) were greater in PG-VF and PBG compared to SLG. These preliminary results suggest that restoring heterogeneity to rangelands through novel grazing management strategies can promote pollinator populations and floral resources.

Beyond the Genetic Code: Identifying Core Resistance Signatures to Fusarium Head Blight in Wheat

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Fusarium Head Blight (FHB), commonly known as "wheat scab," is a devastating fungal disease that threatens the yield and quality of wheat across North Dakota and the globe. While some wheat varieties can naturally fight off the infection, the underlying genetic mechanisms remain complex and difficult to track. Our research aims to identify the specific "defense tools" or differentially expressed genes (DEGs) that allow resistant wheat to survive while others fail. Using high-resolution gene activity profiling (RNA-seq), we compared eight hard red spring wheat cultivars (Wheaton, ND2710, Alsen, Rollag, Steele-ND, Glenn, Sumai 3, and PI277012) over a two-year study. By grouping these varieties into Highly Resistant (HR), Moderately Resistant (MR), and Highly Susceptible (HS) categories, we isolated the "core" signatures of defense. Our analysis revealed a massive shared response of 9,531 genes activated by all varieties, which likely represent a basic, but often insufficient, stress reaction. More importantly, we pinpointed 438 "HR-unique" genes, which are high-priority candidates that are active only in the most resistant lines A key highlight of our study is the inconsistency of some cultivars, which showed strong resistance in one year but shifted behavior in the next. To understand this variability, we are examining known resistance markers like Fhb1 and Fhb5. Furthermore, we are overlaying methylation data to see if "epigenetic switches" are turning these defense genes on or off based on environmental conditions. This work, currently being validated through precision laboratory tests (RT-qPCR), provides a roadmap for breeders to develop more consistent, scab-resistant wheat varieties for North Dakota producers.

Geographically-Weighted Explainable AI Framework for Bus Crash Severity Prediction in Heterogeneous Transit Environments

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More than 15,000 large-bus crashes occur annually across the United States, yet the AI-powered safety tools now reshaping transit infrastructure continue to apply spatially uniform models, treating rural highway corridors and dense urban intersections as equivalent risk environments. As transit agencies pursue Vision Zero commitments, the gap between where crashes are predicted and where KSI events actually occur remains a critical and costly blind spot. This study introduces GWXGBoost, a Geographically-Weighted XGBoost classifier that adapts to local conditions by weighting nearby crashes more heavily at each prediction point, marking the first application of geographically-weighted ensemble learning to transit safety. Applied to 9,201 bus crash records from Minnesota Crash Mapping Analysis Tool 2 (MnCMAT2) form 2016–2025, the framework is validated via spatial block cross-validation to prevent geographic data leakage. GWXGBoost achieved a 57% improvement in KSI prediction (AUPRC = 0.277 vs. 0.177) over a global baseline. Interrupted time series analysis confirmed COVID-19 as a structural break (Chow F = 17.26, $p < 0.001$), revealing a persistent 61-crash-per-month reduction that has fundamentally reset the safety baseline Minnesota transit operators must plan against. Spatial analysis identified a 3.07× KSI rate differential across Minnesota's geographic regimes, with Central Minnesota emerging as a high-risk hot spot. TreeSHAP maps revealed that bus driver behavior drives KSI outcomes in rural outstate corridors, while bus-corridor speed governs Metro district risk, findings that demonstrate a single statewide safety training program misallocates resources. The framework's locally-interpretable, geographically-resolved risk maps provide transit agencies with auditable justification for safety resource allocation, directly reducing the institutional and legal exposure that accompanies opaque AI deployment in public infrastructure.

How Can We Solve Fargo's Problem with Alcoholism? A Lesson from American History! A Lesson from American History!

NASIH ALAM
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In my oral presentation, in the first minute I will discuss what alcoholism is, and how it has affected Fargo over the years. Then, in the next couple of minutes, I will show how Fargo has been rocketed with problems of alcoholism since the late 19th century. While reflecting on the past events against alcoholism in Fargo, from minutes 4-6, I will highlight the role played by Elizabeth Preston Anderson, founder president, Women's Christian Temperance Association (WCTU, North Dakota). In the 7th minute, I will shed light on three major highlights from Anderson's campaigns against Alcohol Problems in Fargo. In the last minute, I will share three solutions to reduce the problems of alcoholism in Fargo. I would like to take the opportunity to present my ideas in short sentences and simple English.

RAGE inhibition sensitizes BRAF mutant melanoma cells to vemurafenib

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Background: BRAF mutations are present in over half of melanoma tumors, making vemurafenib a targeted treatment option for these patients. However, resistance to vemurafenib often develops within 7 months of treatment. Cytotoxic treatments can trigger the release of RAGE ligands, including HMGB1, from melanoma cells. These ligands interact with the receptor for advanced glycation end products (RAGE) on surrounding cells in the tumor microenvironment, activating STAT3, PI3K/AKT signaling, and autophagy, which contribute to drug resistance. We hypothesize that blocking the interaction of RAGE with its ligands enhances the sensitivity of melanoma cells to vemurafenib by reducing cell proliferation, autophagy, and signaling pathways regulated by PI3K/AKT and STAT3. Method: We investigated the synergistic effects of vemurafenib in combination with the RAGE inhibitor FPS-ZM1 in the WM115 human melanoma cell line using the Combenefit software. Cell viability was assessed using resazurin salt, cellular toxicity using CellTox-DNA-binding dye, and proliferation using Ki-67 expression by immunofluorescence staining. AKT and STAT3 signaling were analyzed by Western blot, while the level of HMGB1 and autophagic flux is under investigation. Result and conclusion: Our data demonstrate that inhibition of RAGE significantly reduces the viability of WM115 cells and proliferation under vemurafenib treatment, enhancing the overall synergistic effect and efficacy. Treatment with vemurafenib increased the cell death. Since dead cells can release HMGB1, our next goal is to determine the level of HMGB1 in cells. While vemurafenib effectively reduced the MAPK/ERK pathway, it concurrently increased AKT phosphorylation, which may contribute to reduced drug sensitivity in this cell line. Notably, co-treatment with the RAGE inhibitor FPS-ZM1 reduced the phosphorylation of AKT and further decreased STAT3 activation. Collectively, these findings suggest that RAGE inhibition sensitizes melanoma cells to vemurafenib by decreasing activation of the AKT and STAT3 signaling pathways. Currently, we are investigating whether the HMGB/RAGE axis facilitates the autophagy-induced vemurafenib resistance.

Automated Phenotyping to Identify Sclerotinia Basal Stalk Rot in Sunflower

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Basal stalk rot (BSR), caused by *Sclerotinia sclerotiorum*, is a major constraint to sunflower production and breeding efforts. Greenhouse-based screening for BSR resistance is often limited by labor-intensive and subjective visual assessments of wilting and plant mortality. To address these limitations, an automated phenotyping workflow was developed in 2025 to enable objective, high-throughput disease assessment. A gantry-mounted RGB imaging system was implemented to capture time-series images of inoculated sunflower plants over a 28-day period post-inoculation. Images were systematically organized by time point and used to train a YOLOv12-based object detection model for automated identification of BSR symptoms. The optimized model achieved approximately 90% detection accuracy, enabling consistent symptom detection and quantitative tracking of disease progression. Model performance declined under conditions of significant leaf overlap across adjacent tray cells, and the current pipeline is limited to single-genotype trays. Ongoing work focuses on expanding validation across diverse sunflower genotypes and improving model robustness to support scalable, reproducible BSR resistance screening for sunflower breeding programs.

Impact of Altering Maternal Gut Microbiota through Feeding Limited High-Forage and High-Concentrate Diets on Offspring Microbiome Development in Beef Cattle

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Maternal gut microbiota plays a critical role in shaping immune, metabolic, and developmental programming of offspring beginning at early embryonic stages, making it a central component of the Developmental Origins of Health and Disease (DOHaD) concept. Increasing evidence from human and animal studies, including cattle, suggests that manipulating the maternal microbiome during gestation may improve offspring health, productivity, and developmental outcomes. The present study evaluated the effect of maternal diet on microbiome composition in beef heifers and the subsequent microbial development of their calves. A total of 119 beef heifers were assigned to high-forage (HF) or high-concentrate (HC) diets during gestation. The HF diet contained 75% forage and 25% concentrate, whereas the HC diet consisted of 75% concentrate and 25% forage. Diets were provided from pre-breeding until calving, and all heifers were bred using male-sexed semen from a single sire. Animals were managed to achieve targeted weight gain throughout gestation, and individual feed intake and behavior were recorded. Microbial samples, including ruminal fluid, vaginal swabs, and deep nasopharyngeal swabs, were collected from dams at multiple time points from pre-breeding through postpartum. Steer calves born to these dams were monitored for growth performance and microbial development, with ruminal and fecal samples collected from birth through 372 days of age. Bacterial communities were analyzed using 16S rRNA gene sequencing (V3–V4 region). Maternal diet significantly influenced ruminal, fecal, vaginal, and nasopharyngeal microbiota throughout gestation (PERMANOVA, $P < 0.001$), with HF-fed heifers showing greater microbial richness in gastrointestinal samples. Differential abundance analysis identified diet-associated genera in ruminal communities, including Xylanibacter, Rikenellaceae RC9 gut group, Christensenellaceae R-7 group, and Prevotellaceae UCG-001, while fecal microbiota were dominated by Oscillospiraceae UCG-005, Bacteroides, and Alistipes, taxa associated with fiber degradation and short-chain fatty acid production. Calves born to HF and HC dams exhibited significant differences in ruminal microbiota during early life, indicating transgenerational effects of maternal nutrition. These results demonstrate that maternal diet during gestation influences offspring microbial succession, with potential implications for feed efficiency, rumen function, and long-term animal performance.

The Economic Impact of Roundabout Installations on Nearby Businesses: Evidence from Minnesota

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Roundabouts are increasingly adopted across the United States as a safer and more efficient alternative to traditional signalized intersections. However, having these safety and operational benefits, proposed roundabout projects frequently face opposition from nearby business owners and local stakeholders who fear that changes in traffic patterns, reduced vehicle speeds, limited turning movements, and temporary construction disruptions may reduce customer accessibility and negatively affect local economic activity. Concerns about potential revenue losses can influence public opinion and delay or prevent the implementation of intersection improvements. Despite these concerns, rigorous causal evidence on the local business impacts of roundabout conversions remains limited, with much of the existing literature relying on descriptive case studies or short-term observational analyses. This study evaluates the economic impact of roundabout installations on nearby business revenues in the state of Minnesota using a staggered difference-in-differences framework that accounts for heterogeneous treatment timing and dynamic adjustment patterns. Leveraging a longitudinal dataset of establishment-level revenue records covering the period 1997–2024, we employ the Callaway–Sant'Anna difference-in-difference (CSDID) estimator to compare businesses located within 0.5 miles of newly installed roundabouts as the treated group and businesses located between 1 and 3 miles from the same intersections as the control group. Event-study analyses show no statistically significant revenue effects following roundabout installation. Results are consistent across small, medium, and large businesses. Overall, the findings suggest that roundabouts do not impose economically meaningful harm on nearby businesses over the short to medium run. These results offer important implications for transportation planners and policymakers by addressing a common source of community resistance and supporting the continued use of roundabouts as a safety-enhancing, and economically neutral intersection design.

Evaluating the Impact of Population Structure on Genomic Selection Across Market Classes in Dry Bean (*Phaseolus vulgaris* L.)

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Genomic selection (GS) has the potential to accelerate genetic gain in dry bean (*Phaseolus vulgaris* L.) breeding programs; however, its effectiveness may be influenced by pronounced population structure associated with diverse market classes and major gene pools. Germplasm within the North Dakota State University (NDSU) dry bean breeding program is structured across seven market classes and two major genetic gene pools, Andean and Mesoamerican, with additional differentiation within the Mesoamerican gene pool corresponding to Durango and Jalisco race types. This hierarchical genetic structure may influence genomic prediction accuracy and the transferability of marker effects across breeding targets. This study aims to evaluate whether explicitly accounting for population structure improves genomic selection performance in a structured dry bean breeding population. Genome-wide marker data generated from an approximately 3.8K trait-based SNP chip will be used to characterize genetic structure and relatedness among breeding lines. Genomic prediction will be conducted for key agronomic and phenological traits including seed yield, seed weight, days to maturity, plant height, among others. Principal component analysis and clustering approaches will be used to quantify differentiation among gene pools and market classes. Both parametric and nonparametric genomic prediction models will be evaluated. Parametric models will include genomic best linear unbiased prediction (GBLUP) and ridge regression BLUP (rrBLUP), while nonparametric approaches will include reproducing kernel Hilbert space (RKHS) regression. Models will be implemented under multiple scenarios, including pooled analyses across all lines, pooled models incorporating principal components as fixed effects, and stratified models fit within gene pools and market classes. Prediction ability will be assessed using repeated cross-validation schemes designed to reflect realistic breeding decisions, including both within-market-class prediction and prediction across genetically structured subpopulations. This research will determine whether modeling population structure improves genomic prediction accuracy, reduces bias in marker effect estimation, and enhances the utility of genomic selection for parent selection and line advancement in dry bean breeding. Results will provide practical guidance for implementing genomic selection in structured breeding programs and contribute to improved breeding efficiency and genetic gain in dry beans.

Passive UHF RFID Temperature Sensing Using a Thermal Expansion-Based Dipole Resonator

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A passive ultra-high-frequency (UHF) radio frequency identification (RFID) temperature sensor based on a zinc-molybdenum (Zn-Mo) integrated dipole resonator is presented in this study. The proposed sensor uses geometry deformation to provide intrinsic temperature readings by taking advantage of the difference in thermal expansion coefficients between molybdenum and zinc. Measurable variations in impedance and reflection coefficient throughout the UHF band are caused by the bimetallic resonator's uneven expansion, which modifies its effective electrical length as temperature changes. To ensure effective RF power transfer and dependable chip activation, the resonator is made to match the near-conjugate impedance of a commercial RFID chip at 915 MHz. The temperature-dependent behavior of the sensor is examined using coupled electromagnetic and thermal-mechanical simulations spanning a temperature range of 273 K to 773 K. The results demonstrate a robust and repeatable variation in S-parameters and input impedance with temperature, confirming the sensing capability of the proposed structure. The sensor remains fully passive, low-cost, and compatible with standard UHF RFID readers, making it suitable for applications such as cold-chain monitoring, food logistics, pharmaceutical storage, and environmental sensing where scalable and low-power temperature tracking is required.

