The 10th Annual Conference of the Arkansas Bioinformatics Consortium (AR-BIC)

AR-BIC 2024

We are an Arkansas Collaborative Community in Bioinformatics Research

https://ar-bic.aralliance.org/

Real-World Impact of AI

February 26-27, 2024

Conference Center
Wyndham Riverfront Little Rock
North Little Rock, Arkansas

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AR-BIC 2024: Real-World Impact of AI

Established in 2014, the Arkansas Bioinformatics Consortium (AR-BIC) is an Arkansas-centric community that facilitates communication and collaboration among researchers to leverage the state's expertise and resources in data sciences and bioinformatics. While celebrating 10 years of this annual conference, leading experts will convene to share and discuss the transformative impact of AI in addressing real-world challenges. They will illustrate how AI is reshaping scientific research, influencing regulatory decision-making, and driving meaningful changes in public health and beyond. The 2-day conference will be held at Wyndham Riverfront Little Rock, February 26 - 27, 2024, https://ar-bic.aralliance.org/.

Organized and supported by:

Arkansas Bioinformatics Consortium (AR-BIC)

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*University of Arkansas (UA)
*University of Arkansas at Little Rock (UALR)
* University of AR for Medical Sciences (UAMS)
* University of Arkansas at Pine Bluff (UAPB)

**Funding for this conference was made possible, in part, by the Food and Drug Administration through grant 1R13FD005304-02, views expressed in written conference materials or publications and by speakers and moderators do not necessarily reflect the official policies of the Department of Health and Human Services; nor does any mention of trade names, commercial practices, or organization imply endorsement by the United States government.*

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- Room A: Cloud-based Training
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- AWS HealthOmics

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Dr. Shuk-Mei Ho	(4:00 pm – 4:45 pm)
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Break: 5:30 pm – 6:00 pm

Welcome Reception and Poster Session (6:00 pm – 8:00 pm)

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- Room A: Careers in Medicine
- Room B: Careers at FDA

Breakout Sessions (9:00 am – 10:30 am)

- Room A: AI for NLPs
- Room B: AI Ethics

Break: 10:30 am – 11:00 am

Breakout Sessions (11:00 am – 12:30 pm)

- Room A: AI in Informatics
- Room B: Interpretable AI

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GENERAL INFORMATION

Venue and Date

- Wyndham Riverfront Little Rock: 2 Riverfront Pl, North Little Rock, AR 72114
- February 26-27, 2024 (Monday and Tuesday)

AR-BIC Advisory Council 2023-2024

- Arkansas Biosciences Institute (ABI): **Bobby McGehee**
- Arkansas Economy Development Commission (AEDC): **Jennifer Fowler**
- Arkansas Research Alliance (ARA): **Bryan Barnhouse (Chair), Amy Hopper Swan, Michelle Barnes**
- Arkansas State University (ASU): **Travis Marsico**
- National Center for Toxicological Research (NCTR): **Tucker Patterson, Weida Tong, Dongying Li**
- University of Arkansas (UA): **Margaret McCabe**
- University of Arkansas at Little Rock (UALR): **Brian Berry**
- University of Arkansas for Medical Sciences (UAMS): **Shuk-Mei Ho**
- University of Arkansas at Pine Bluff (UAPB): **Mansour Mortizavi**

Scientific Program Committee (2023-2024)

- Arkansas Research Alliance (ARA): **Bryan Barnhouse, Michelle Barnes, Amy Hopper Swan, Douglas Hutchings**
- Arkansas State University (ASU): **Asela Wijeratne**
- Center for Drug Evaluation and Research, Food and Drug Administration, **Shraddha Thakkar**
- National Center for Toxicological Research (NCTR): **Weida Tong (Chair), Huixiao Hong, Steven Foley, Joshua Xu, Dongying Li**
- University of Arkansas (UA): **Samantha Robinson, Douglas Rhoads, Jimmy Abbas**
- University of Arkansas at Little Rock (UALR): **Mary Yang, John Talburt**
- University of Arkansas for Medical Sciences (UAMS): **Shuk-Mei Ho, David Ussery**
- University of Arkansas at Pine Bluff (UAPB): **Grace Ramena, Vinay Raj**

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- Scientific Program: Weida Tong (Weida.Tong@fda.hhs.gov)

PROGRAM AGENDA

DAY 1 – FEBRUARY 26, 2024

10:00AM – 1:00PM **Registration and Poster Setup**

10:30AM – 12:00PM ***Pre-Conference Workshops A & B (Parallel)***

- **Workshop A: Cloud-based Training modules for Data Sciences (Room A)**
  Instructor: Dr. Stephanie Byrum, Associate Professor, University of Arkansas for Medical Sciences

  Description: This workshop will introduce the NIGMS Sandbox cloud-based training modules, how to setup an account, create a compute engine using Google cloud, and access 12 different data science training modules. A working demonstration of the Biomedical Imaging Analysis training module will be presented.

- **Workshop B: AI and Machine Learning Made Easy with JMP (Room B)**
  Instructor: Dr. Russ Wolfinger, Director of Scientific Discovery and Genomics, and Dr. Wenjun Bao, Chief Scientist and Director of Advanced Analytics R&D, JMP Statistical Discovery, SAS Institute Inc

  Description: This workshop features new developments in JMP Pro software to provide you direct access to two of the most powerful libraries for AI and Machine Learning: Torch and XGBoost. The primary motivation is to enable busy scientists and engineers to interactively and quickly wrangle data and build state-of-the-art predictive models without having to write code in Python or R. This often affords dramatic gains in efficiency in understanding, predicting, and explaining complex scientific systems, leading to better discoveries and progress and mastery of difficulties like overfitting and deployment. The dynamic graphical interfaces and workflows are designed from deep experience gained and battle tested over years engaging with a worldwide customer base and in dozens of data science competitions. We show examples from a variety of scientific fields using image, text, and tabular data.

12:15PM – 1:45PM ***Pre-Conference Workshop C***

- **Workshop C: Deep Learning Based Analysis**
  Instructor: Nan Gabriel, Solutions Architect, Healthcare and Life Sciences, Amazon Web Services

  Description: This workshop focuses on using the Graphical User in AWS Console to complete tasks and demonstrate the capabilities of AWS HealthOmics Storage and Ready2Run Workflows. Some experience with AWS, genomics data types, and genomics data analysis is expected but not a strict requirement.