Intranasal Spray as a Treatment for Alzheimer's Disease

MATHEUS BELIN

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Alzheimer's disease (AD) affects more than 55 million people worldwide and imposes an economic burden exceeding $1 trillion annually. It is characterized by amyloid beta (Aβ) accumulation, tau pathology, neuroinflammation, and cognitive decline. Apolipoprotein E2 (ApoE2) has been shown to reduce these disease-associated features; however, its effective delivery to the brain remains a major challenge due to the blood–brain barrier. We developed an intranasal spray containing layered double hydroxide (LDH) nanoparticles for brain delivery of the pApoE2 gene. Magnesium aluminum chloride (MgAlCl-LDH) nanoparticles were synthesized by co-precipitation and dual-functionalized with mannose (Man) and penetratin (Pen) to enhance brain targeting and cellular uptake. LDH exhibited a positive surface charge (25–35 mV), enabling efficient binding, encapsulation (>85%), and protection of negatively charged DNA. Their nanoscale size (< 200 nm) facilitates cellular internalization and transport across biological barriers. In vitro studies in brain endothelial cells, primary astrocytes, and neurons demonstrated high biocompatibility, efficient cellular uptake, and successful gene delivery using both pGFP and pApoE2. LDH-Man-Pen enhanced uptake and gene expression ($p < 0.001$). In neuronal models expressing AD-associated mutations (MAPT^P301L and APPSwe), LDH-Man-Pen/pApoE2 reduced Aβ and tau levels ($p < 0.001$). In vivo studies (n=6/group, IACUC20250074) demonstrated that intranasal administration enabled effective brain delivery. While non-functionalized LDH did not significantly increase ApoE2 expression, LDH-Man-Pen markedly enhanced ApoE2 levels in the brain ($p < 0.001$). Biodistribution studies confirmed improved brain targeting, and safety was validated through hemolysis assays, serum biomarkers (AST, ALT, creatinine, troponin), and histological analysis of major organs. No significant systemic toxicity or pro-inflammatory response was observed. Therapeutic efficacy was evaluated in disease models. In 6-month-old 5xFAD and PS19 mice, LDH-Man-Pen/pApoE2 reduced Aβ and tau levels, respectively, while improving cognitive performance (Y-maze spontaneous alternation and total arm entries) and increasing synaptic markers (synaptophysin and PSD-95) ($p < 0.001$). In 24-month-old wild-type mice, treatment reduced pro-inflammatory cytokines (TNF-α, IL-6, IL-1β), particularly in the brain, and improved synaptic integrity. This study demonstrates that an intranasal spray increases brain ApoE2 levels, improves brain function, and reduces key features of Alzheimer's disease. This approach offers a safe, non-invasive strategy to overcome major barriers in brain-targeted therapy and advance treatment of the disease.

North Central Agriculture Producers' Perceptions of Clean Energy Tractors

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To ensure the sustainability of agriculture, research and investment in clean energy technology. are growing. To ensure investment in technology is matched by producers' willingness to adopt it, it is necessary to understand agricultural producers' perceptions of clean-energy tractors. Using an exploratory, qualitative approach, interviews were conducted with 17 agricultural producers to understand their perceptions of clean-energy tractors. Guided by Rogers' Diffusion of Innovation Theory (2003), the data were analyzed and aligned with the theory's components. It was found that producers in the North Central United States do not see a relative advantage in adopting clean-energy tractors at present. They view the technology as complex and incompatible with their operations. The findings of this study should guide future investment in clean-energy technology, as well as help industry navigate the rollout of new technology with producers.

Improving Corn Production Under Acidic and Drought-Stressed No-Till Soils Using Integrated Soil Amendments

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Abstract Dryland corn production is expanding in western North Dakota due to early-maturing hybrids and widespread adoption of no-till systems. Although no-till improves soil conservation and long-term soil structure, prolonged use of ammonium-based fertilizers without soil mixing can accelerate surface soil acidification. Corn (*Zea mays* L.) is moderately sensitive to low soil pH, and acidic conditions may restrict nutrient uptake and root development, intensifying drought stress in semi-arid environments. Baseline soil analysis (0–6 in) at the study site confirmed moderately acidic conditions (pH 5.3), emphasizing the need for management strategies that address both soil acidity and water stress.A field experiment was conducted during the 2025 growing season at the Dickinson Research Extension Center under dryland conditions (mean annual precipitation ≈396 mm). Corn was planted in early May, and eight treatments were arranged in a randomized complete block design with four replications: Control, Lime, Biochar, AMF, Lime+Biochar, Lime+AMF, AMF+Biochar, and Lime+AMF+Biochar. Relative Leaf Water Content (RLWC) was measured at 93 Days After Planting (DAP), corresponding to late vegetative growth, while Leaf Area Index (LAI) and grain yield (adjusted to 15.5% moisture) were determined at 124 DAP near physiological maturity. Soil moisture (0–6 in) was also evaluated. Data were analyzed using ANOVA with mean separation by Fisher's LSD ($\alpha = 0.05$). Grain yield differed significantly among treatments ($P < 0.05$). The Lime+AMF+Biochar treatment produced the highest yield (142.6 bu ac^{-1}), approximately 6% greater than the control (134.6 bu ac^{-1}), and significantly higher than Lime+Biochar and AMF+Biochar. Surface soil moisture did not differ among treatments ($P = 0.69$), although block effects were significant ($P < 0.001$). In contrast, RLWC and LAI were significantly influenced by treatment ($P < 0.05$), with Lime+AMF recording the highest RLWC (96.2%) and AMF producing the greatest LAI (0.62). Overall, the findings indicate that no single amendment works best in isolation; instead, combining strategies appears essential for improving productivity in acidic, moisture-limited no-till systems.

Picasso with Pixels: How Computers Create Beautiful and Realistic Scenes

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The use of ray tracing in computer graphics to simulate realistic lighting pushes the limits of modern hardware to render photorealistic, computationally expensive scenes. While previously considered computationally infeasible, recent hardware advancements have prompted the capability to render high-quality, dynamic scenes in near-real time. This paper overviews the fundamental implementation of a path tracer and explores the optimization of light source representations within a Monte Carlo framework. We introduce a Gaussian volumetric lighting model that treats lights as 3D probability distributions and performs comparative analysis against traditional disk proxy models. Our research evaluates the utility of these models through the comparison of visual variance (noise), computational efficiency, and robustness across diverse scene and lighting configurations. Specifically, we examine the interaction of these light models with specular and fuzzy-metallic surfaces. Further, we illustrate the efficacy of Importance Sampling over uniform distributions. We derive specific Probability Density Functions for Gaussian volumes and showcase how targeted sampling can achieve low-variance images with significantly fewer samples than naive uniform methods. The results of this study underscore the inherent trade-offs between photo-like accuracy and computation speed, and they serve as a guide to navigating the ideal balance between image fidelity and rendering performance.

Empirical Validation of Keystone Taxa in Salinity-Stressed Synthetic Communities Reveal Genetic Drivers of Keystoneness

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Keystone taxa play a central role in influencing community structure and functions, yet experimentally validating keystoneness in microbial communities remain a major challenge. Although co-occurrence network inference can help identify putative keystones, distinguishing ecological keystone taxa from spurious correlations require mechanistic validation. Here, we combined synthetic community (SynCom)-based experiments with multi omics approaches to mechanistically validate keystone taxa and investigate their genomic and functional drivers. We initially assembled an 82-member SynCom from highly saline (10 dS/M) soils collected from Langdon Research and Extension Center, North Dakota, USA and used network analysis to identify candidate keystones across salinity gradients. Thereafter, to evaluate causal roles, we assembled a reduced 20-member SynCom containing three species-resolved putative keystones (*Arthrobacter oryzae, Rossellomorea marisflavi, Sphingobium xenophagum*) that overlapped between SynCom and field-soil networks, and generated targeted dropout communities lacking individual or combined keystone taxa. Whole genome sequencing of all three taxa and RNA-Seq profiling of *Arthrobacter oryzae* under varying salinity were also performed. Network connectivity declined significantly when all three were dropped out, and individual dropouts pointed *Arthrobacter* as the primary keystone. Genomic profiles of the keystones were abundant in disordered protein regions and regulation pathways, indicating a high degree of metabolic plasticity. RNA-Seq data of *Arthrobacter* indicated global metabolic streamlining, with salinity-induced upregulation of membrane proteins, chaperones, ATP synthesis and translation apparatus, and downregulation of non-essential housekeeping functions. Together, these findings provide a reproducible framework for species-level mechanistic validation of keystone taxa and highlights their disproportionate governance over SynCom resilience, with implications for microbiome engineering.

Decoding Human Response to Flood Warning Cues Through Immersive Virtual Reality

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Floods are among the most frequent and destructive natural disasters, posing significant threats to lives, infrastructure, and communities worldwide. Understanding how individuals perceive and respond to disaster warning cues is critical for improving public preparedness and emergency communication strategies. This study investigates how different combinations of flood-related cues influence risk perception and evacuation decision-making. Specifically, three categories of warning cues were examined: environmental cues (visible floodwater intrusion), auditory cues (emergency sirens), and informational cues in the form of Wireless Emergency Alerts (WEA) and Integrated Public Alert and Warning System (IPAWS)–style messages. An immersive virtual reality (VR) environment was used to simulate realistic flood scenarios in a safe and controlled experimental setting. Fourteen participants familiar with the Fargo Downtown area experienced eight systematically designed flood scenarios, each representing a unique combination of cues. After each scenario, participants evaluated perceived severity, personal vulnerability, protective intentions, and evacuation likelihood using visual analog scales and indicated whether they would evacuate immediately. Results revealed that visual water cues had the strongest influence on participant perception and decision-making compared to sirens or alerts alone. Scenarios combining visible water with sirens or alerts produced the highest evacuation agreement rates, with up to 93% of participants choosing immediate evacuation. These findings highlight the critical role of visible environmental cues in motivating protective action during flood emergencies. The results suggest that emergency communication systems can be strengthened by integrating visual risk information, such as animated flood maps, augmented reality–based flood projections, and live camera feeds of flood-prone locations, alongside traditional auditory and informational alerts.

Fate of 15N-Labeled Urea Applied In-Season for Corn in Eastern North Dakota

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Nitrogen (N) fertilizers represent a major investment for North Dakota cropping systems as evidenced by the 890,000 tons of N used by producers in 2024 alone. If these inputs are to be beneficial to the producer and not harmful to the environment, they must be managed efficiently. To evaluate the efficacy of split-N applications, 15N-labeled fertilizer was applied to three different soil types in eastern North Dakota, including an irrigated sand, a smectite rich clay, and clay loam developed on glacial till above a marine bedrock unit of shale. Treatments included a single application of 140 lbs ac-1 broadcasted at planting and two treatments with 30% applied at planting and 70% applied in-season as a surface dribble, where the entirety of one treatment (Split-15N) is 15N-labeled and only the first application of another treatment is 15N-labeled (Split-1st15N). Plant tissue was dried, ground and analyzed for total N content and atom % 15N to determine the portion of applied fertilizer taken up by the crop. Preliminary data shows no significant difference in N concentration or dry matter production between treatment, though there were significant differences between sites. Isotopic data shows an increase in fertilizer 15N uptake efficiency from a split application for both corn grain and stover, and that in season applications were more effective for crop uptake at all three locations. This data also shows that a significant portion of the N taken up by plants comes from the soil, but in cases of split application, a higher proportion of N take up comes from fertilizer.

VIP Deficient Mice are Resistant to Diet-Induced Obesity (DIO)

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Obesity is a chronic disease with a rapidly increasing prevalence. Currently, more than 42% of adults are affected by obesity, and this rate is projected to increase to approximately 50% by 2050. Vasoactive intestinal peptide (VIP) is a 28 amino acid gut hormone involved in regulating appetite and energy homeostasis . Notably, the amino acid sequence of VIP is 100% identical across most mammals, including humans, rodents, and livestock, highlighting its important physiological role. Glucagon-like peptide-1 (GLP-1), a related peptide within the secretin/glucagon superfamily, is widely used to treat obesity and diabetes. Given the rapidly increasing prevalence of obesity, identifying additional pathways that regulate energy balance is of significant interest. Our laboratory has observed that VIP knockout (KO) mice exhibit gut microbiota dysbiosis similar to that reported in inflammatory bowel disease mouse models and appear noticeably leaner than their wild-type (WT) littermates. Based on these observations, we hypothesized that VIP-deficient mice would be resistant to diet-induced obesity (DIO). To test this hypothesis, male and female VIP WT, heterozygous (HET), and KO mice ($n \leq 5$ per group) were fed either a low-fat or high-fat diet ad libitum for 12 weeks. Food intake, water consumption, and body weight were monitored weekly. At week 17, blood, tissue samples (liver, kidney, and jejunum), and fecal samples were collected for further analysis. VIP KO mice were highly resistant to diet-induced obesity, gaining only ≈40% of the body weight observed in WT mice ($p \leq 0.0001$). Furthermore, 16SrRNA sequencing of fecal samples revealed significant differences in bacterial richness in KO mice compared to WT mice, independent of sex. Bacterial abundance also increased under the high-fat diet in a genotype-independent manner. Together, these findings suggest that VIP signaling is an unexpected regulator of metabolic homeostasis and may represent a novel therapeutic target for obesity and metabolic disease.

Evaluating Rust Severity in Dry Beans: A Comparison of High-Throughput Phenotyping and Traditional Scoring for GWAS

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The NDSU breeding program continues to focus on improving yield and disease resistance in dry beans (*Phaseolus vulgaris* L.). Besides field trials, lines are tested in greenhouse screenings for diseases like common bean rust (*Uromyces appendiculatus*). Visual assessment remains the standard for measuring disease severity and differentiating resistant and susceptible lines; however, genotypes with intermediate resistance are more challenging to score consistently. Therefore, this study evaluated whether a greenhouse high-throughput phenotyping platform using imaging, image segmentation, and deep learning could detect disease severity patterns similar to those from visual scoring. The study also examined whether this imaging method could identify the same genomic regions as the traditional visual approach in genome-wide association studies (GWAS). A panel of 355 genotypes, including preliminary and advanced yield-trial lines, germplasm lines, and cultivars, was tested in an augmented design with replicated checks. Plants were inoculated in the greenhouse with urediniospores of *Uromyces appendiculatus* race 20-3, following the protocol described by Erfatpour et al. (2025). Disease severity was assessed through RGB imaging and a conventional 1–9 visual scoring scale (Schoonhoven and Pastor-Corrales, 1987). Data were analyzed using both a nine-category scale and a simpler three-category grouping. The relationship between traditional visual scoring and high-throughput phenotyping was evaluated with correlation analysis, mean absolute error (MAE), and root mean square error (RMSE). Genome-wide association analyses employed GEMMA (GLM and MLM) and the GAPIT model to identify loci associated with resistance. The imaging platform showed a strong positive correlation with visual scores on the nine-class scale ($r = 0.791$) and captured a broader range of phenotypic variation. Reducing data to a three-class scale simplified classification while maintaining high effectiveness for breeding, enabling quick identification and removal of susceptible genotypes. GWAS using both visual and imaging data consistently identified a major signal on chromosome 11 corresponding to the Ur-11 resistance locus, while a possible signal on chromosome 1 needs further investigation. The consistent signals across methods show that the imaging platform can reliably identify the genetic basis of rust resistance.

How Do Grapevines Withstand North Dakota's Challenging Winters?

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Cold temperature injury is a major constraint in grape production and accounts for substantial economic losses across the United States. In cold regions such as North Dakota, midwinter cold hardiness is essential for vine survival. However, climate change is altering temperature patterns and advancing bud break timing, increasing the risk of frost injury even in regions not traditionally considered cold-limited. As seasonal temperature fluctuations become more frequent, understanding both midwinter hardiness and deacclimation behavior is critical for sustainable vineyard management. This research examines cold hardiness and bud break phenology in interspecific grapevine populations to better understand how genetic background influences winter survival and frost susceptibility. In addition to advancing fundamental knowledge, collecting bud break phenology data provides practical value for growers by identifying genotypes that deacclimate earlier and are therefore more vulnerable to late spring frost. Such information can guide cultivar selection, pruning timing, and other cultural management decisions, directly supporting agronomic decision making under variable climatic conditions. Bud cold hardiness was quantified using differential thermal analysis, and genotypes were assigned to five cold-hardiness classes based on relative lethal temperature thresholds. Bud break timing and developmental progression were characterized using the BBCH scale to quantify deacclimation patterns under divergent environmental cues. Substantial variation in midwinter hardiness and deacclimation timing was observed among genotypes. Importantly, vines that were highly cold hardy in midwinter were not always those most resistant to spring frost, underscoring the need to evaluate both traits together. This foundational study supports cultivar development and agronomic decision making aimed at improving resilience and sustainability under increasing climate variability.

Natural Antagonism: A Potential Tool for Managing Root Rot in Pulses

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Root rot is one of the most destructive diseases of pulse crops worldwide. It is caused by a combination of fungi, oomycetes, and bacteria. In the Northern Great Plains, *Fusarium* spp. are the predominant members of the root-rot disease complex. Preliminary studies on Fusarium spp. infecting lentil indicated that instead of forming a virulent disease complex, some *Fusarium* species inhibit each other when co-inoculated. To investigate whether we are able to find similar competitive interactions for *Fusarium* spp. infecting chickpea, we collected a total of 94 Fusarium species, that belonged to 6 different species, namely *Fusarium oxysporum, Fusarium solani, Fusarium acuminatum, Fusarium equiseti, Fusarium redolens*, and *Fusarium avenaceum*, from field surveys in 2022 and 2023. Since *F. equiseti* has been previously reported to be weakly or non-pathogenic on chickpea, it was not included in the greenhouse pathogenicity tests. Representative isolates of the remaining five species, *F. oxysporum, F. solani, F. acuminatum, F. redolens,* and *F. avenaceum* were tested in single- species inoculations and 26 different multi-species combinations (10 two-species, 10 three-species, 5 four-species and 1 five-species combinations), to assess their virulence potential on chickpea. While single species inoculations and most multi-species inoculations were highly virulent, three out of ten possible two-species combinations showed a reduced level of virulence when compared to virulence potential of the corresponding single strain inoculations. We are currently introducing different fluorescence markers to the *Fusarium* strains that are members of the combinations that displayed the lowest as well as highest virulence potential and we will use quantitative PCR assays to quantify the relative biomass of each strain during co-infection. Understanding the dynamics of these interactions will provide insight into how *Fusarium* species form and act as disease complexes and may ultimately guide biocontrol strategies that exploit natural antagonism among strains to reduce root rot severity.

Photochemical Fate of Painting Materials on Solid Surface using Far-UVC (222 nm) and UVC (254 nm)

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Far-UVC (222 nm) irradiation is increasingly used for microbial control, yet its potential to transform surface-bound organic additives is poorly constrained, leaving a significant research gap. This study investigates the effects of far-UVC irradiation (222 and 254 nm) on organic additives (biocides and phthalates) as thin films on quartz and evaluates matrix effects in two paint binders (wall and furniture paints) using isoproturon and diethyl phthalate (DEP) applied either as a surface mixture or as a surface deposit on cured surfaces. On quartz, 222 nm increased normalized photolysis rate constants (k, cm2 mJ-1) for all compounds, with UV222/UV254 ratios of 1.24–5.51-fold for biocides and 1.55–6.52 for phthalates (e.g., diuron: 8.64×10-4→1.57×10-4; di n butyl phthalate: 2.30×10-3→3.72×10-4 at 222→254 nm). Parallelly, aqueous experiments were conducted to determine photolysis rate, molar absorptivity (ε), and apparent quantum yield (Φ). In water, larger ε and Φ at 222 nm often coincided with faster decay (e.g., carbendazim showed ε222=20863 M-1cm-1 and Φ222=0.01498 versus ε254=11086 and Φ254=0.00234, paralleling k increases (1.05×10-3→1.29×10-4)). Additionally, observed higher ε and Φ at 222 nm in water might also explain the reason why we observed faster decay of selected compounds at 222 nm in the solid surface. Paint binders preserved the advantage of 222 nm but showed matrix dependence. In wall paint, isoproturon exhibited 2.04- and 1.43-fold enhancement for the mixture and deposit, respectively, while DEP showed 1.87- and 2.36-fold enhancement. Similarly, furniture paint showed 1.71- and 1.91-fold enhancement for isoproturon and 2.75- and 1.65-fold enhancement for DEP in mixture and deposit conditions, respectively. Overall, Far-UVC (222 nm) shows promise for air disinfection; however, results indicate that it can accelerate the photochemical degradation of paint additives, underscoring the need to account for material stability and potential by-product formation in indoor environments.

Assessing Reliability of Soybean Yield Stability Metrics in the U.S. Central–North Region

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The statistical analysis of Genotype x environment interactions (GEI) is closely linked with quantitative estimations of yield stability, a key target in soybean breeding programs. Numerous stability metrics have been proposed to quantify yield stability across environments. However, the minimum number of years needed to obtain consistent temporal stability for selection decisions remains unclear. We aimed to (i) identify how many years of multi-environmental trial (MET) data are required for reproducible and consistent temporal yield stability and (ii) compare four commonly used stability parameters. We analyzed soybean MET data from the private seed company GDM, comprising 18 genotypes evaluated across >300 locations in North Dakota, Minnesota, and South Dakota from 2019 to 2025. Stability was quantified using Finaly-Wilkinson regression (slope bi), deviation from regression Eberhart and Rusell (S^2di), Wricke's ecovalence (Wi2), and Francis and Kannenberg (CV%). Stability quantified from multiple year combinations (2, 3, and 4 years) were compared against a 5-year benchmark to assess reliability, using RMSE, RRMSE, and CV. The accuracy improved consistently from 2 to 4 years of data. Francis and Kannenberg, and Finlay Wilkinson showed the lowest RRMSE and CV across year combinations. Francis and Kannenberg, and Finlay-Wilkinson presented better KGE. Overall, Wricke's ecovalence showed the worst performance. The outcomes of this study guide breeders and growers on data requirements and stability metrics that best support genotype selections and potential commercial release in the U.S. Central-North Region.

Intercropping Cabbage and Onion as a Pest Management Strategy

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Insect damage and contamination is a major contributor to cabbage crop losses. Various cabbage pests feed on roots, stems, and leaves, resulting in stunted growth and unmarketable heads. Intercropping systems with diverse crops have demonstrated decreased insect damage compared to monoculture cropping systems. Many *Allium* species have been used in diverse cropping systems due to their repelling effect on insect pests. Onions release volatile organic compounds that can deter herbivores and may have a positive impact on neighboring plants. Understanding the strength of these compounds and their corresponding effect is limited. For this experiment, various high and low sulfur-producing onion cultivars were chosen to assess their effectiveness in preventing insect damage in a cabbage field intercropping system. Eight treatments will include cabbage control with and without insecticide, row intercropped cabbage and onion plots with two different high sulfur onion cultivars and two low sulfur cultivars, and two low sulfur onion intercropped plots with insecticides. This will be a randomized complete block design with four replications conducted in Absaraka, ND. The two low sulfur onion cultivars are 'Candy' and 'Walla Walla', and the two higher sulfur onions are 'Cortland' and 'Dakota Tears'. The cabbage cultivar is 'Golden Acre'. The expected results of this trial could demonstrate that the higher sulfur-producing onions significantly reduce insect damage on cabbage compared to lower sulfur-producing onion cultivars. This study may support the idea that onion plants can protect important vegetable crops from insect pest activity. This could result in reduced crop losses, insect damage, and contamination, which correlates with increased crop marketability and producer profits. On a wider scale, this provides a basis for an organic pest management alternative to pesticide use, leading to a decrease in insect resistance, negative environmental, and health effects.

Life Cycle Inventories for Sustainable Crop Production

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Camelina (*Camelina sativa* (L.) Crantz) is a promising oilseed crop for renewable biofuel production, due to its short life cycle, low input requirements, stress tolerance, and high seed oil content (30–40%). In the United States, biofuels may qualify for federal clean fuel tax credits if their production demonstrates >50% greenhouse gas (GHG) emissions reductions compared to fossil fuel production. Modelling carbon intensity (CI) at the farm level is therefore essential to certify emissions reductions to access tax incentives. This study developed a cradle-to-farm-gate life cycle inventory (LCI) for the agricultural phase of camelina production, evaluating impacts of biostimulants and soil amendments on CI, yield, and economic outcomes. In contrast with full life cycle assessment (LCA), this LCI omits midpoint and endpoint impact characterizations. The LCI was constructed using representative input rates, production practices, and emission factors from the literature and expert consultations. These data were integrated into a Microsoft Excel-based calculator to estimate energy use and CI contributions from individual inputs, management practices, and field emissions. Field data from a camelina experiment in eastern Montana were utilized to populate and demonstrate a use-case for this calculator. Scenario analyses evaluated how hypothetical yield increases could affect CI. Results highlighted synthetic fertilizer production, field emissions, and harvest operations as the largest CI contributors, while biostimulants contributed minimally. Systems that can achieve yield improvements, while reducing synthetic fertilization via use of biostimulants, may achieve net GHG reductions. This LCI and calculator provide a decision-support toolset and a foundation for future LCA studies.

A iRGD-Targeted Liposome Delivering Adavosertib for Ovarian Cancer Treatment

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Background: Ovarian cancer is the most lethal gynecological cancer. It is second leading cause of death among gynaecological malignancies, 5-year survival rate of only 31%. Ovarian cancer is heterogeneous collection of malignancies, among which most common type is high-grade serous ovarian cancer, which comprises 75% of total cases. Adavosertib (ADA) has been shown to have potential efficacy against ovarian cancer. However, administration of the ADA solution often fails to control tumour growth due to poor tumour distribution. So, to overcome this issue, non-targeted and targeted nanocarriers were extensively formulated for enhanced delivery of chemotherapeutics to the tumour. In our study, we prepared iRGD-conjugated liposomal formulations of ADA and investigated its antitumoral efficacy against ovarian cancer cell lines. iRGD is a cyclic 9 amino acid long peptide which has deeper tumour penetrating, tumour homing and higher uptake capabilities. Method: Solid phase peptide synthesis method was used for iRGD peptide synthesis. Targeted and non-targeted liposomes were prepared using a thin film hydration method. Liposomes were then dialyzed against deionized water for 8 hours to remove unencapsulated drugs. Conjugation was examined using CD. The size and surface charge of the liposomes were measured using the Zetasizer Nano ZS instrument. Encapsulation efficiency was determined by HPLC and loading was calculated. Stability study was done for 5 weeks, and the formulations were stored at 4°C and for 4 hours, and the formulations were stored at 37°C. In vitro cytotoxicity assay and biocompatibility assay was performed using the SKOV-3 and MA-148 cells. Results: Size and charge of ADA-liposome were 110.4 ± 0.9 nm and -20.5 ± 1.9 mV, respectively, size and charge of iRGD-ADA-liposome is 115.27 ± 3.22 nm and -21.22 ± 2.43 mV respectively (n=4). The encapsulation efficiency for ADA-liposome and iRGD-ADA-liposome were 67.63% and 64.12%, respectively. Cytotoxicity was compared to free drug solution, ADA-liposome, iRGD-liposome against SKOV-3 and MA-148 cells. Conclusion: We have successfully formulated ADA loaded unconjugated and iRGD-ADA-liposomes with high encapsulation efficiency and loading. Liposomes were stable at 4° C and at room tremperature with 10% serum containing media throughout the study period. Liposomes successfully lowered IC50 as compared to solution.

Understanding PFAS Removal Using Clay Materials and Ion Interactions

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Per- and polyfluoroalkyl substances (PFAS) are a large group of synthetic chemicals widely used in industrial processes and consumer products due to their exceptional resistance to heat, water, and oil. However, the strong carbon-fluorine bonds that make PFAS useful also render them highly persistent in the environment, earning them the name "forever chemicals." As such, developing effective and sustainable methods for PFAS removal from water has become an urgent research priority. In this study, we investigate how naturally formed clay minerals, specifically montmorillonite, interact with PFAS under different physiological conditions. Batch adsorption experiments were conducted to evaluate PFAS removal at different pH environments. Clay samples were prepared under varying surface charge conditions (using NaOH and HCl), and PFAS concentrations were determined by liquid chromatography–tandem mass spectrometry (LC-MS/MS). PFAS removal increased with carbon-chain length. PFOS showed the highest removal efficiency (>70%), while PFBA showed the lowest (7–12%), indicating that longer hydrophobic chains promote stronger adsorption. For PFAS with the same chain length, sulfonates generally adsorbed better than carboxylates, highlighting the role of the functional headgroup. Computationally, the results showed that sodium ions can influence PFAS adsorption by interacting with their charged headgroups, but they may also limit effective attachment due to strong hydration effects. Modifying the ionic environment by introducing chloride ions improved PFAS removal efficiency. Overall, the findings suggest that ion composition plays a key role in controlling PFAS adsorption onto clay surfaces and can be optimized to enhance water treatment performance.