2:00PM – 2:15PM **Opening Remarks**

- **Opening Remarks:** Bryan J. Barnhouse, President & CEO, Arkansas Research Alliance

2:15PM – 5:30PM ***Plenary Session***

Chair: Dr. Weida Tong, Director, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, US FDA

2:15 – 3:00PM ***The ToxAIcologist Is In – Ask Anything!*** Dr. Thomas Hartung, Director, the Center for Alternatives to Animal Testing, Johns Hopkins University

3:00 – 3:45PM ***Data Science: Making Safety Part of Drug Design,*** Dr. Ruth Roberts, Director and Cofounder, ApconiX; Chair and Director of Drug Discovery, University of Birmingham, UK

3:45 – 4:00PM **Break**

4:00 – 4:45PM ***Can AI Heal? Unpacking the Hype and Hope of AI in Public Health,*** Dr. Shuk-Mei Ho, Vice Chancellor for Research & Innovation; Professor, Department of Pharmacology and Toxicology, University of Arkansas for Medical Sciences

4:45 – 5:30PM ***Enhancing Dementia Studies with AI and Informatics: Strategies for Mining Big BioHealth Data,*** Dr. Li Shen, Professor and Deputy Director of Division of Informatics, Department of Biostatistics, Epidemiology and Informatics, Perelman School of Medicine, University of Pennsylvania

5:30PM – 6:00PM **Break**

6:00PM – 8:00PM ***Welcome Reception and Poster Session***

DAY 2 – FEBRUARY 27, 2024

8:00AM – 9:00AM ***Breakfast and Career Development Roundtables (Parallel)***

- **Roundtable A: Careers in Medicine (Room A)** – Dr. Bobby McGehee, Distinguished Professor, University of Arkansas for Medical Sciences; join to learn the ins and outs of medical school applications, admissions, and experience.

- **Roundtable B: Careers at the FDA (Room B)** – Dr. Tucker Patterson, Director, National Center for Toxicological Research, US FDA; join to learn about the vast career opportunities within the FDA, the world's premier regulatory agency for public health and safety.

9:00AM – 10:30AM ***Breakout Sessions 1 & 2 (Parallel)***

SESSION 1: AI FOR ANALYZING UNSTRUCTURED DATA (ROOM A)

Chair: Dr. Huixiao Hong, National Center for Toxicological Research, US FDA

Description:
Unstructured data refers to data that doesn't have a predefined structure or format, such as text documents, images, audio recordings, and videos. Analyzing unstructured data is a common and valuable application of artificial intelligence (AI). AI can be used to extract meaningful insights, patterns, and knowledge from unstructured data. When analyzing unstructured data, it's essential to use the appropriate AI techniques and tools based on the specific requirements of projects or business goals. Recently, many AI techniques and approaches have been emerging for analyzing unstructured data, including natural language processing techniques that enable the analysis of text data, such as BERT, GPT-3 and their successors which are proficient at tasks such as text classification and summarization; sentiment analysis AI techniques that determine the emotional tone or sentiment expressed in textual data to assist gauge public opinion and

customer feedback; text mining and information retrieval approaches that extract valuable information from large volumes of text data, such as keyword extraction, topic modeling, and document clustering; and named entity recognition methods that identify and classify entities such as drug terms, genes, and proteins within unstructured text. This session provides a lineup of experts in application of AI for analyzing unstructured data to share their research, findings, and opinions and to discuss the possibility and likelihood of advancing AI techniques and approaches to promote and improve analysis of unstructured data.

9:00 – 9:30AM ***Automatic Text Classification of Drug-induced Liver Injury Using Document-term Matrix and XGBoost,*** Dr. Wenjun Bao, JMP Statistical Discovery, SAS Institute Inc

9:30 – 9:50AM ***BERT-Based Language Model for Extracting Drug Adverse Events from Social Media***, Dr. Fan Dong, National Center for Toxicological Research, US FDA

9:50 – 10:10AM ***Enhancing Quality of Drug Terms in Rxnorm to Empower Artificial Intelligence for Analysis of Unstructured Textual Data,*** Dr. Wenjing Guo, National Center for Toxicological Research, US FDA

10:10 – 10:30AM ***Towards Robustly Measuring Bias in Input Embeddings,*** Magnus Gray, National Center for Toxicological Research, US FDA

SESSION 2: AI ETHICS: CONSIDERATIONS AND RECOMMENDATIONS FOR PURSUING POSITIVE IMPACT (ROOM B)

Chair: Dr. Samantha Robinson, University of Arkansas, Fayetteville

Description:
Following the recent release of ChatGPT, Bard, and Bing Chat, debate and discussion about artificial intelligence (AI) ethics has broadened in scope. The risks posed by new AI applications are risks that are now being faced head on by government, industry, and academia. Everywhere that has embraced the rapid development, and the utility of AI must also carefully consider the ethical implications of its use. With recent technological advancements and the increasing availability of real-world data, there is widespread consensus that discussions about AI ethics must move beyond explainability/interpretability and fairness/bias. AI is one of the most impactful technologies developed but, without consideration of the problems existent in present-day AI applications and concerted efforts to find solutions to these problems, the safety of AI (especially in high-stakes settings) will remain uncertain. This session will serve as a forum for scientists, educators, philosophers, and practitioners from across our state to share insights about AI ethics and discuss how, with ethics in mind, we can harness the power of AI for the public good.

9:00 – 9:30AM ***Concepts, Measurements, and Mitigations of Bias in Artificial Intelligence***, Dr. Leihong Wu, National Center for Toxicological Research, US FDA

9:30 – 9:50AM ***(Informational) Privacy and Oppression***, Dr. David Barrett, University of Arkansas, Fayetteville

9:50 – 10:10AM ***AI Needs the Humanities***, Dr. Zachary Stine, University of Central Arkansas

10:10 – 10:30AM ***Integrating Ethics in the Statistics Classroom and Beyond***, Dr. Samantha Robinson, University of Arkansas, Fayetteville

10:30AM – 11:00AM **Break**

11:00AM – 12:30PM Breakout Sessions 3 & 4 (Parallel)

SESSION 3: AI IN INFORMATICS (ROOM A)

Co-Chairs: Dr. Mary Yang & Dr. John Talburt, University of Arkansas at Little Rock

Session Description:

In this era of data abundance and rapid advancements in Artificial Intelligence (AI) technologies, the dynamic synergy between AI and informatics has emerged as a driving force for profound breakthroughs. Across the multifaceted landscape, encompassing Bioinformatics, Health Informatics, Information Quality, and Toxicological Informatics, and extending beyond, AI has risen as a potent catalyst, reshaping our comprehension, expanding our capabilities, and magnifying our overall impact. In this session, we will unveil the boundless potential of AI in various informatics domains, exploring AI's transformative capabilities and its potential to tackle critical challenges in informatics while driving innovations. It serves as a platform for collaboration and networking, facilitating opportunities that arise when diverse informatics fields converge with AI technologies.

11:00 – 11:30AM OmniTrustAI: Revolutionizing AI with the Train Once, Apply Anywhere Framework, Dr. Xiaowei Xu, University of Arkansas at Little Rock

11:30 – 11:50AM The Art of Possibility: Blending Human Augmentation, and Generative AI for Creative Mastery, Dr. Mariofanna Milanova, University of Arkansas at Little Rock

11:50 – 12:10PM Exploring Spatial Omics with Machine Learning, Dr. Juexin Wang, Indiana University

12:10 – 12:30PM AI in Drug Discovery, Challenges and Opportunities, Dr. Cesar Compadre, University of Arkansas for Medical Sciences

SESSION 4: INTERPRETABLE AI: DATA DRIVEN AND MECHANISTIC MODELING (ROOM B)

Chair: Dr. Hao Zhu, Tulane University, New Orleans, LA

Session Description:

Addressing the safety aspects of new chemicals has historically been undertaken through animal testing studies, which are expensive and time-consuming. Computational toxicology is a promising alternative approach that utilizes machine learning (ML) and deep learning (DL) techniques to predict toxicity potentials of chemicals. Although the applications of ML and DL based computational models in chemicals toxicity predictions are attractive, many toxicity models are "black box" in nature and difficult to interpret by toxicologists, which hampers the chemical risk assessments using these models. The recent progress of interpretable ML (IML) in the computer science field meets this urgent need to unveil the underlying toxicity mechanisms and elucidate domain knowledge of toxicity models. In this new modeling framework, the toxicity feature data, model interpretation methods, and the use of toxicity knowledgebase in IML development advance the applications of computational models in chemical risk assessments. The challenges and future directions of IML modeling in toxicology are strongly driven by heterogenous big data and newly revealed toxicity mechanisms. The big data mining, analysis, and mechanistic modeling using IML methods will advance artificial intelligence in the big data era to pave the road to future computational chemical toxicology and will have a significant impact on the risk assessment procedure and public health.

11:00 – 11:30AM Guidelines for Trustworthy AI, Dr. Fred Prior, University of Arkansas for Medical Sciences

11:30 – 11:50AM Reproducible AI for Supporting Regulatory Applications – A Case Study, Dr. Ting Li, National Center for Toxicological Research, US FDA

11:50 – 12:10PM Back to The Future: Using AI to Incorporate Human Data in Chemical Hazard assessments, Dr. Alexandra Maertens, Johns Hopkins University

12:10 – 12:30PM Interpretable AI: Data Driven and Mechanistic Modeling For Chemical Toxicity and Drug Safety Evaluations, Dr. Hao Zhu, Tulane University

2:00 – 2:45PM Dialogue with FDA Principal Deputy Commissioner and NIEHS/NTP Director

- **Moderator:** Dr. Tucker Patterson, Director, National Center for Toxicological Research, US FDA
- **Speakers:**
  - Dr. Namandjé N. Bumpus, Principal Deputy Commissioner, US FDA
  - Dr. Richard Woychik, Director, National Institute of Environmental Health Sciences (NIEHS) & National Toxicology Program (NTP)

2:45 – 3:30PM Panel Discussion: Arkansas Bioinformatics Consortium (AR-BIC) – The Past, Present and Future.

- **Moderator:** Dr. Weida Tong, Director, Division of Bioinformatics and Biostatistics, National Center for Toxicological Research, US FDA
- **Panellists:**
  - Dr. William Slikker, Former Director, National Center for Toxicological Research, US FDA
  - Jerry Adams, Former President, Arkansas Research Alliance
  - Dr. Shraddha Thakkar, Project Manager and Principal Investigator, Center for Drug Evaluation and Research, US FDA

3:30 – 4:00PM **Award Announcements and Concluding Remarks**

Poster Abstracts

(In alphabetical order by topic area and presenter's last name)

Topic Area:

Topic Area A:

Computational and Theoretical Models

Poster Number: 1

Impact of a Trauma Focused School on Social Emotional Assets Resilience and Trauma Symptom Behaviors

Obed Asare[1], Samantha Robinson[2*], Kristi Perryman[3], Alfieri Ek[2], Joseph Moretto[3]

1. Department of Sociology and Criminology, University of Arkansas, Fayetteville, AR, USA
2. Department of Mathematical Sciences, University of Arkansas, Fayetteville, AR, USA
3. Department of Counseling, Leadership, and Research Methods, Fayetteville, AR, USA

[*]Corresponding author

Background: Adverse childhood experiences (ACEs) can negatively impact children's health, academic achievement, and behavior. Trauma-focused schools aim to create healing environments for students with trauma histories using interventions like child-centered play therapy (CCPT). However, limited research has examined such schools' effectiveness.

Methods: Fifteen K-5 students and teachers at a trauma-focused charter school completed pre- and post-assessments during an 18-month timeframe from January 2021 to May 2022. Students completed the Social Emotional Assets and Resilience Scale (SEARS-C) and teachers completed the SEARS teacher form (SEARS-T). Additionally, the Trauma Symptom Checklist for Young Children (TSCYC) was completed for each student.

Results: SEARS-C total sum scores, while not statistically significant, increased from pre to post with a medium effect size, indicating some improvement in overall emotional regulations and resiliency. An analysis of SEARS-T scores revealed significant overall improvements and, specifically, revealed improved in teacher perception of childrens' self-regulation. Despite these positive signs, TSCYC scores revealed increases in Atypical Responses (ATR) and Post-traumatic Stress-Intrusion (PST-I) scores. Directional and non-directional correlational analyses between the scales provided insight into how these measures were related and how each influenced the other in this particular sample of children.

Conclusions: Preliminary evidence suggests trauma-focused educational environments incorporating CCPT may improve resilience while some trauma-related behaviors in students with ACEs might not change or might even be worsened. Further research with larger samples is warranted.

Keywords: Adverse childhood experiences, Trauma-informed schools, Resilience, Child-centered play therapy**,** Survey statistics

Poster Number: 2

Resilience to Covariate Shift: Evaluating the Impact of Model Complexity on Mortality Prediction with MIMIC Data

Buddhika Jayawardana[1], Paul Rogers[1], Zhiyuan Lu[1], Hyeonju Kim[1], Dong Wang[1*]

1. National Center for Toxicological Research, US FDA, Jefferson, AR USA

[*]Corresponding author

Background: The rapid progress of machine learning algorithms has led to the creation of clinical decision support systems, including mortality prediction models for prioritizing patient care. However, a significant challenge arises from potential covariate shift due to differences in covariate distribution between the training and target populations. Despite the pivotal role of covariate shift in affecting model performance, there is a lack of detailed studies quantifying its impact and proposing effective mitigation strategies.

Methods: Our empirical investigation, using MIMIC-III and MIMIC-IV datasets, examines the influence of covariate shift on mortality prediction for adult ICU patients. Two setups for model training were employed: ICD9 models and Full models, utilizing demographic variables, ICD9 chapters, severity of illness scores, and organ dysfunction scores. Three classifiers—XGBoost, Logistic Regression, and SVM—were chosen for evaluation. Calibration procedures, including Sigmoid, Beta, and 5-fold methods, were applied to enhance prediction accuracies.

Results: The findings highlight the impact of covariate shift on ICD9 models, revealing that Full models constructed with a large number of covariates are less affected by these shifts. Furthermore, the results emphasize the effectiveness of improving the performance of the models, specifically with XGBoost, by carefully integrating a small portion of the target domain in both the training and calibration phases.