‘Here We Go, Another Professor with Their Special Way of Doing Their Things’: Promoting Social Metacognition in a CURE using a Modified Scrum Framework

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Let’s be honest – sometimes working in a group is terrible. Group work commonly comes with a suite of frustrations like unequal contribution from group members, disorganization, lack of communication, and poor time management leading to group procrastination. However, learning to overcome these frustrations is crucial to being an effective collaborator — a crucial skill for student success both during their undergraduate education and after graduation. Previous work has shown scaffolding the development and use of social metacognitive regulation skills during group work can improve student outcomes with enhanced course and group engagement, increased performance on high stakes assessments and projects, and reporting an overall better experience with their group — all while avoiding, or addressing, those common issues with group work. Course-based undergraduate research experiences (CUREs) often require group work, leaving room for the potential for students to experience these common group work frustrations. We implemented a modified Scrum framework in a biology education research (BER) CURE to scaffold the development of social metacognitive regulation skills aiming to improve the group work experience. Students were invited to participate in a focus group (n=5) to reflect on their semester and how Scrum impacted their group’s working dynamic and process. Using thematic analysis we found evidence of planning, monitoring, and evaluating: the phases of metacognitive regulation. We also found Scrum was an effective framework to encourage student autonomy and ownership over their research project, important outcomes of a CURE.

Comparing Modern and Historic Wild Bee Diversity in the North Dakota Sandhills

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Bees (Hymenoptera: Apoidea: Apiformes) are crucial pollinators for natural and agricultural systems in North Dakota and excellent indicators of prairie ecosystem health. As agricultural land use intensifies and climate shifts across the Northern Great Plains, natural systems may experience changes in the diversity and abundance of bees. However, tracking changes in bee populations over time is challenging, as there are few historical datasets. Extensive surveying of bees conducted in the Sandhills from 1910-1950 represents a unique opportunity to evaluate changes in bee communities over time. The goal of our study was to evaluate the current bee community in the Sandhills and compare it to historic records. We conducted bee surveys from May 1 through September 7, 2025 at sixteen sites within two locations: ten at the Ekre Grassland Preserve and six at Brown Ranch. Sites representing six different microhabitat types varying in topography, floral resources and soil moisture were chosen to maximize diversity of bees captured. We collected bees bimonthly by sweep-netting all flowering plants at each site as well as targeted sweeping of specific plant species. We have currently identified 125 bee species, including 10 new North Dakota state records. These results suggest that the Sandhills are a hotspot of bee diversity, and that some bees may be expanding their range into North Dakota. Continued examination of our data will focus on evaluating the changing bee community of the Sandhills and their relationship with native plants, providing insight into factors that affect bee diversity and abundance in the region.

Stochastic Model for the Internal Transfer Kinetics of Cargo in Carriers with Two Compartments

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Lipid vesicles and related nanocarriers often contain two compartments, such as the inner and outer leaflets of a bilayer membrane between which amphipathic molecules can migrate. We develop a stochastic model for describing the transfer kinetics of cargo between the two compartments in an ensemble of carriers, neglecting inter-carrier exchange to focus exclusively on intra-carrier redistribution. Starting from a set of rate equations, we examine the Gaussian regime in the limit of low cargo occupation where Gaussian and Poissonian statistics overlap. We derive a Fokker–Planck equation that we solve analytically for any initial cargo distribution among the carriers. Moments of the predicted distributions and examples, including a comparison between numerical solutions of the rate equations and the analytic solutions of the Fokker–Planck equation, are presented and discussed, thereby establishing a theoretical foundation to study coupled intra- and inter-carrier transport processes in mobile nanocarrier systems.

Nanoplastics Release from Coffee Pots while Brewing

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Coffee is one of the most widely consumed beverages in the world and is generally considered safe when enjoyed in moderation. Using single-use coffee pods has become a common and convenient way to prepare coffee at home and in workplaces. However, there is growing concern about whether tiny plastic particles or chemical compounds may be released from these pods during brewing. This study examined the possible release of nano plastics from use of coffee pods under different brewing conditions. A total of 60 empty coffee pods were prepared by completely removing the coffee grounds and carefully rinsing them with tap water and ultrapure water. To avoid contamination, all equipment and surfaces were cleaned with methanol, and two initial blank brewing cycles were run before collecting samples. Brewing was carried out under two different conditions: (1) 8 oz volume, intense strength, and extra-hot temperature; and (2) 4 oz volume, low strength, and low temperature. For each condition, 20 blank samples (without pods) and 20 samples brewed with empty pods were brewed for comparison. All samples were filtered using ultrafiltration (100 kDa filter) and then further concentrated by ultracentrifugation. The remaining samples were transferred to the Pyrolysis cups and dried at 60 °C in an oven and analyzed using pyrolysis–gas chromatography–mass spectrometry (Py-GC/MS). In addition, the brewed coffee pods were analyzed using Fourier-transform infrared spectroscopy (FTIR) to study their material composition. By comparing blank samples with pod-brewed samples under different conditions, this study aimed to better understand whether nano plastics or polymer-related compounds are released from coffee pods during the brewing process.

Yield Prediction and Efficient Selection in Canola (*Brassica napus* L.) using Vegetation Indices

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Remote sensing techniques with the potential application of vegetation indices for yield prediction and indirect selection of high-yielding genotypes have been successful in several crops. In this study, diverse canola genotypes in the field trial were evaluated for vegetation indices and yield over two years (2022-2023) at Carrington and Langdon in North Dakota. Multispectral images were taken at multiple growth stages, and 38 vegetation indices (VIs) were extracted. Among the VIs, nine (NDVI, VEG, GRRI, NGRDI, NDRER, MGRVI, VDVI, VARI, OSAVI) showed strong positive correlations (r = 0.42-0.74) with seed yield, and effective indirect selection at the end of the flowering stage. Furthermore, PCA and K-means clustering effectively summarized spectral diversity and effectively grouped the genotypes. Broad-sense heritability of selected indices ranged from 17% to 41%, indicating genetic potential and improvement. Yield prediction for the unseen test population, ENET, and LASSO outperformed Ridge Regression, MLR, PLSR, and RF, achieving a strong predictive performance with a coefficient of determination (R2) of 0.66 and root mean squared error (RMSE) of 413-415 kg ha-1. Notably, in a validation test, VIs-based selection shares at least 77.8% (14 out of 18) of the genotypes across all models, as if the selection were based on harvest yield, which supports the effectiveness of the selection. Overall, this research highlights the effectiveness of UAV-based multispectral imaging for identifying vegetative indices that contribute to seed yield, thereby accelerating breeding efforts and enhancing selection efficiency.

Influence of Hormonally Induced Diapause Termination on Adult Longevity, Cellular Aging, and Oxidative Stress in the Solitary Bee, *Osmia lignaria*

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In the blue orchard bee (*Osmia lignaria*), reproductive diapause is an obligatory physiological state enabling winter survival. The diapause phase plays an important role in regulating cellular aging, as evidenced by significantly longer telomeres in post-diapause individuals. However, it is unknown whether cellular aging is influenced by the timing of diapause itself or by the process of emergence following diapause completion. To examine this, we hormonally terminated diapause early using the juvenile hormone analogue pyriproxyfen and evaluated the post-termination effects on adult longevity, cellular aging, and oxidative stress. The freshly capped O. lignaria nests containing developing larvae were kept in an incubator at 25°C and 75% relative humidity. As they entered diapause, four different treatment groups were established: pyriproxyfen treatment (5ug/bee), control (pre-chilled), acetone (vehicle) control, and a control (chilled) in which bees emerged after diapause. Cumulative emergence under pyriproxyfen treatment reached 100% after seven days for males and six days for females. Post-treatment longevity was significantly influenced by treatment ($p < 0.005$), where pyriproxyfen-treated bees lived longer than bees that emerged after diapause completion, suggesting an upstream physiological relevance of early diapause termination. Telomere length differed significantly between pyriproxyfen- and control (pre-chilled) bees, suggesting that early termination affects cellular aging. Oxidative stress was evaluated in three treatment groups using the antioxidant capacity (TEAC assay) and lipid peroxidation (MDA assay). These results suggest that early emergence does not disrupt oxidative homeostasis. Taken together, our findings provide evidence that diapause termination via endocrine disruption may reshape longevity and cellular aging.

Chloride Removal from Produced Water Impacted Groundwater using AEM-Facilitated Electrokinetic Treatment

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Produced Water (PW) is the aqueous byproduct of oil and natural gas extraction and is often characterized by elevated concentrations of inorganic ions, particularly chloride, which pose significant ecological risks. This study evaluates the effectiveness of membrane-based electrokinetic treatment for chloride reduction in PW. Three synthetic chloride solutions (1000–3000 mg/L) were treated for 24 h in an anion exchange membrane–assisted electrokinetic cell operated at a constant current density of 0.65 mA/cm² using titanium-coated platinum electrodes. The results indicate that chloride removal efficiency depended on chloride concentration and treatment time. At low chloride concentrations, removal exhibited a strong linear correlation with time, whereas higher concentrations showed a statistically significant non-linear pattern. Mass balance analysis further confirmed effective chloride transport, evidenced by a decrease in chloride mass in the catholyte and a corresponding increase in the anolyte. Overall, the findings highlight the potential of this electrochemical process for passive chloride treatment in PW.

A Multi-Modal Deep Learning Approach to Decoding the Satellite-Management-Environment Data Handshake for Sustainable Yields

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Accurate in-season yield forecasting is critical for optimizing nitrogen application and enhancing food security, yet traditional models often struggle with the irregular temporal frequency of satellite data and the complex interactions between management practices and weather shocks. This research develops a "Time-Aware" Hybrid Neural Network that integrates multi-source temporal data with static experimental factors to provide high-resolution yield predictions at the subplot level. The study utilizes a seven-year dataset (2019–2025) comprising PlanetScope 3-meter satellite imagery and localized weather telemetry. To address the challenge of irregular satellite acquisition, we developed a Temporal Convolutional Network (TCN) augmented with a Multi-Head Self-Attention mechanism. Unlike standard interpolation methods that smooth over critical biological signals, our model utilizes raw daily-of-year (DOY) features to anchor 32-step sequences of Vegetation Indices (NDVI, GNDVI, EVI, OSAVI) and meteorological variables. This temporal branch is integrated via late fusion with a Static MLP Branch encoding management variables, including tillage (T/M/N), crop type (Corn/Soybean), and fertilizer source (Manure vs.

Mineral). The hybrid architecture outperforms traditional regression baselines by capturing the non-linear "handshake" between environmental stress and management resilience. The Attention mechanism specifically identifies the grain-filling phenological window (August–September) as the primary determinant of yield variance. Preliminary evaluations using Huber Loss demonstrate superior robustness against outliers compared to standard MSE, particularly in years with extreme weather volatility. By accurately quantifying how specific tillage and fertilization strategies mitigate climate-induced yield gaps, this model provides a scalable tool for precision agriculture.

North Dakota Agricultural Microbiome as a Driver of Soil Health and Wheat Productivity

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Agricultural ecosystems function as integrated units in nature, where soil health, microbial diversity, and management practices operate together to determine crop yield. Belowground microbial communities play an indispensable role in regulating nutrient availability, decomposing organic matter, and imparting biotic and abiotic stress tolerance to plants. To enhance resource availability for plants, farmers commonly adopt management practices such as tillage and the application of fertilizers and pesticides; however, these interventions can also disrupt soil structure and reshape microbial communities. Soil health, governed by soil physical, chemical and microbial parameters, ultimately determines crop productivity. Despite this complexity, the relationships of crop productivity with microbial diversity, soil health, and management practices are often studied in isolation. As a result, the integrated effects of these factors on crop yield prediction remains insufficiently understood. To address this gap, we conducted extensive sampling across 201 wheat fields from 51 counties in North Dakota. Sampling was performed at three time points over the wheat growing season, resulting in a dataset of 603 samples that included soil physicochemical properties, multi-domain microbial community data, aboveground biomass, grain yield, weather parameters, and management practices, making it one of the most comprehensive agricultural microbiome projects in the world. Our results indicated that under moderate management intensity, prokaryote community evenness can act as a predictor of wheat grain yield ($p = 0.039$, $R = 0.2$). Under low management intensity, prokaryote evenness was negatively associated with yield, indicating accelerated resource utilization by microbes under limited nutrient availability ($p = 0.0042$, $R = -0.43$). Notably, grain yield was comparable under moderate and high management intensity, and it was lowest in low management intensity due to resource limitation. To further investigate the multi-associated relationship between the variables, we developed a structural equation model (SEM) to predict yield. The SEM revealed that moderate management intensity decreases prokaryote evenness, but improves soil health, which in turn positively influence wheat grain productivity. Overall, this study provides a comprehensive regional scale assessment of microbial community dynamics and highlights their role as predictors of crop yield under varying management practices.

Short Term Impacts of Grazing Winter Cereal Cover Crops on Cropping Systems and Profitability

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Cover crops (CC) as part of integrated crop livestock systems may extend the grazing season in the Northern Great Plains and offset costs of CC establishment. The objective of this study was to determine the effects of grazing CC on crop performance, soil health, and profitability. At Central Grasslands Research Extension Center near Streeter, ND, nine 1.8 ha plots were established and assigned: dual (fall and spring) grazing (DG), spring grazing (SG), or no grazing (NG), which was split to include no CC. Fall 2022 and 2023, winter rye was planted as a CC. Fall 2024 and 2025 winter rye, winter wheat, and winter triticale strips were planted in each CC plot. In fall 2022, and spring 2023, 2024, and 2025, CCs were grazed at 0.6 animal unit months (AUMs), 3.36 AUMs, 0.98 AUMs, and 0.56 AUMs, respectively. Grazing was deferred fall 2023 and 2024 due to low biomass. Winter cereal biomass production was evaluated pre- and post-grazing. Fall grazing did not impact spring CC biomass. Winter rye produced the greatest spring biomass, followed by winter wheat. Winter triticale biomass was low due to winter kill. Grazing did not alter soil chemical or physical properties. Cover crops significantly reduced weed cover. Weed suppression was unaffected by grazing. In 2025, corn grain yield was significantly lower in triticale CC strips. Soil volumetric water was highest in NG plots throughout the growing season. A partial budget estimated the economic effect of CC establishment, cash crop yield, and livestock production. Grazing either resulted in a net income or provided a return on CC investment across all years. Grazing CC is heavily dependent on planting date, temperature, and precipitation, but can extend the grazing season in the spring, reducing feeding costs without negatively impacting soil health or crop performance.