Conclusions: Models that include a wide range of covariates demonstrate resilience to a covariate distribution change between training and testing domains, resulting in a decreased vulnerability to its impacts. In contrast, smaller models are more exposed to a negative effect when faced with a covariate shift.

Keywords: Covariate Shift, MIMIC data, Machine Learning, Model Calibration

Poster Number: 3

Effects of Measurement Error in Student Pre-Post Test Score on the Recovery of the Estimates of Teachers or Schools Value-Added Scores

Merlin J Kamgue[1], Samantha E. Robinson[2*]
[1] Department of Counseling, Leadership, and Research Methods, University of Arkansas
[2] Department of Mathematical Sciences, University of Arkansas, Fayetteville, Arkansas, USA
*Corresponding author

Background: Value-added models (VAMs) are statistical approaches that estimate a teacher's effectiveness at raising or lowering student performance on standardized tests. Using past scores, VAMs project a child's future performance. That projection is then compared to the student's actual results. VAMs compare each student's new test scores to past scores and chiefly control differences in students' backgrounds. The difference is the "value" that the teacher added or subtracted. While we may believe in the precision and reliabilities of those tests, this does not negate that, as all measurement tools (e.g., standardized tests) contain error(s). However, scholars seldom consider standard error of measurement (SEM) in VAMs.
Methods: The present study uses a Monte Carlo simulation design to investigate the impact of standardized tests' reliability (i.e., from perfect to less reliable) and the effect of sample size at the classroom level, number of years (or grades), number of teachers on estimates of teacher effectiveness produced by VAMs. **Results:** While results are pending at present, we anticipate to observe differential impacts of various tests upon teacher effectiveness based upon reliability, sample size, and various classroom and school-level factors.
Conclusions: The answers to our research questions will guide educational shareholders and school administrators in using VAMs for high-stakes decisions if substantial errors are observed in ranking or classifying teachers. VAMs have been used for retention and removal decisions, merit or performance pay, and re-shuffling teacher responsibilities. Under certain conditions, for example, the presence of measurement error in student test scores will result in VAMs mis-categorizing teachers as ineffective or highly effective and/or produce inaccurate or unstable estimations of teachers' effectiveness. Those inaccuracies, in turn, may impact the miscategorized teacher's pay in districts using, for example, the pay-for-performance systems.

Keywords: VAMs, standardized tests, reliability, SEM, Bayesian

Poster Number: 4

HTJ2K as a Default Storage Format for Medical Images

Utkarsh Rai[1], Lawrence Tarbox[1]*

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*Faculty Advisor

Background: Healthcare systems around the world store large volumes of medical images, like X-rays or scans. The largest public archive currently has 30.9 million radiology images. These images are high quality and use a lot of space making them difficult to store and share.

Image compression comes with two main challenges, loss in the quality of the image and additional resources needed to compress currently existing images. Efficient storage and fast decoding are essential because these images serve as primary inputs for training various AI models solving important medical challenges like tumor detection and treatment assessments.

Methods: Our project proposes using a recently introduced image format, high-throughput JPEG 2000 (HTJ2K), for lossless compression of these images. This new format allows you to see a blurry version first which gradually gets clearer. This is very handy when you are dealing with slow internet or huge files. A single image file holds several copies of gradually improving resolutions and medical researchers can pick from any of these, without having to duplicate their datasets.

Results: Depending on the type of scan and noise in the images, we achieved a compression ratio in the range of [1.3,6.95] for our samples; with a median value of 3.375.

Conclusions: Our project provides open-source tools to convert medical images to HTJ2K, methods for users of the images to decode, view and use them as necessary and pipelines that system architects can use to model medical image storage using HTJ2K format such that they are easy to maintain.

Poster Number: 5

Utilizing the Horseshoe Prior for Exploratory Factor Analysis in Studies of Fatalism

James T. Roddy[1], Samantha Robinson[1*]

1. Department of Mathematical Sciences, University of Arkansas, Fayetteville, AR USA

[*]Corresponding author

Background: The concept of fatalism, or the belief in the inevitability of events, is a significant area of study in psychological research. Traditional exploratory factor analysis (EFA) methods have limitations in dealing with complex, high-dimensional data typically encountered in fatalism studies. This research aimed to apply the horseshoe prior, a Bayesian approach, to enhance the effectiveness of EFA in this context.

Methods: The study employed a Bayesian EFA framework using the horseshoe prior to analyze survey data from 2000 participants regarding their beliefs and attitudes towards fatalism. Data were analyzed using the probabilistic programming language Stan for Bayesian inference.

Results: The horseshoe prior in EFA improved the identification of latent factors associated with fatalism beliefs. It effectively distinguished relevant factors from noise, resulting in a more data driven and interpretable factor structure.

Conclusions: The utilization of the horseshoe prior in EFA provides a robust and efficient approach for analyzing complex psychological constructs like fatalism. This method offers an advanced analytical tool for psychologists and researchers, allowing for more nuanced and accurate interpretations of factors underlying human beliefs and behaviors.

Keywords: Horseshoe Prior, Exploratory Factor Analysis, Fatalism, Bayesian Statistics, Psychological Research.

Poster Number: 6

A stochastic model for scheduling of tenders for pediatric vaccines in low- and middle-income countries

Nicholas M. Uhorchak[1]*, Ruben A. Proano[2], Sandra Eksioglu[1], Fatih Cengil, [1] Burak Eksioglu[1]

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Background: Pediatric vaccine tendering in low and low-middle income countries is an effort which continues to receive support from organizations such as UNICEF (United Nations Children's Fund), PAHO (Pan American Health Organization), and GAVI (Gavi, the Vaccine Alliance). These organizations coordinate vaccine tenders to ensure that enough supply is available in the market at the lowest possible prices, in a way that is equitable, efficient, and accessible. This complex problem involves trade-offs between multiple objectives while ensuring that vaccine availability, demand, and logistical constraints are met.

Methods: We propose a multi-stage stochastic optimization model to capture the dynamics of decision making in a stochastic environment. This model helps us address the following research questions: What should the optimal sequencing and scheduling of vaccine tenders be to enhance affordability and profit? What is the optimal tender procurement schedule for single/multiple antigen(s) scenario? We use several sources of real-life data to validate the model and address our research questions.

Results: Our analysis shows that scheduling of tenders and tender duration is affected by the available manufacturing capacity, the cost of a tender, the number of antigens in a vaccine, and the cost of producing a vaccine. The model prioritizes the production of vaccines that contain multiple antigens, such as the Pentavalent and Hexavalent vaccines. Early in the planning period, the model selects tenders with long duration to minimize costs. In later periods, short duration tenders are scheduled to meet excess demand for vaccinations.

Conclusions: The use of optimization models, such as stochastic programming, assists decision making under uncertainty. The corresponding solutions are robust and have lower expected costs. These models lead to higher quality when scheduling pediatric vaccine tenders, and can help to overcome the deterministic nature of linear programs alone. Stochastic programming results in a more robust solution, after considering variability inherent in this process.