Evaluating the Impact of Pollen and Nectar Availability on Sunflower Insect Visitation with Floral eDNA

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The analysis of residual arthropod DNA from flowers is a developing technique that can elucidate plant-arthropod interactions. We collected environmental DNA (eDNA) from sunflowers varying in pollen availability and floret length (nectar accessibility) to determine how floral resources affect the diversity of arthropod visitors. Many pollinators and natural enemies are attracted to flowers with greater nectar accessibility and pests to flowers with pollen, but how floral resources affect these groups within the same system is understudied and experiments that independently manipulate pollen and nectar are lacking. Our field experiment was conducted in Casselton, ND August-September 2024 and 2025. We collected eDNA from short floret male-fertile (n=18), short floret male-sterile (n=17), long floret male-fertile (n=24), long floret male-sterile (n=23), and wild (n=5) sunflowers by washing heads in water and targeted the COI gene with a general arthropod primer set in metabarcoding analysis. We cleaned and processed metabarcoding results: exact sequence variant (ESV) identifications were vetted and read count data converted to presence/absence for diversity analysis. We identified 125 distinct taxa across 13 orders and 49 families and categorized them into functional groups. General pests (e.g. thrips, aphids) and sunflower-specific pests were the most prevalent groups and only one bee was detected due to primer compatibility. More taxa were detected on sunflowers with long florets than those with short florets or wild sunflowers, although pollen availability had no impact. Pairing eDNA results with traditional arthropod sampling will clarify whether differences are artifacts (e.g. uneven DNA degradation) or related to floral treatments.

Productivity of Winter Camelina in Regional Cropping Systems

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Winter camelina (*Camelina sativa* (L.) Crantz) is an oilseed crop that is grown in limited acres across the country. Camelina requires less inputs than other oilseed crops, but also yields about half as much as similar crops, such as canola (*Brassica napus* L.). To determine if certain crop sequences can improve camelina seed yield, as well as providing many other benefits to the environment, field experiments were conducted in Hickson and Prosper, ND in 2023. The crops include early maturing sunflower (*Helianthus annuus* L.), spring wheat (*Triticum aestivum* L.), and soybean (*Glycine max* (L.) Merr). In 2023, sunflower and spring wheat were planted in the spring and winter camelina was planted in the fall. Soybean and sunflower were double cropped in 2024 of certain treatments. Evaluations included soil total and organic carbon and nitrogen and bulk density, plant height, seed and oil yield, seed oil and nitrogen content, plant biomass nitrogen content, and fatty acid profile. Wheat and sunflower yields showed no significant differences between treatments in 2023. Camelina oil content and crude protein was not significant in any sequence or location. In Prosper, camelina yields were highest following sunflower, particularly in camelina-unfertilized treatments (788 kg/ha). In 2024, the camelina was harvested in mid-July and resulted in a failed double-cropping. Land equivalent ratio were used to determine productivity of cropping sequences, with the most productive being spring wheat – winter camelina + N – sunflower. Carbon intensity was not reduced by the inclusion of winter camelina instead of fallow in sequences including wheat, sunflower, and soybean. This data will allow for a better understanding of where winter camelina can benefit common northern Great Plains crop sequences.

How do Students Process and Answer Unconventional Integrals?

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Integrals can be conceptualized with an infinitesimal or limit definition, and holding a certain conceptualization may change how someone frames and solves an integral problem. We present excerpts from two different interview studies where we asked second-semester calculus-based intro physics students integral questions. Student utterances and differing answers to these selected questions led us to define two conceptual resources concerning infinitesimals, which correspond to the different definitions of integration. These conceptual resources align with the theoretical backgrounds leveraged in math or in physics, showing a distinction between the two disciplines. To investigate further, we collected free response answers to two integral questions from University Physics II and Calculus II courses. We report the proportions of students answering with each conception in each course setting. This work highlights subtle differences in students' interpretation of integration within contexts and areas for future study.

Plant-Soil Feedbacks, Microbial Shifts and Nutrient Changes in Kentucky Bluegrass Invasion

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The grassland of Northern Great Plains (NGP) is a significant ecosystem in North America that supports high biodiversity and provides various valuable ecological services. However, these prairies are increasingly degrading and threatened by invasive species, especially Kentucky bluegrass (*Poa pratensis*), that are reducing native plant abundance and changing community structure and ecosystem function. While the above-ground effects of invasion have been well studied and less is known about the below-ground processes that may help invasive species become dominant. This study focused on how plant-soil feedbacks, soil microbial communities, and nutrient changes are linked to Kentucky bluegrass invasion in grasslands. In a controlled experiment, we compared Kentucky bluegrass (KBG) with four native species, including two forbs (*Achillea millefolium* and *Rudbeckia hirta*) and two grasses (*Pascopyrum smithii* and *Bouteloua gracilis*). We measured plant growth traits such as height, tiller number, chlorophyll content, and shoot biomass. We also examined changes in bacterial and fungal soil communities over time, along with changes in soil nutrients, especially carbon-to-nitrogen (C:N) ratios. We hypothesized that Kentucky bluegrass would change plant-soil interactions by shifting microbial communities and nutrient conditions in ways that support its own invasion. Our results showed that Kentucky bluegrass changed both bacterial and fungal communities when grown with native plant mixtures. When grown alone in monoculture, it also shifted the dominant microbial community in ways that may help its own growth and spread. We also found that native grasses and Kentucky bluegrass had more similar microbial communities than native forbs, probably because of differences in their functional traits. These results suggest that soil microbial shifts are an important part of Kentucky bluegrass invasion and that using a diverse mix of native grasses and forbs may improve resistance to invasion. Overall, this study shows that both above- and below-ground interactions are important for understanding invasion dynamics and for developing better restoration strategies in NGP grasslands.

Rethinking PFAS Pollution: Proteins as Potential Binding Platforms

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Per- and polyfluoroalkyl substances (PFAS), commonly known as "forever chemicals," are persistent environmental contaminants that pose serious risks because of their high mobility, exceptional chemical stability, and resistance to degradation. Their widespread presence in water systems underscores the urgent need for innovative and sustainable remediation strategies. In this context, abundant natural proteins offer a promising and environmentally benign route as bio-adsorbents.

Here, we investigate ovalbumin (OVA), the major protein in chicken egg white (>50% of total protein), as a potential bio-adsorbent for PFAS in aqueous environments. Using a combination of experimental techniques and molecular-level characterization, we show that OVA exhibits measurable affinity toward a range of PFAS compounds. The strength of these interactions depends strongly on PFAS molecular structure, with long-chain PFAS displaying greater affinity than short-chain analogs. Binding is driven primarily by hydrophobic and electrostatic interactions, which promote association of PFAS molecules with specific regions on the protein surface. Computational simulations further support these findings, identifying arginine and lysine residues as key binding sites and revealing that both fluorination and headgroup chemistry significantly influence binding behavior. Thermodynamic analysis confirms that the interactions are favorable, as indicated by negative enthalpy (ΔH) and Gibbs free energy (ΔG) values. Taken together, these results highlight the potential of OVA as a versatile biomolecular platform and provide molecular insights into protein-PFAS interactions in water. This work establishes a foundation for the development of protein-based and biomimetic strategies for PFAS capture, contributing to more sustainable approaches for mitigating PFAS contamination in aquatic systems.

Ligand-Controlled Optical Properties of Copper(I) Complexes for Biological Sensing

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Copper(I) diimine complexes have emerged as promising candidates for bioimaging and chemical sensing due to their highly tunable photophysical properties, which arise from the balance between metal-to-ligand charge-transfer (MLCT) and ligand-centered (LC) π–π^* excited states. In this work, density functional theory (DFT), time-dependent DFT (TDDFT), and nonadiabatic molecular dynamics (NAMD) with incorporated spin-orbit coupling were employed to investigate a family of $[Cu(N^\wedge N)_2]^+$ complexes featuring bipyridine-type ligands systematically modified through π-conjugation extension and electron-donating substituents. NAMD was used to quantify electron-vibrational couplings contributing to MLCT and LC excited states, revealing how ligand substitution influences intersystem crossing and internal conversion pathways that determine excited-state relaxation, emiss and emission lifetimes—effects not captured by static electronic structure methods alone. The analyses of absorption spectra and the electron-hole pairs contributing to the lowest energy transitions show that increasing ligand conjugation and electron-donating strength decreases the energy of LC π^* orbitals and enhances Cu–N orbital overlap, stabilizing MLCT states and producing pronounced red shifts from 400 nm to 500 nm with high oscillator strengths. This behavior is consistent with experimental data for analogous complexes reported. Reduced nonadiabatic coupling for electron and hole relaxation from MLCT to LC states further indicated suppressed nonradiative decay and prolonged excited-state lifetimes. Our results demonstrate how targeted ligand design can effectively control charge-transfer character and optical performance in Cu(I) complexes. Gained information will be useful for designing materials for biosensing in the NIR range, enabling deeper tissue penetration and reduced autofluorescence in bioimaging and other light-driven applications.

Electrolyte Dilution Alters Electrical Response During Acute Hyperhydration: Evidence from Bioimpedance Spectroscopy

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Acute changes in hydration status do not always lead to electrical impedance variations in the physiologically expected direction. Electrolyte dilution and other short-term physiological processes may alter tissue resistivity independently of changes in total body water (TBW), potentially affecting bioimpedance-based estimates of body fluid compartments. This study evaluated the behavior of Cole model parameters obtained from bioimpedance spectroscopy (BIS) during experimentally induced acute hyperhydration. Sixteen healthy volunteers were measured using a whole-body BIS system (Xitron Hydra 4200). After a baseline measurement, participants ingested three doses of mineral water (≈300 mL each) at 10-minute intervals, with BIS measurements performed after each dose. The results showed that extracellular and intracellular resistance values did not consistently decrease as expected with increased body water volume. The observed responses suggest that transient changes in tissue resistivity, likely related to electrolyte dilution, may temporarily predominate over volumetric effects. These findings indicate that BIS-based fluid estimates may be unreliable shortly after fluid intake, and measurements should be interpreted with caution under acute hydration conditions.

Innovative Microbial Disinfection Using Far-UVC Light

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The most common chemical means of wastewater treatment have harmful disinfection byproducts. Wastewater treatment plants have begun adopting UV disinfection as a safer and, at times, cheaper alternative, though direct contact with UVC light is harmful to human skin, and the lamps aren't as effective against enveloped viruses or certain vegetative bacteria. Far-UVC emits 222nm wavelength UV rays that do not harm human tissues. This study examines the effectiveness of Far-UVC microbial disinfection when treating synthetic wastewater dosed with varying concentrations of nitrate. Resuspended cell solutions were made using model bacteria, and then those solutions were dosed with nitrate and treated with Far-UVC light. By growing the bacteria on agar plates and comparing the growth to control samples that did not contain nitrate, we've found that nitrate can inhibit the treatment efficacy of Far-UVC light.

Identification and Characterization of Ligand Specific RAGE Antagonists Based On Monoclonal Antibodies

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The receptor for advanced glycation end products (RAGE) is a cell surface receptor belonging to the immunoglobulin superfamily and is capable of binding multiple ligands. It is widely expressed across various cell types, including epithelial and endothelial cells, neurons, hepatocytes, vascular smooth muscle cells, and immune cells. The full-length RAGE protein comprises a variable-like (V) domain and two constant type domains (C1 and C2), a short transmembrane segment, and a cytoplasmic tail. The V domain serves as the primary ligand-binding site, although certain ligands can also interact with the C1 and C2 domains. Originally named for its first identified ligand, advanced glycation end products (AGEs), RAGE has since been recognized to bind a diverse array of ligands, including HMGB1, S100 proteins, amyloid β peptides, MAC-1, C1q, phosphatidylserine, lysophosphatidic acid, and nucleic acids. Beyond its role as a cell surface receptor, RAGE's ability to engage multiple ligands positions it as a key regulator in numerous pathological conditions, including Alzheimer's disease, neurodegeneration, cardiovascular disease, cancer, and diabetes. Targeting RAGE to block specific ligand interactions holds therapeutic potential across multiple diseases. This study aims to identify and characterize monoclonal antibody-based ligand-specific RAGE antagonists as therapeutic interventions in RAGE associated diseases. The NanoLuciferase (LgBiT-smBiT) complementation assay was utilized to investigate RAGE-ligand interactions. For this purpose, HEK293 cells were stably transfected with an LgBiT-tagged RAGE receptor. To complement the LgBiT, smBiT-tagged S100B and HMGB1 were employed, as both ligands are known to bind RAGE. Following complementation of LgBiT and smBiT, luciferase activity was measured upon the addition of the NanoLuciferase substrate furimazine. Blockade of S100B and HMGB1 binding to RAGE by specific anti-RAGE antibodies was assessed based on changes in luminescence signals. We successfully generated HEK293 cell lines stably expressing functional RAGE-LgBiT. Additionally, smBiT-tagged S100B and HMGB1 proteins were successfully constructed, expressed, and purified. The interaction between RAGE-LgBiT and smBiT-tagged proteins effectively reconstituted the NanoLuciferase enzyme activity. Furthermore, the NanoBiT system demonstrated the ability to detect competition with untagged S100B. We successfully screened panel of monoclonal anti-RAGE antibodies demonstrating competition with S100B ligands using this assay.

Investigation of Adhesion and Friction of PDMS-based Materials at Nanoscale using AFM

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The adhesion and friction behavior of soft materials at small scales is critical to the performance of advanced technologies, including microdevices, biomedical systems, and soft robotics. Polydimethylsiloxane (PDMS) serves as an ideal model system due to its tunable viscoelastic properties, chemical stability, and widespread use in engineering applications. Understanding these interfacial properties is essential for controlling surface interactions and optimizing material performance. Although adhesion and friction in soft materials have been widely studied at micro- and macroscales, their nanoscale characterization remains limited. Atomic Force Microscopy (AFM) enables high-resolution measurement of these interactions and provides a framework to interpret results through contact mechanics models. However, the viscoelastic nature of soft polymers introduces time-dependent deformation and energy dissipation, posing challenges for accurate quantification. In this work, the role of viscoelasticity in governing nanoscale adhesion and friction of PDMS is investigated. By incorporating silica nanoparticles, the viscoelastic properties of PDMS are systematically tuned, enabling direct correlation between material response and interfacial behavior. The results reveal a clear relationship between adhesion and the viscoelastic parameter (tan δ), indicating that adhesion is strongly influenced by the material's energy dissipation characteristics. Additionally, a consistent trend is observed between adhesion and friction, where increased adhesion corresponds to higher friction forces. These findings demonstrate that viscoelasticity is the dominant factor controlling nanoscale tribological behavior in soft polymers and must be explicitly considered in modeling and design. This study provides fundamental insight for the development of optimized materials in applications such as anti-fouling and anti-icing coatings, MEMS, and bioengineering systems.

Pricing the Unpredictable: Disasters, Currency, and Financial Risk

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The devastation caused by an earthquake or hurricane is not limited to physical damage; ecosystems are destroyed, communities disperse, and billions of dollars are lost. Recovery is slow, and rarely occurs without money traveling across borders. Governments, businesses, and communities need financial tools to recover. Catastrophe bonds are specifically designed to transfer financial risk associated with disasters from insurers to investors worldwide. The problem is that such investors deal in different currencies, sit in different nations, and are subject to sudden changes in interest rates. The majority of current models just do not deal with all of it at once when pricing these bonds fairly. The currency exchange rates fluctuate rather than flowing smoothly. When a crisis strikes, a currency changes in ways that are impossible for a gradual model to predict. We develop a framework that takes into account: abrupt variations in currency rates, interest rates that fluctuate widely between nations, all combined into a single pricing formula for foreign exchange options; the fundamental block that Catastrophe bonds rely on. Our model performs better under actual market conditions when tested against two well-known models. The distinction is important because mispriced bonds result in investors assuming hidden risk, communities receiving less assistance, and the system as a whole being somewhat less reliable. As the frequency of disasters rises due to climate change, measures like these become increasingly important for strengthening global financial stability.

Detecting Earlier, Reaching Further: Optimizing Breast Cancer Screening in Rural North Dakota

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Cancer remains one of the most significant public health concerns in the United States, with approximately half of the men and one-third of women expected to develop the disease in their lifetime. Among all types, breast cancer in particular stands out due to its high prevalence in new cases and cost. In the U.S., over 300,000 new cases are projected in 2025, with treatment expenses reaching nearly 30 billion only in 2020. While early detection can significantly improve survival rates and reduce costs by up to one-third, many individuals face barriers to timely screening. Out-of-pocket expenses and limited access to healthcare services contribute to delayed diagnoses. In some cases, treatment costs for breast cancer can exceed $120,000. These challenges are especially pronounced in North Dakota, where breast cancer incidence rates among women are above the national average, and rural populations often lack access to preventive care. This study proposes the use of mathematical programming to strategically deploy mobile health units across North Dakota. The goal is to improve early detection rates and reduce both mortality and the economic burden on underserved populations. The proposed model could serve as a blueprint for other rural states facing similar disparities in cancer outcomes.

Relationship between Body Fat Percentage and Hip and Shoulder Mobility in Division I Female Softball Players

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Research suggests that body composition may influence how well athletes move, which in turn can affect both performance and injury risk. Previous research has shown that female softball players with a higher body mass index (BMI) often have reduced rotation ability in their hips and shoulders. However, it is unclear whether such a relationship exists between body fat percentage specifically and joint mobility in softball players. Therefore, the purpose of this study was to examine whether body fat percentage is associated with shoulder and hip internal rotation (IR) and external rotation (ER) range of motion reductions in Division I (D1) female softball players. Nineteen DI female softball players (19.7±1.0 years; 172 ±6.4 cm; 71.38 ±9.7 kg) participated in this study. Their ability to rotate both shoulders and hips internally and externally was measured using an electronic goniometer. Additionally, body fat percentage was measured using a bioelectrical impedance device. The results showed that a higher body fat percentage was related to reduced internal rotation of the hip on the dominant side, the side used most frequently during play ($r = -.49$; p-value = 0.03). This correlation was found to be moderate and significant. However, similar relationships between body fat percentage and joint mobility were not found for the non-dominant side hip IR ($r = -.23$; p-value =0.34), dominant side hip ER ($r =.03$; p-value = 0.88), non-dominant side hip ER ($r= -.21$; p-value = 0.39). Additionally, no significant correlations were found between body fat percentage and shoulder internal and external range of motions ranges. The findings of this study suggest that higher body fat percentage may be linked to reduced internal rotation of the dominant hip in female softball players. Hip rotation plays an important role in movements such as pitching, hitting, and throwing in softball. Consequently, reduced hip mobility may influence movement mechanics and efficiency during play, potentially affecting performance or increasing injury susceptibility in female softball players. This study contributes to the understanding of how body composition can affect joint mobility, which is crucial for sports performance enhancement and injury risk reduction in softball players.

In Vitro Mutation of Raspberry Species Using Chemical Mutagen Ethyl Methane-Sulfonate (EMS)

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Raspberry, belongs to the genus *Rubus* in the Rosaceae family. The genus Rubus consists of more than 740 species distributed worldwide. Raspberry fruits can be used for fresh consumption, frozen and processed products, such as jellies, juices, jams, and desserts. The narrow genetic diversity within the genus *Rubus* remains a primary constraint in raspberry breeding programs. This study focuses on in vitro mutation induction using the chemical mutagen ethyl methane-sulfonate (EMS) to expand genetic variation and mitigate chimerism in two raspberry cultivars, 'Prelude' and 'Polana'. In vitro leaf and nodal segments were treated to a range (0%, 0.1%, 0.25%, 0.5%, 0.75%, and 1.0%) of EMS concentrations. EMS treated explants were cultured on Woody Plant Medium (WPM) containing 20 g/l sucrose, 6.5 g/l agar, 200 mg/l Polyvinylpyrrolidone (PVP), and 1.0 µM thidiazuron (TDZ) to facilitate shoot regeneration. Following successful shoot development and subsequent In vitro and ex vitro rooting, the research has currently reached the critical stage of acclimation. Rooted plants were first grown in the culture room and are now transitioning from controlled culture room conditions to the greenhouse environment. Final evaluations will involve determining survival rates and characterizing morphological variations in leaf structure, cane development, and fruit quality within both greenhouse and field settings. This research emphasis that in vitro mutation induction using chemical mutagen could be a useful tool to develop genetic variations that have potential for breeding and germplasm improvement of raspberries and other *Rubus* species.

How University Archives in Fargo-Moorhead Help Local Communities

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University archives are often understood as places that preserve the records and history of a single institution. However, their value extends beyond campus boundaries. This project examines how university archives in the Fargo-Moorhead area serve local communities and contribute to the broader public good. Focusing on repositories such as North Dakota State University, Minnesota State University Moorhead, and Concordia College, this study asks how these archives support people outside the university, including local historians, genealogists, museum workers, journalists, researchers, and community members. Using a comparative case study approach, this research explores the public-facing roles of university archives through reference services, outreach activities, exhibits, digital collections, collaborations, and community partnerships. It also considers how archivists balance institutional responsibilities with wider public access, engagement, and representation. By examining both physical and digital access, this project highlights the ways archives function as community resources rather than closed academic spaces. This study argues that university archives play an important role in preserving regional memory, supporting local research, encouraging public history work, and strengthening connections between campuses and surrounding communities. In a region like Fargo-Moorhead, where universities are closely connected to local cultural life, archives help document not only institutional history but also the stories, identities, and experiences of the broader public. This research contributes to conversations in public history and archival studies by showing that university archives should be understood as active civic institutions. Their significance lies not only in what they preserve, but also in how they make those materials meaningful and accessible to people beyond the university.

Low-Cost RF Sensing

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Farmers and researchers have long relied on laboratory-based methods to monitor soil health and detect early signs of plant stress. While effective, these methods often require expensive equipment and significant time, making them difficult to use regularly or at scale. This research explores low-cost RF sensing as a more accessible alternative, using RF resonator-based sensors to measure soil pH and plant volatile organic compounds (VOCs). Two sensors were designed and tested. The first uses cellulose nanofiber to detect soil pH changes, and the second uses MXene to detect plant VOCs. Both work on the same principle that changes in pH or VOC levels alter the dielectric properties of the sensing material, producing measurable shifts in the RF resonator's frequency response. To validate the VOC sensor, soybean plants grown in both controlled and uncontrolled environments were tested. Results showed clear and distinguishable differences in RF amplitude response between baseline readings and plant samples, confirming that the sensor responds to the presence of VOCs and can detect variation between samples. These findings support the potential of low-cost RF sensing combined with nanomaterials as a practical pathway for agricultural monitoring. Future work will focus on further experimental validation and advancing toward a deployable monitoring system.

Fluopyram Sensitivity in *Fusarium virguliforme* Isolates Associated with Soybean (*Glycine max* L.) Sudden Death Syndrome

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Sudden death syndrome (SDS), caused by *Fusarium virguliforme*, is an emerging disease of soybean in North Dakota and causes significant yield losses across the United States. Fluopyram, a succinate dehydrogenase inhibitor fungicide (FRAC 7), has been registered in the U.S. since 2014 as a seed treatment for SDS management. This study aimed to assess the in vitro sensitivity of *F. virguliforme* isolates to fluopyram to evaluate potential shifts in sensitivity. A total of 44 isolates were collected from three counties in North Dakota (Cass, Dickey, and Richland), where the disease was prevalent in 2024 and 2025. Twelve isolates collected from Iowa, Michigan, and Minnesota prior to 2014 were used as baseline isolates in the study. Technical-grade fluopyram was added to half-strength potato dextrose agar at concentrations of 0, 1, 5, 10, 25, 50, and 100 µg a.i. mL^{-1}. A 4-mm mycelial plug was placed at the center of each plate, and incubated in the dark at 21 ± 2°C for 10 days. Colony diameters were measured to calculate percent mycelial growth inhibition and EC_{50} (effective concentration that inhibits mycelial growth by 50%) values. The experiment was conducted twice using a completely randomized design. Mean EC_{50} values for baseline and North Dakota isolates were 2.04 and 1.72 µg mL^{-1}, respectively. No significant difference was observed in the overall mean EC_{50} between baseline and North Dakota isolates ($P = 0.52$), indicating ND isolates are sensitive to fluopyram, and it remains an option for SDS management.

Design of a Denim-Based Wearable Antenna and Frequency Detuning Analysis on a Hand Phantom

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This paper presents the design and analysis of a wearable microstrip patch antenna operating at 5.5 GHz using denim fabric as the substrate. The antenna is initially designed and optimized in free space, achieving a resonance at 5.5 GHz with a return loss of 42.37 dB. To investigate wearable performance, the antenna is placed on a realistic phantom hand model at both the front and back sides. Due to the dielectric loading and losses introduced by the human tissue, the antenna resonance shifted from its original frequency. The detuning behavior is analyzed and compared for different placements. The results highlight the importance of considering body effects when designing textile antennas for wearable applications.

Optimizing Fungicide Spray Programs Against Cercospora Leaf Spot (CLS) of Sugarbeet

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Cercospora Leaf Spot (CLS) caused by fungal pathogen, *Cercospora beticola* is the most economically significant disease of sugarbeet especially in warm and humid periods of the Red River Valley. Due to its polycyclic life cycle, CLS can rapidly cause epidemics within the fields when not controlled. Along with tolerant varieties, growers rely on fungicide application at or around row closure followed by subsequent applications throughout the season. However, unnecessary application can cause increased production costs thereby reducing profit margins. This project focuses on the relationship of spray programs differing in application timing and fungicide selection to resulting CLS infection severity, root yield and recoverable sugar. Fungicide programs evaluated varied in initial application and interval between the subsequent applications. Replicated small-plot field experiments were conducted in a randomized complete block design in 2025 near Foxhome, MN and Kragnes, MN. Ten treatments, including a nontreated control, were tested on a CLS-tolerant (CR+) and susceptible Non-CR+ varieties. Initial application timings were either Mid-June, Late June, Early July, Disease Onset or 3-5% CLS Severity. The result illustrated higher CLS rating and significantly greater disease severity in nontreated plots compared to treated plots. Regardless of the varieties, early fungicide application and 14-day intervals early in the season provided better CLS control and increased recoverable sugar, but not always at a statistically significant level in this experiment. These results support current fungicide program recommendations to manage CLS in Minnesota and North Dakota, indicating economic benefits for sugarbeet growers from risk-averse CLS management programs.

The Lived Experiences of Women Teachers in Hutterite Colony Schools: Negotiating Faith and Educational Policy

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This phenomenological study explores the lived experiences of women teachers working in Hutterite colony schools in the United States. Situated within dual systems of accountability—state-regulated public education and Hutterite religious governance—these educators navigate complex cultural, linguistic, and gendered expectations in their daily work. While colony schools comply with state curriculum standards, teacher certification requirements, and accountability measures, they simultaneously operate within communal structures shaped by religious doctrine, patriarchal leadership, and trilingual language practices. This study seeks to understand how women teachers experience and make meaning of their professional roles within these intersecting systems. This research uses semi-structured interviews to examine how participants describe their instructional responsibilities. Particular attention is given to how teachers experience gendered authority, moral expectations, and the affective dimensions of classroom life. The study also explores how educators interpret and adapt state-mandated curriculum within religious boundaries, and how they experience tensions between professional standards and communal norms. The findings show that teaching in Hutterite colonies is an ongoing reflection of the relationship between faith and policy, care and authority, community cohesion, and external accountability. Participants describe their feelings as caring for students and are shaped by both constraint and agency. The narratives describe how professional identity develops through reflective negotiation of cultural expectations, linguistic boundaries, and institutional power structures. By centering the voices of women teachers, this study contributes to scholarship on faith-based schooling, gendered educational labor, and culturally responsive pedagogy in rural contexts. It extends phenomenological research into underexamined communal educational settings and offers insights for teacher preparation programs, policymakers, and educational leaders seeking to support educators working within religiously organized environments.