Keywords: Stochastic Programming, Vaccine tender, Hypothetically Coordinated Vaccine Market, Optimization.

Topic Area B:

Disease Detection and Management

Poster Number: 7

Identifying the Weeds Hosting Viruses during Winter Season at the University of Arkansas at Pine Bluff Farm

Elijah Agene and Sathish K. Ponniah*
Department of Agriculture, University of Arkansas at Pine Bluff, Pine Bluff, AR, United States of America

*-Corresponding Author

Sweet potato is one of the profitable crops grown in Arkansas. It is rich in nutrients, vitamins, and fiber. But one of the major limitations of sweet potato production is viral infections. However, weeds have proven to be a destructive mechanism to the growth of this important crop by serving as a host of sweet potato viruses. The rapidly evolving nature of these viruses proved to reduce the yield of sweet potato estimated up to 25-40%. The transmission of the virus is mainly attributed to aphid-borne sweet potato feathery mottle virus (SPFMV) and whitefly-borne sweet potato chlorotic stunt virus (SPCSV). It has been suspected that weeds could be reservoirs of sweet potato virus. Previous results from other researchers showed that some common weed species that can serve as reservoirs of viruses include Morning Glory (*Ipomoea purpurea*), Bindweed (*convolvulus arvensis*), and Jimsonweed (*Datura stramonium*). This study aims to investigate the spread and transmission of the virus across weed species which may act as potential host perpetuating the virus. Field experiments were conducted in the winter on the UAPB sweet potato farm and the results showed some weeds which harbored these potyvirus, weeds collected for analysis were *Vicia sepium, Lamium aplexicaule, Poa annua L. Rumex acetosella,* and *Cynodon dactylon*. These weeds were collected from the University of Arkansas at Pine Bluff (UAPB) farm. The objective of this research is to investigate whether weed species may be reservoirs of viruses and to identify specific weed hosts that may contribute to their spread. After collecting weed samples from sweet potato cultivated fields, the potyvirus was detected using Reverse Transcriptase-Polymerase Chain Reaction (RT-PCR). The findings from this study identified that *Cynodon dactylon* (also known as Bermuda grass) was one of the weed species hosting the sweet potato viruses.

Keywords*:* Potyvirus, RT-PCR, *Cynodon dactylon.*

Poster Number: 8

Spatial Modeling Highlights Risk Factors of Colorectal Cancer Screening Patterns and Outcomes in Arkansas

Johnna K. Berryhill[1,3] , Xiao Huang[4], Sudeepa Bhattacharyya[2,3]*

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Background: There is a well-established link between social determinants of health (SDOH) and cancer incidence and survival rates. Arkansas, a rural state which has some of the worst reported health outcomes in the country, had the 8th highest incidence rate of colorectal cancer (CRC) in the US, and the 6th highest mortality rate from colorectal cancer (American Cancer Society, 2021). Previous studies have shown that cancer screening rates are positively correlated with reduced cancer incidence and mortality. In this study, our primary objectives were to assess the impact of demographic, social, and environmental determinants on CRC screening and mortality outcomes in Arkansas.

Methods: The data used for this study was obtained from the Arkansas All Payers Claims Database (APCD). CRC patients from the Arkansas Cancer Registry were linked to medical claims data and death certificate data. A Fine-Gray survival analysis was performed controlling for factors such as race, gender, age, and screening patterns to examine the impact of these factors on survival rates and determine the hazard of CRC-related death for different demographic groups. Additionally, this study employs a geographically weighted regression model at the census-tract level to analyze the disparities in CRC screening rates across the state of Arkansas.

Results: Patient subgroups at a higher risk for CRC related mortality were identified through the survival analysis. Those who were diagnosed with CRC at a late stage have a significantly higher hazard of CRC-related death than those who were diagnosed at an early stage (hazard ratio 5.997 (4.99-7.20)). Males diagnosed with CRC were found to have a significantly higher hazard of CRC-related death than females with CRC (hazard ratio 1.15 (1.01-1.30)). Our geographically weighted regression analysis revealed that certain census-tract level environmental and social determinants uniquely affect colorectal cancer screening rates across Arkansas.

Keywords: Colorectal Cancer, SDOH, Survival Analysis, GWR, Spatial Analysis

Poster Number: 9

Prognostic Role of Tumor Associated Macrophage Markers CD204, CD68 and CD163

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Background: The M1 and M2 macrophage polarization and role in the cellular microenvironment contributes to metabolic processes and the progression or suppression of chronic and fatal diseases. Tumor associated macrophages (TAM) such as CD204, CD68 and CD163 play an important role as markers in many forms of cancer and other inflammatory diseases affecting the liver, lung etc. The expression of macrophage markers is becoming more significant in understanding the role of the macrophages in the different diseases.
Methods: We studied the literature for the differential expression of CD204, CD68 and CD163 macrophage markers in different diseases to gain insights into their role and relationships in macrophage polarization to elucidate their potential as prognostic indicators. We also performed a molecular and clinical characterization of these macrophage markers from genomic databases and reported meta-analyses.
Results: Our findings suggest that a differential expression of the CD204, CD68 and CD163 markers has a significant impact on the outcome of patients' survival especially in solid cancers. Some macrophage markers are reported to be host protective in some disease states, but there is also compelling evidence that some play a role in the pathophysiology of other diseases. Endoplasmic reticulum (ER) stress response may provide important insights into the conflicting role of some of these macrophage markers.
Conclusions: The potential for these macrophage markers to be used as individual prognostic indicators must be evaluated further extensively. Therapeutic strategies based on or combined with macrophages have the potential to improve the treatment efficacy of cancer and other diseases.

Key Words: Macrophages, CD204, CD68, CD163, Tumor, Prognosis

Poster Number: 10

Knowledge Acquisition Methods Identify Diagnostic Patterns of Cognitive Impairment in Parkinson's Disease

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Background: Parkinson's disease (PD) with minor to major cognitive impairment (PD-MCI) is difficult to characterize because of diverse clinical presentations. A diagnosis of PD-MCI can be obtained from the interpretation of established global screening assessments, like the Montreal Cognitive Assessment (MoCA) and patient health information. There is evidence that the patient's pattern of performance on the MoCA holds prognostic importance rather than the designated scoring protocol, but our lack in understanding of clinical reasoning creates a barrier to gleaning potentially vital relationships within the data.

Methods: We conducted a 60-minute semi-structured interview of neurologists (n = 5) and clinical neuropsychologists (n = 1) specializing in PD. Using the 'think aloud' interview technique we asked them to verbalize their thought process of determining a diagnosis of PD-MCI as they reviewed patient health files. A total of eight patient health files were created containing a MoCA exam and deidentified patient health information from a neuropsychological report. The patient files were grouped into three groups of three to gather at least two clinical opinions on each file. The interviews were coded by JE and FP using iterative coding methods.