Assessing the Landscape Performance of Urban Riverfront Parks: A Geospatial Framework Applied to Fargo, North Dakota

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Urban riverfront parks are critical infrastructure that provide significant environmental benefits, particularly for stormwater management and flood risk mitigation. Through floodplain restoration and the integration of green infrastructure (such as riparian buffers, bioswales, and native vegetation), these parks can reduce surface runoff, enhance water retention capacity, lower peak flood elevations, improve water quality, and support urban biodiversity. Projects such as Tom Hanafan River's Edge Park in Council Bluffs, Iowa, and Portage Lakefront and Riverwalk in Indiana demonstrate how Midwestern riverfront parks use restored floodplains and green infrastructure to manage stormwater, enhance habitat, and strengthen ecological resilience. For flood-prone cities like Fargo, these parks play a crucial role in supporting community resilience to increasing climate risks. However, Fargo's riverfront parks have not yet been systematically assessed for their stormwater and flood management performance. Without such evaluation, it is difficult to guide future riverfront park design and riparian restoration. Performance assessment is also essential to demonstrate the value of parks and link design strategies with measurable ecological and hydrological outcomes that support long term resilience. To address this gap, this study aimed to develop and apply a GIS-based landscape performance assessment framework to evaluate Fargo's urban riverfront parks along the Red River with respect to stormwater and flood management. The framework utilized high-resolution remote sensing for land cover classification, field surveys for green infrastructure delineation, NDVI for vegetation health assessment, and DEMs for hydrological modeling. Spatial outputs included pollutant hotspot maps, runoff heatmaps, soil erosion risk maps, and runoff pathway models. A set of stormwater modeling tools was used to quantify the landscape performance, such as InfoWorks ICM and the EPA Stormwater Calculator. The resulting analyses evaluated performance metrics under varying rainfall events, such as total runoff, runoff retained by vegetated buffers, and pollutant loads. These findings supported ranking Fargo's parks, developing design scenarios to improve their performance, and formulating guidelines for future park planning and riparian restoration in flood-prone regions. By offering a transparent and repeatable evaluation method, the study supported evidence-based decision-making for the design, restoration, and management of riverfront parks in Fargo and comparable urban contexts.

Intrinsically Disordered Regions (IDRs) as Regulatory Hotspots in Pancreatic Cancer

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Pancreatic ductal adenocarcinoma (PDAC) is the most predominant form of pancreatic cancer and is one of the deadliest forms of all cancers, with a 5-year survival rate of about 13%. While traditional cancer research has focused on structured protein domains (for example, KRAS in PDAC), intrinsically disordered regions (IDRs) have emerged as critical regulatory elements in oncogenic signaling and have been largely unstudied in pancreatic cancer research. Here, we present an integrative computational pipeline to systematically characterize the role of IDRs in frequently mutated and differentially expressed genes in PDAC. Specifically, we used sequence-based disorder prediction (Metapredict), mutation mapping, molecular recognition feature (MoRF) analysis, post-translational modification (PTM) profiling, and subcellular localization profile (DeepLoc2) to compare frequently mutated PDAC proteins against wildtype proteins within over- and under-expressed gene sets obtained from COSMIC, GEPIA2, cBioPortal, and UniProt databases. Our data indicates that pancreatic cancer-associated proteins have significantly more extended IDRs (>100 amino acids) than other tumor types. Within the group of somatic mutations, 30% were found to be localized within disordered regions, and the percentage of high impact mutations was disproportionately high within disordered regions. Interestingly, nonsense and frameshift mutations produced significant effects on both disorder and predicted subcellular localization properties. Disordered features analysis of clinical survival datasets (from TCGA) reveals that proteins that are unfavorable to patient survival typically have higher disordered content, establishing the clinical significance of protein disorder. Furthermore, prediction of liquid–liquid phase separation (LLPS) propensity demonstrated a strong positive correlation between high phase separation potential and unfavorable survival-associated proteins. These data suggest that IDRs within PDAC associated proteins are structurally and biologically relevant as targetable "hotspots" and need further experimental investigation as potential therapeutic targets.

Foam Fractionation of PFAS from Landfill Leachate Using a Membrane Electrochemical Reactor

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The effective removal of PFAS from chemically complex landfill leachate remains a significant challenge for the solid waste industry. To address this, a membrane electrochemical reactor (MER) was investigated for PFAS removal from landfill leachate at low pH (≈2.0) in the anode chamber. The MER achieved 95.6 % PFAS removal from landfill leachate within seven hours of operation, with 98.3 % of perfluorosulfonic acids (PFSA) and 85.5 % of perfluorocarboxylic acids (PFCA) removed from the leachate. Short-chain PFSAs ($C \leq 6$, 92.5–99.1 %) were removed more efficiently than PFCAs ($C \leq 6$, 80.8–90 %), possibly due to their stronger affinity for the air–water interface, which enhanced foam-based separation. Long-chain PFAS ($C > 6$) showed near-complete removal (96.1–100 %). Importantly, PFAS precursors such as fluorotelomer carboxylic acids and perfluoroalkane sulfonyl fluorides were not detected in defoamed leachate, suggesting their removal through both oxidative transformation and foam-phase partitioning in the MER. Simple pH adjustment to 2.0 using concentrated H2SO4, conducted for comparison with the MER, resulted in 83.1 % of PFAS separation into foam and 11.3 % into settled solids. Additionally, short-chain PFAS were separated into foam (59.2–84.7 %) and settled solids (5.7–13 %), while long-chain PFAS showed similar trends with 78.3–86 % in foam and 5.3–18.2 % in settled solids. The addition of 0.1 M NaHCO3 before pH adjustment enhanced foam formation, increasing PFAS separation in foam to 92.5 %. This study highlights MER's effective PFAS removal performance without any solid precipitate generation. Further research should explore the effect of MER operational conditions and leachate–PFAS chemistry on the treatment performance.

Genetic Mapping of a Novel Rust Resistance Gene in Common Bean (*Phaseolus vulgaris* L.) Cultivar ND Twilight

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Bean rust (caused by *Uromyces appendiculatus* Pers.) is considered one of the most economically important diseases of common bean (*Phaseolus vulgaris* L.), with significant seed yield losses worldwide under severe infections. The pathogen has a complex life cycle involving sexual recombination which paves the way for the emergence of new races. This underscores the need for the identification of novel resistance loci to develop resistant bean cultivars. More than 20 rust resistance genes belonging to the Ur-series have been identified, and at least 10 of these have been genetically mapped with their loci distributed across chromosomes Pv01, Pv04, Pv06, Pv07, Pv08, and Pv11. 'ND Twilight' is a black bean cultivar that has shown a resistant response to predominant races of bean rust in North Dakota. However, it was unclear if the rust resistance in ND Twilight is conferred by previously known genes or from an unknown source. A biparental F2 population was developed by crossing UI 114 (susceptible) with ND Twilight (resistant) to evaluate its response to race 20-3 and to map genomic regions associated with resistance through bulked segregant analysis. Preliminary results suggest that the resistance is controlled by a single recessive gene ($\chi^2 = 0.89$, $p = 0.35$). A major QTL conferring rust resistance was identified on Pv04 between 4,750 and 5,037,474 bp, spanning approximately 5.0 Mb. To our knowledge, this is the first report of a recessive gene–mediated resistance in common bean against *U. appendiculatus*. Future studies will involve validation, fine-mapping and cloning of this locus to understand the genetic mechanism of resistance and the development of molecular markers for its future deployment in bean cultivars.

Evaluating the Efficacy of Virtual Fencing to Implement Patch Grazing

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Virtual fencing systems utilize digital fence boundaries and global positioning system (GPS)-enabled collars or ear tags to manage movement of grazing animals. Auditory and electrical stimuli are used to keep individual animals within the VF-designated boundaries. While VF technologies are commonly evaluated to determine their effects on livestock production outcomes, an added benefit may be their ability to promote heterogeneity-based grazing patterns. These grazing patterns can help combat biodiversity loss on working landscapes. However, successful grazing management for heterogeneity requires effective cattle containment throughout the grazing period. The objective of this study was to determine VF's efficacy in containing cattle during patch grazing. This trial was conducted at three study sites across North Dakota (one site in 2023, an additional site in 2024, and another additional site in 2025). Cattle with VF collars grazed for an average of 150 days between June and October. Four pastures were divided into quadrants using VF and cattle were permitted to graze one quarter, then one half, then three quarters of the pastures, excluding one quarter. This pattern created a gradient of disturbance by varying grazing intensity over space and time, impacting vegetation structure. Collars sent location data every ≈15 minutes, and containment within the VF was calculated as the percentage of all collar location signals from within the VF boundary. The average virtual fence containment rate was 74.7% ($n = 523$), ranging from 72.3% ($n = 237$) to 84.8% ($n = 95$) between years and 65.8% ($n = 207$) to 84.6% ($n = 283$) between sites. Site, year, rotation, pasture, and individual differences in containment rate were all highly significant ($P < 0.001$). In 2025, the virtual fence patch grazing (VF-PG) cows gained an average of 0.442 lbs/day more than cows under season long grazing (SLG) ($P < 0.001$). There was no significant difference in average daily gain (ADG) between the calves of VF-PG and SLG cows. Forage production and utilization data were collected at CGREC in 2025 and, while virtual fence containment was effective enough to produce a visual difference in forage production, it did not have statistically significant impacts on forage production or utilization.

Seed Decay in Soybean: Implications for Animal Health

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Seed decay in soybean (*Glycine max* L.) is primarily caused by fungal pathogens such as *Diaporthe* (*Phomopsis*) *longicolla*, *Cercospora kikuchii*, and species of Fusarium. Warm and humid conditions during the late reproductive stages, delayed harvest, and poor post-harvest storage can favor pathogen infection. These pathogens degrade seed tissues, reduce seed quality, and reduce grain yield. Despite *D. longicolla* being an important seed decay pathogen, there is limited information available regarding the metabolites it produces and their potential effects on animal health. Therefore, in this study, untargeted metabolomic profiling was performed on two isolates of *D. longicolla* obtained from diseased soybean plants sampled from commercial fields and cultured in potato dextrose broth to characterize their secondary metabolites. The analysis revealed that cytochalasin derivatives (P and N), along with fumonisin B, were significantly upregulated in both isolates, whereas zearalanone was significantly upregulated in only one isolate ($P < 0.05$) compared with the non-inoculated control (potato dextrose broth). These findings suggest that *D. longicolla* may produce metabolites, such as fumonisin B and zearalanone, similar to those previously reported in *Fusarium* spp., highlighting the need for further investigation into their potential impact on animal health.

Enhancing Construction Site Safety using Safety-Aware Motion Planning for Autonomous Cranes

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Construction sites are busy environments where cranes operate close to workers, vehicles, and heavy equipment. Most cranes are still controlled by human operators. Because of blind spots, limited visibility, and complex site conditions, accidents can occur when cranes move too close to people or objects. Autonomous crane systems have the potential to improve safety and efficiency on construction sites. However, many existing motion planning methods for automated cranes focus mainly on finding the shortest or fastest path. These methods often do not account for how close the crane moves to workers or equipment, which can create safety risks. This research presents a safety-aware motion planning method for autonomous tower cranes. The goal is to generate crane paths that are both efficient and safe. The proposed method adds an adaptive safety margin to the Rapidly Exploring Random Tree Star (RRT*) motion planning algorithm. This safety margin increases the cost of paths that move too close to obstacles such as workers, vehicles, or construction equipment. As a result, the planner prefers paths that keep a safer distance from these objects while still moving efficiently. To test the method, a simulated construction site was created with a 3-degree-of-freedom (DoF) tower crane. The proposed method was compared with a standard RRT* and a dilation-based safety method. The comparison used several metrics, including safety cost, path length, success rate, and planning time. The results show that the proposed method produces safer crane paths while maintaining similar path efficiency and planning time. This study shows that adding safety awareness to motion planning can help improve autonomous crane operations and reduce safety risks on construction sites.

Understanding How Wheat Fights Off Major Disease: Stem Rust

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Stem rust, caused by *Puccinia graminis* f. sp. *tritici* (Pgt), is a major wheat disease threatening global wheat production. To identify novel sources of resistance against foreign rust races, 497 durum lines were evaluated at both seedling and adult stages. Three durum accessions; PI192711, PI383416, and PI520392, showed resistance to three foreign rust races: TTKSK, JRCQC, and TRTTF, respectively. Recombinant inbred line (RIL) populations at F5 developed by crossing these accessions with Rusty were used to detect genomic regions associated with resistance. iSelect 90K SNP assays were used to genotype these populations, and high-density linkage maps were constructed using JoinMap. Composite interval mapping (CIM) identified three quantitative trait loci (QTLs) on chromosomes 3B and 7A against the TTKSK race in PI192711/Rusty population. A single QTL on chromosome 2A contributing 78.23% of phenotypic variation against the TRTTF race, and another QTL on 4A contributing 61.30% variation against JRCQC, were mapped from the PI383416/Rusty population. PI520392/Rusty population identified three QTLs on chromosomes 2B, 5B and 6A against the TRTTF race contributing 24.35%, 29.3% and 26.93% phenotypic variation, respectively. Among these eight QTLs identified in this study, five of them overlapped with earlier reported Sr genes, while three mapped to novel regions. Allele-effect plots showed that resistance to TTKSK in the PI192711/Rusty population required combined presence of all three reported QTLs, whereas in the PI520392/Rusty population each of the three QTLs individually conferred a comparable level of resistance to TRTTF. QTL on 7A mapped approximately within 6.21cM interval which corresponded to 5.7Mbp in Svevo v2 reference genome with 111 high-confidence (HC) genes with a few potential candidate genes for disease resistance. While QTL on 5B mapped approximately 7.03cM candidate region corresponding to 13.10Mbp with 193 HC genes and QTL on 4A mapped between 8.19cM region with 87 HC genes in Svevo v2 genome.

Organic Micropollutants Removal from Wastewater Recycling Concentrate by Far-UVC (222 Nm)-Based Advanced Oxidation

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Far-UVC at 222 nm using KrCl* excimer lamps represents an emerging technology for advanced oxidation of organic micropollutants (OMPs). This study investigated the efficiency of UV222-based AOPs for removing OMPs in reverse osmosis concentrate (ROC). Photolysis experiments were performed using a KrCl* excimer lamp, and its performance was compared with that obtained with a low- pressure mercury lamp. UV222/AOP achieved, on average, 8–15-fold higher fluence-normalized degradation rates than UV254 for carbamazepine, DEET, caffeine, and 1,4-dioxane. With only 30–60 % reduction in ROC compared to that of DI water, the decay rates of OMPs revealed high resilience of 222 nm irradiation in complex matrices. Observed rates were 1.4–2.3 times higher than calculation based on direct photolysis, confirming additional reactive species-mediated oxidation.