Results: Six distinct patterns describing features of patient performance on a MoCA and relationships to health data from a neuropsychological report were extracted. In addition, the patterns were compiled to create a list of individual features of importance describing the heuristic data elements from the patterns. The distinct patterns can be characterized by quantifiable parameters to form a vector for input into a machine learning algorithm.

Conclusions: The patterns of patient performance as interpreted by the clinical professionals holds deeper information on cognition than the composite score of the MoCA. The distinct patterns of patient performance identified through iterative coding of the interviews reveals important relationships of PD cognitive pathology currently unexplored.

Keywords: Parkinson's disease, knowledge acquisition, cognitive assessment, pattern recognition

Poster Number: 11

The Acquired *pco* Gene Cluster in *Salmonella enterica* Isolated from Retail Meat Confers Tolerance to Toxic Levels of Copper

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Background: Non-typhoidal *Salmonella enterica* have acquired heavy-metal resistance genes due to the use of heavy metals, such as copper and silver, in animal feed for their antimicrobial and growth promotion properties. The *pco* gene cluster has been detected in several non-typhoidal *S. enterica* isolated from human clinical cases and foods of animal origin. Yet, the role of the *pco* cluster on the physiology of *S. enterica* remains poorly understood. The present study examines the role of *pco* gene cluster in *S. enterica* copper resistance.
Methods: The Non-typhoidal S. enterica isolates used in this study were isolated from retail meat. Two isolates: SL-3 and SL-4, contain *pco* cassette. The SL-4 *pcoABCD* deletion mutant was constructed using allelic exchange mutagenesis. Wild type *S. enterica*, SL-3, SL-4, and SL-4*ΔpcoABCD* were tested for copper tolerance in LB medium supplemented with 800 or 2000 µM $CuSO_4$ and incubated for 3 or 6 days at 37°C. Growth was monitored by measuring the optical density of each culture or by Alamar Blue assay. To test the impact of *pco* cassette on replication in macrophages, RAW264.7 macrophages were infected with all strains at multiplicity of infection of 1.
Results: Deletion of *pcoABCD* genes inhibited growth of *S. enterica* in high-copper medium, but only under anaerobic environment. As expected, the loss of *pcoABCD* genes did not impact silver resistance. The survival of *S. enterica* in RAW264.7 macrophages was not affected by the loss of *pcoABCD* genes.
Conclusions: This study indicates that the acquired *pco* cluster is crucial for copper detoxification in *S. enterica*, but it is not essential for intracellular replication within macrophages.

Keywords: *Salmonella enterica*, *pco* cluster, copper resistance, heavy metals

Poster Number: 12

Stretchable and Conductive Thin Films of PEDOT:PSS/Ionic Liquid Composite

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Background: The field of flexible electronics is one of the most interesting areas for research due to the wide scope of applications in flexible electronics for health care, energy, displays, and sensor devices. Numerous studies have been conducted to develop flexible materials for electrodes, but they are very rigid, expensive, and pose a potential environmental issue.

Methods: In this study, an eco-friendly conductive polymer is mixed with ionic liquids for the development of free-standing thin film as a flexible conductor. Furthermore, we investigated the effect of different anions of ionic liquids on the polyethylene dioxythiophene:polystyrene sulfonate (PEDOT:PSS) composite film. Ionic liquids composed of the same cation with different soft and hard anions are employed to develop highly stretchable and conductive films. Thin films are developed using the drop casting method and the physical properties of the films are studied using XPS, AFM, and SEM. A four-point probe is used to investigate the conductivity, and the stress strain measurement is performed to determine the mechanical strength of the film.

Results: The conductivity and flexibility of the free-standing thin film prepared using PEDOT:PSS and ionic liquids composite mixture depicted enhanced properties. The effect of different anions in the ionic liquids is evident. The soft anion exhibited tremendous increase in conductivity as well as in stretchability. The conductivity of the free-standing thin film increases as the ionic liquid's weight percent increases in the composite materials.

Conclusions: This study is very useful to optimize the development of future flexible electronics materials. The ions of ionic liquids make significant changes in the mechanical strength as well as the conductivity of the film. The optimization of ionic liquids' ions is essential to attain highly stretchable and conductive films for flexible health care and other electronic devices.

Keywords: Thin films, flexible electronics, PEDOT:PSS, ionic liquids.

Poster Number: 13

Globodera Pallida RHA1B Protein Functions as a Meta-Effector, Manipulating the Stability of Other Pathogenic Nematode Effectors

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Background: The Potato Cyst Nematode (*Globodera pallida*) is a plant-parasitic nematode (PPN) significantly impacting potato yield. Like other PPNs, *G. pallida* employs numerous effector proteins that play a crucial role in altering host cell functions and suppressing defenses. The recently identified RHA1B protein from *G. pallida*, functioning as an E3 ubiquitin ligase, suppresses effector-triggered immunity by ubiquitinating plant target proteins. Interestingly, the targeting of host defense proteins for degradation to enhance virulence may not be the only function of RHA1B. This research investigates the potential role of the RHA1B as a meta-effector - an effector that regulates the stability and activity of other effectors. Specifically, we tested the influence of RHA1B on five other effector-molecules (MEs) clustering with the *RHA1B* gene on one of the putative "effector islands".
Methods: In this study, we cloned *G. pallida* ME1-5 effectors and employed an *Agrobacterium*-mediated transient expression system in *Nicotiana benthamiana* to co-express them with RHA1B. Western-blotting was utilized for protein detection. We also conducted a Hypersensitive Response suppression assay to better understand the role of MEs in nematode parasitism.
Results: Co-expression assays of *ME* genes with *RHA1B* variants in *N. benthamiana* revealed that the stability of ME-1 and ME-4 was significantly reduced by the E3 ligase activity of RHA1B. We also found that ME-4 can suppress HR triggered by different resistant proteins. Although the molecular mechanism remains to be uncovered, this data suggests RHA1B's role as a master regulator in the effector network.
Conclusions: The selective destabilization of MEs by RHA1B suggests a regulatory level in the effector network. The full spectrum of RHA1B's regulatory capacity requires further elucidation, particularly its influence over other effectors that do not physically cluster together. Future research focusing on genome-wide direct effector-effector interactions will enhance our understanding of plant-nematode dynamics and inform control strategies.

Keywords: *Globodera pallida*, RHA1B effector, Meta-effector networks, Molecular plant pathology.

Poster Number: 14

Enhanced Bacterial Eradication: Integrating Antibiotics with Photothermal Therapy

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Background: The surging issue of bacterial resistance to conventional antibiotics poses a significant threat to public health worldwide. Traditional treatments are increasingly ineffective, leading to a rise in persistent infections and deaths. This study focuses on addressing the urgent need for innovative treatments by exploring a novel approach that combines two distinct antibacterial mechanisms in a single therapeutic compound.
Methods: This research involves the synthesis of a novel compound integrating a commercial antibiotic with a near-infrared dye. The dual-action compound aims to deliver a chemical killing mechanism along with a photothermal killing mechanism. The study assesses the efficacy of this combination in neutralizing our model bacteria, Escherichia coli, using 96-well plates treated with drug and bacteria to simulate infection environments. The effectiveness of the compound is measured through bacterial inhibition concentration.
Results: Preliminary findings indicate a significant enhancement in the eradication of our model bacteria, excluding resistant bacteria as we have not reached that step yet. The compound's dual mechanism ensures the destruction of bacteria through chemical means while the photothermal component targets the resistant cells, reducing the likelihood of bacterial growth.
Conclusions: The combination of chemical and photothermal therapies in a single compound represents a promising advancement in the fight against multi-drug resistant bacteria. This innovative approach holds potential for the development of more effective treatments, addressing the critical need for strategies that outpace the evolving resistance patterns of pathogenic bacteria.

Keywords: Antibiotic Resistance, Photothermal Therapy, Bacterial Eradication, Combined Therapies, Multi-Drug Resistance.

Poster Number: 15

Exploring the Association between Gut Microbiome-Produced Bile Acid Profile, Circulating Lipid Profile, and Neuropsychiatric Symptoms in Patients with Parkinson's Disease: *A Metabolomics and Informatics Study*

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Background: Patients with Parkinson's Disease (PD) can experience Neuropsychiatric Symptoms (NPS) before motor symptoms. Over 50% exhibit depression, anxiety, and cognitive impairment at the time of motor diagnosis, emphasizing the need to understand NPS in PD development. Studies suggest that gut microbiota-produced secondary bile acids influence lipid homeostasis and mitochondrial function in individuals experiencing anxiety and depression. Given the clear gut-brain axis in PD based on the Braak Hypothesis for the pathologic progression of PD, our hypothesis is that bile acid and lipid profiles will differ in individuals with PD exhibiting more severe NPS.

Methods: Participants are being enrolled from the University of Arkansas for Medical Sciences Movement Disorders Clinic. After obtaining written informed consent, participants undergo a blood draw to sample bile acid and lipid profiles. All participants also undergo a complete Parkinson's disease exam with the Unified Parkinson's Disease Rating Scale (UPDRS), as well as assessments of their NPS with the Hamilton Anxiety Rating Scale (HAMA), Hamilton Depression Rating Scale (HDRS), and the Montreal Cognitive Assessment (MoCA). Gait is evaluated using the Timed Up and Go on an instrumented gait mat (Protokinetics Zeno Walkway). Metabolomic samples will be analyzed as a single batch once all participants are enrolled.

Results: To date, 29 participants have been enrolled (20 PD and 9 non-PD controls). In the currently enrolled cohort, there were no significant differences in age or sex between the PD and control groups. HDRS (HC 3.11±3.10; PD 8.53±6.00, p=0.007) and HAMA scores (HC 3.34±3.04; PD 6.47±4.39, p=0.013) differed between the two groups. There was a correlation between total UPDRS scores and HDRS (0.68, p=0.02) and HAMA scores (0.59, p=0.08).

Conclusions: In our study, quantifiable differences exist between PD and control participants, and a range of results on the HAMA, HDRS, and MoCA scores will allow us in the future to determine whether NPS symptoms in PD are related to metabolomic profiles.

Keywords: Parkinson's disease, Neuropsychiatric symptoms, Depression, Anxiety, Cognition

Poster Number: 16

Evolution of Antibiotic Resistance in Gram-Negative Bacteria

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Background: The E. Coli K12 strain is not the most aggressive strain, however, it allows us to establish a foundation of understanding as to how gram-negative bacteria adapt to antibiotics. Established antibiotics have been used and analyzed for effectiveness at disseminating the bacteria. A number of antibiotics have been tested to discover which is the most effective, as well as factors that potentially inhibit or facilitate the bacterial resistance.

Methods: The research was conducted over approximately half a year, including literature reviews, experimentation, data collection, and analyses. A minimum inhibitory concentration test (MIC) was utilized to determine the lowest concentration of an antimicrobial agent hindering growth of bacteria in the medium. A MIC test was performed using Broth dilutions. A fractional inhibitory concentration index (FIC) was also utilized to test whether antibiotics have synergistic effects. Four established antibiotics and three newly synthesized antibiotics were evaluated. The experimentation for this project included the cultured K12 strain of E. coli under a controlled environment.

Results: The study showed significantly lower MIC's for Cu(Ipr)(3,4'-dodpa)PF6 and Cu(IMes)Cl with 16 µg/mL and 32 µg/mL respectively. The lower MIC signifies that a lower quantity of the drug is necessary for inhibiting the growth. Kanamycin and ampicillin were also found to have lower MIC values in comparison to streptomycin and penicillin. The results indicate that the K12 strain already has a level of resistance to streptomycin and penicillin.

Conclusions: With the newfound comprehensive understanding of antibiotic resistance of gram-negative bacteria, this project is paramount in developing countermeasures against bacterial resistance. Genetic mutations and adaptive mechanisms have been observed in relation to bacterial evolution. With the knowledge obtained from this research, other researchers will be able to identify new drug targets and synthesize novel antibiotics or mixtures of drugs that can stay ahead of bacterial resistance.

Keywords: Antibiotic Resistance Gram-Negative Bacteria

Poster Number: 17

The Road from Animal Models to New Approach Methods for Protecting Human and Animal Health

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Background: There is interest in the use of alternative methods to supplement or supplant animal use in basic biomedical, pharmacological, and regulatory research. New approach methods (NAMs) refer to any technology, methodology, approach, or assay used to understand effects and mechanisms of drugs or chemicals with a focus on the 3Rs. The purpose of this work was to provide a balanced view of the current state of use of animal models and NAMs as approaches to development, safety, efficacy, and toxicity testing of drugs and chemicals.

Methods: A working group of toxicology experts from the Scientific Liaison Coalition (SLC) representing academia, industry, and government, used the scientific literature and their experience and expertise to review the state of the science on animal use and NAMs.

Results: The working group found that there is historical value in animal use for many biological discoveries. An examination probed successes and challenges in selecting the appropriate animal model for deciphering mechanism of action, identifying adverse effects, or understanding disease processes. Next, we summarized *in vitro* replacement assays, including the importance of engineered microsystems and newer human cell-based assays that, combined with computational models, advance the potential to improve mechanistic understanding and regulatory decision-making for human toxicity. Finally, we assembled a list of limitations of animal use and NAMs.

Conclusions: While it is unlikely that all animal studies will be able to be replaced entirely, with the continued advancement in NAMs, it is possible that NAMs will likely be an important component by which discovery, efficacy, and toxicity testing of drugs and chemicals is conducted and regulatory decisions are made. The participation of biologists, computational modelers, toxicologists, and veterinarians looking at alternatives from a multifactorial perspective will propel the field forward, likely using both animal models and NAMs.