Presence of nitrate increased degradation of the OMPs, whereas fulvic acid caused inhibition due to light attenuation and radical scavenging. These results illustrate the strong potential of KrCl*-based far-UVC AOPs for efficient ROC treatment.

Food Insecurity Trajectories in Mothers with Depression: A Randomized Trial of Cash Transfers

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Food insecurity affects 13.5 million U.S. households and disproportionately burdens low-income families with young children (USDA, 2023). Although maternal depression is a well-established correlate of food insecurity (Whitaker et al., 2009; Karpyn et al., 2020), few studies have examined how depression operates as both a stable individual difference and a time-varying state in shaping food insecurity trajectories, or whether unconditional cash transfers can alter these trajectories over time. This study used data from Baby's First Years study (BFY), a randomized controlled trial in which 1,000 low-income mothers were assigned to receive either high ($333/month) or low ($20/month) unconditional cash transfers beginning shortly after their child's birth. The analytic sample comprised 949 mothers across four U.S. metropolitan areas (New York, New Orleans, Twin Cities, and Omaha), providing 2,693 observations at child ages 1, 2, and 3. Food insecurity was measured on a 0–6 scale and maternal depression was assessed using the PHQ-8. Multilevel growth models with person-mean decomposition were used to disaggregate within-person and between-person effects of depression on food insecurity trajectories. Results indicated that food insecurity declined significantly over time ($b = -0.008$, $p = .010$). Maternal depression was the strongest predictor. The between-person effect ($b = 0.196$, $p < .001$) was 3.5 times larger than the within-person effect ($b = 0.055$, $p < .001$), explaining about 30.5% of between-person variance. This suggests that chronic depression functions as a stable risk factor for food insecurity rather than merely a reactive response to temporary hardship. A marginally significant Treatment × Time interaction ($b = -0.009$, $p = .053$) indicated that families receiving higher cash transfers declined in food insecurity 2.2 times faster than controls, converging to similar levels by age 3 despite higher baseline food insecurity. These findings suggest that unconditional cash transfers may accelerate recovery from food insecurity, particularly for families with the greatest initial need, and underscore the importance of pairing economic interventions with mental health support.

The Relationship between Tumor Hypoxia and Metastasis in Pancreatic Ductal Adenocarcinoma

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Hypoxia in solid tumors is associated with reduced intra-tumoral transport, drug-resistant cancer stem cells, increased treatment difficulty, and consequently, poor patient prognosis. Nanoparticles have the potential to penetrate solid tumors and release the encapsulated drugs in hypoxic niches. This study aims to investigate the effects of hypoxia on cancer stemness, metastasis, and the tumor microbiome employing three-dimensional spheroids of patient-derived pancreatic cancer cells. Subsequently, we will mitigate hypoxia by delivering oxygen through cerium oxide nanoparticles and determine the effect on cancer stemness. We will also deliver a broad-spectrum antibiotic through polymer nanoparticles to understand the effects of altered microbiome composition on drug resistance and metastasis. Since cancer metastasis involves blood flow, we constructed a 3D-printed bioreactor (designed by computational fluid dynamics simulation) that functions at high flow rates. We will use this in vitro metastasis model to probe the roles of oxygen and antibiotic delivery in reducing cancer metastasis.

A Novel CNN-Based Approach for Soil Nutrient Prediction Using Hyperspectral Imaging

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Soil nutrient management plays a vital role in sustainable agriculture, directly influencing crop yield and food security. Traditional methods for estimating soil nutrients like nitrogen (N), phosphorus (P), and potassium (K) are time-consuming and requiring extensive laboratory analysis. This study aims to develop an efficient and accurate method for soil nutrient prediction using hyperspectral imaging. Hyperspectral imaging captures high-resolution spectral and spatial data, enabling comprehensive analysis. Soil samples were collected from two diverse locations in North Dakota representing varying soil properties and management zones. Samples underwent laboratory analysis for nutrient content and hyperspectral imaging in the range of 400-1700 nm. The data was further processed and classified into nutrient categories based on laboratory results. After testing different machine learning (ML) and deep learning (DL) nutrient prediction models, a convolutional neural network (CNN) model is developed to predict soil nutrient status, with integration of advanced deep learning techniques like CNN neural architecture search (NAS) models to optimize prediction performance. These novel approaches aim to improve the accuracy and reliability of soil nutrient prediction, addressing limitations such as variability in spectral data and environmental noise. The CNN-NAS models achieved a prediction accuracy of 0.83 showing the potential of artificial intelligence for efficient soil nutrient monitoring, offering a cost-effective, real-time solution for precision agriculture. By exploring the integrated use of hyperspectral imaging and cutting-edge CNN models, this study contributes to the advancement of digital agriculture.

The Use of Single Residue Targeted Mutagenesis to Identify Lysines within Replication Factor A1 (Rfa1) Required for Checkpoint Activation, a Critical Step in Preventing DNA Mutation and Cellular Disease

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DNA replication and mitosis/cell division follow a pathway (i.e., the cell cycle) with essential quality control checkpoints to ensure chromosomal DNA is complete and intact before proceeding to the next phase in the cycle. Replication Factor A (RFA) is an essential single-stranded DNA binding complex that recognizes damaged DNA and recruits repair proteins while also activating a DNA damage checkpoint.

Checkpoint activation allows time for damage repair to occur in G2 phase and prior to chromosomal division in M phase (mitosis), thus ensuring the integrity of the genome that is passed on to daughter cells. RFA has been demonstrated to be essential for cells to activate the G2/M checkpoint. Furthermore, our lab has shown that the Rfa1 subunit (616 amino acid protein containing 39 lysine residues) is critical for this activation. This was shown using an Rfa1 (lysineless) mutant that cannot be post-translationally modified at lysines, which subsequently also cannot activate the checkpoint efficiently. This leads to increased mutation frequency and the potential for cellular disease. My research utilized in vitro site-directed mutagenesis to restore specific lysine (or combinations of lysine) residues in the Rfa1 lysineless mutant. These now lysine-containing Rfa1 forms were introduced into the yeast Saccharomyces cerevisiae through a plasmid shuffle technique, and DNA damage was induced by expression of an endonuclease in the cell that breaks chromosome III. The ability to restore checkpoint activation following DNA damage when the proper Rfa1 lysine residue(s) was restored was assayed by microscopy. Our studies show that checkpoint activation likely requires modification of as few as one specific lysine residues in Rfa1. Our data also indicate that the locations (amino acid positions 170, 180, and/or 411) of lysine modification lie in non-structured regions of Rfa1. Further testing will conclusively determine if sumoylation of Rfa1 is the modification of lysine required and if a particular sumoylated form (e.g., mono-, di-, tri-) of Rfa1 is necessary for activating the G2/M checkpoint. This data will allow for a better understanding of how cells monitor DNA damage and prevent mutations that ultimately lead to disease.

Exploring the Professional Experiences of English Language Learner High School Teachers in a Rural State: A Qualitative Investigation

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The purpose of this research was to explore the perceptions and experiences of high school teachers in North Dakota who teach English Language Learners (ELL). Using the transcendental phenomenological method, we interviewed seven teachers with between 10 and 23 years of experience working with ELL students. Ecological systems theory (EST) was employed to capture specific elements and processes present in the school environment that assist or hinder ELL teachers as they fulfill their work responsibilities and support the resettlement of New Americans. The findings revealed the complex and multifaceted role of ELL teachers, which is affected by multiple ecological factors and duties that extend well beyond teaching in a classroom. Participants felt supported in their work life by ELL teachers, paraeducators, interpreters, and ELL programs. However, the participants expressed aspects of their work lives that inhibit their ability to assist ELL students, including the exclusive responsibility of ELL, a lack of professional development opportunities, time-consuming language testing responsibilities, and conflicts with mainstream teachers who do not fully understand how to best engage with ELL students. In light of these findings, we offer practical implications for schools to better support ELL teachers and foster inclusive school environments for English learners and New Americans.

Less Plastic, Smarter Design: Reducing Material Use in Bottled Water Packaging

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The consumption of single-use plastic water bottles has surged over the past two decades, yet guidance on improving bottle design remains limited. To address this gap, we investigated how packaging design, bottle size, bottle components, and polymer composition influence the plastic footprint of bottled water, using carbon content as a proxy. Fifteen bottled water brands, ranging from 0.24 L to 9.5 L, were purchased from U.S. retail stores. Large-capacity bottles—particularly the 4 L size—had the lowest carbon content per unit volume, averaging 13.45 ±0.84 g/L. In contrast, largely due to differences in packaging design and body wall thickness, the embedded carbon content of small-capacity bottles showed substantial variability. The carbon content of a 0.5 L bottle varied from an average of 9.48 to 30.99 g/L. Bulky caps and full-body wrappers also significantly increased carbon. Optimizing packaging weight in widely used 0.5 L bottles—from 51.66 to 15.64 g/L—could yield an estimated annual polymer savings of 0.68 million tons. Most bottles analyzed were made of mixed polymers; for instance, 0.5 L bottles typically consisted of 9.68–31.14 g PET/L, 1.19–4.16 g PE/L, 0.29–1.35 g PP/L, 0.40–1.89 g PVC/L, and 0.03–0.08 g PS/L. These findings highlight the potential need for mono-material packaging and standardized design guidelines, emphasizing reduction in polymer content as a practical strategy to lower the footprint of bottled water across its supply chain.

Applying Multimodal Large Language Models to Thermal Imaging for Smart Building Climate Control

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Real-time Clothing Insulation Level Recognition (CILR) is crucial for enhancing thermal comfort and energy efficiency in adaptive HVAC control systems. However, existing solutions either rely on intrusive sensors or extensive labeled datasets, limiting practical deployment. To address these limitations, this study introduces a thermal-image–driven MLLM approach for CILR and evaluates its performance under limited-data conditions. We collected a dataset of 110 thermal images, classified into three insulation levels, including low, moderate, and high. A fine-tuned MLLM (Gemini-2.0-flash-lite) and a conventional convolutional neural network (CNN) reference model were trained on varying subsets of this dataset (20, 50, and 90 images). Experimental results reveal that the fine-tuned MLLM consistently outperforms the CNN across all dataset sizes, achieving accuracy of 70% even with just 20 training images, compared to only 40% by the CNN. With 90 training images, the MLLM's accuracy reached 90%, substantially surpassing the CNN's 75%. These findings highlight the MLLMs' superior generalization capability and data efficiency, driven by its inherent semantic reasoning. Consequently, fine-tuned multimodal MLLMs represent a promising, practical solution for accurate and efficient real-time clothing insulation estimation in smart HVAC applications.

The Structural Characteristics, Functional Properties, and Health Properties of Resistant Starch Derived from Common Beans

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Common beans are widely consumed as a staple food. In beans, starch is the major carbohydrate, typically accounting for approximately 50% of their composition. Resistant starch (RS), a fraction of starch that escapes digestion in the small intestine and is fermented in the large intestine, has been associated with numerous health benefits. However, RS in beans has received relatively little attention. Therefore, the objective of this study was to enhance the RS content of bean starch and to investigate its physicochemical, functional, and health-related properties using isolated native navy bean starch (NS) and red kidney bean starch (KS) as representative samples. The effects of microwave treatment (15 s), enzymatic treatment with pullulanase, and their combination on the physicochemical properties and digestibility of modified bean starches were evaluated and compared with their native counterparts. Overall, pullulanase-mediated debranching and the combined treatment significantly increased RS content, amylose levels, and functional properties such as water-holding capacity in both bean starches. For example, the RS content of NS increased from 16.55% to 30.39%. X-ray diffraction (XRD) analysis revealed that both native and modified starches exhibited an A-type crystalline pattern, except that the combined treatment shifted from A-type to A+V-type crystallinity. In addition, relative crystallinity slightly decreased after modification. These results were consistent with microstructural observations: unlike the smooth surfaces of native starch granules, modified starch granules exhibited fissures and fractures. In terms of health-related properties, enzymatic and combined treatments slightly increased in vitro bile acid-binding capacity. Interestingly, both native and modified starches fell within the low glycemic index (GI) category; however, native starch exhibited a lower estimated GI (eGI) than modified starch. This may be attributed to incomplete hydrolysis of the high-purity starch within the 2-h digestion period. Overall, these findings provide a basis for the development of bean-derived starches as functional health ingredients.

The Role of Alamandine in Cardiometabolic Health and Disease

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Natural processes such as aging and pathologies that alter energy metabolism, like obesity and type II diabetes, are strongly associated with the development of heart disease. Local cardiac insulin resistance has been linked to worsening heart disease even in non-diabetic patients. Angiotensin II (Ang II), a key peptide of the classical renin angiotensin system (RAS), drives cardiac remodeling and hypertrophy. The non-classical RAS, comprised of peptides such as the novel heptapeptide Alamandine (Ala), is currently understood to play a pivotal counterregulatory role of attenuating the detrimental effects of Ang II. This study explores Alamandine and its receptor MrgD in the heart during aging. We are hypothesizing that Alamandine couples with MrgD to protect the heart during aging. In this study, mice were treated with Alamandine. Echocardiography performed showed an improvement in cardiac function in old mice treated with Alamandine. Our results suggest that Alamandine influences the heart in old males through an increase in PKA activity, which leads to elevated phosphorylation of PLB at Ser16. Future studies will further explore the metabolic effects of Alamandine in the aged heart and during metabolic stress.

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thank you!

This event was made possible through the generous funding support of the Office of the Vice President for Research and Creative Activity and NDSU Student Government. Gamma Sigma Delta offers a heartfelt thanks to the Minnesota Soybean Research and Promotion Council as well as to the NDSU College of Agriculture, Food Systems and Natural Resources. We are grateful for their commitment to advancing student research endeavors.

We also extend our sincere appreciation to the many individuals who contributed to the success of this event, our evaluators, volunteers, faculty mentors, and all those who offered their time, expertise, and support. Your dedication helps create meaningful opportunities for our students to showcase their research and grow as scholars.

Thank you for being part of this celebration of student research!

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