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Keywords: NAMs, 3Rs, animal models

Topic Area C:

Drug Safety and Pharmacology

Poster Number: 18

Comparison of the Cellular-Uptake Levels and Bioactivity Among the Various Vitamin E Tocol Isoforms

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Background: The vitamin E family includes eight different vitamers, four tocopherols (α, β, γ and δ) and four tocotrienols (α, β, γ and δ), which are collectively known as tocols. Tocols have been shown to possess radiation protection activity when given prior to radiation exposure. Multiple studies have also shown that, despite the small structural differences between tocotrienols and tocopherols, there are substantial differences in their biological activity, with tocotrienols having more potent biological activity.
Method: In this study, we explored the possibility that the differential activity among the various tocols is related to differences in their cell uptake. Thus, we determined and compared the cellular uptake levels of 6 vitamers including α, γ, δ tocopherols and α, γ, δ tocotrienols in endothelial (HUVEC cells), motor neuron like cells (NSC-34 cells), and hepatocytes (HepG2 cells) by incubating the cells with 5 μM tocols for various incubation periods and then determining the levels of cellular uptake using GC/MS. Then, we used the TBARS assay with rat liver microsomes to measure the intrinsic antioxidant capacity of the tocols. Results: Tocol cell uptake levels are directly correlated with their bioactivity and inversely correlated with their octanol / water partition coefficient. Endothelial cells showed much higher cell uptake levels than the other cell lines.
Conclusion: The results of this study emphasize the importance of cellular uptake in the differential activity of each tocol.

Keywords: Tocopherols, Tocotrienols, radiation, biological activity, Tocols.

Poster Number: 19

Overexpression and Cell-Penetrating Peptide-Mediated Delivery of Cas9 and its Variant(s) for Targeted Genome Editing

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Background: The Clustered, Regularly Interspaced, Short Palindromic Repeat (CRISPR)-associated system (Cas) is a powerful tool that has been used for genome editing. Cas9 is a bacterial RNA-guided endonuclease that cleaves target DNA and modifies a cell's genome. Despite the advantages and promising results of the use of CRISPR-Cas9 as a molecular tool and potential therapeutic protein, the production and purification of the recombinant Cas9 remains a challenge. Following protein expression and purification, delivering the cas9 into the cells is a key concern for many researchers. Typically, cas9 and gRNA are delivered by using either plasmid or viral vectors. However, the plasmid or viral-mediated delivery triggers an undesirable immune response and leads to uncontrolled integration of the plasmid into the host genome. We envision that direct delivery, i.e. conjugating the protein with Cell-Penetrating Peptide (CPP) will lead to endogenous gene disruptions with reduced off-target effects compared to the other delivery methods that require a transfection reagent.
Methods: Our study aims to determine if the vector strains or culture conditions need to be altered based on different Cas9 variants. The Cas9 variants (V743C and S204C) were designed based on Solvent Accessible Surface Area (SASA) measurement which was calculated using the internal SASA measurement method of VMD. Therefore, we methodically evaluate the expression and purification of recombinant Spcas9 and variants through affinity chromatography in four *E.coli* strains (Rosetta, BL21 (regular), BL21-PlysS, and BL21-star). Additionally, this study intends to deliver Spcas9 and variants into the mouse fibroblasts (NIH3T3 cell line) by conjugating the protein with CPP through thiol chemistry.
Results: After optimization of the conditions (temperature and post-induction time), PlysS strain efficiently expressed the Spcas9 and all the other variants.
Conclusions: Overall, the results of this study will suggest if the CPP method will facilitate Cas9-directed genome editing.

Keywords: Cas9, genome editing, cell-penetrating peptide

Poster Number: 20

From Data to Caution: Unraveling Sex Disparities in Opioid Adverse Events Utilizing FAERS

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Background: Due to differences in reproductive physiology, hormone variances, and genetic polymorphisms between males and females, sex emerges as an important factor impacting the adverse events associated with opioids. Despite this, there exists a notable absence of in-depth exploration into sex disparities related to adverse events linked to opioid drugs.
Methods: Our study involved collecting information on available opioid drugs from the literature, followed by mining adverse events through drug names, brand names, trade names, and generic names obtained from Drug Bank. We then categorized the identified adverse events into 27 System Organ Classes (SOCs) using the Medical Dictionary for Regulatory Activities (MedDRA).
Results: Our analysis covered 53 opioid drugs, identifying a total of 7,190,447 adverse events associated with these drugs in FAERS. Of these, 2,777,636 were reported for males and 4,412,811 for females, indicating a higher frequency of adverse events in females. Oxycodone and acetaminophen contributed to the highest frequency of adverse events—approximately 40% for both males and females.
Conclusions: The findings indicate a higher frequency of adverse events in females when using opioid drugs, underscoring the need for caution. This suggests that considering the safety profile can aid in selecting opioid drugs with favorable safety profiles for females, thereby contributing to the improvement of women's health.

Keywords: Opioid Adverse Events, Sex Disparities, FDA Adverse Event Reporting System (FAERS), Drug Safety, Pharmacovigilance.

Poster Number: 21

Generation of a drug-induced renal injury list (DIRIL) to facilitate the development of new approach methodologies (NAMs) for nephrotoxicity

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Background: Drug-induced renal injury (DIRI) can lead to the development of acute kidney injury, chronic kidney disease, or end-stage renal disease, causing over 1.5 million adverse events annually and affecting approximately 26% of the United States population. Currently, the standard biomarkers for DIRI identification are serum creatinine and blood urea nitrogen, both markers are late-stage biomarkers that are known to lack the sensitivity or specificity to detect nephrotoxicity prior to significant loss of renal function.
Methods: For the proper development of alternative nephrotoxic methods, a large drug list with annotated DIRI potential is needed. In this study, we describe the creation of DIRIL, a list of drugs associated with drug-induced renal injury and nephrotoxicity. The Drug-Induced Renal Injury List (DIRIL) was assembled from literature data with specific criteria: it had to be highly curated with a large number of drugs, using comparable methods to annotate DIRI with a binary classification system. Comprised of 317 drugs, 171 were Nephrotoxic (DIRI Positive) and 146 were Non-Nephrotoxic (DIRI Negative).
Results: The DIRIL dataset contains all 14 anatomical drug categories, as classified by the WHO's ATC Classification System. Approximately 91% of the drugs are from 7 of the 14 categories, with drugs related to the Cardiovascular and Nervous systems categories being most predominant. Antivirals for Systemic Use (J05), Antineoplastic Agents (L01), and Psychoanaleptics (N06) were the most predominant among the therapeutic categories, with 19% of drugs combined. We also found that, while methods like the Rule-of-Two (RO2) and Biopharmaceutics Drug Disposition Classification System (BDDCS) are known to be successful in the evaluation and severity classification of Drug Induced Liver Injury (DILI), these methods have proven to be ineffective in the classification of a drugs nephrotoxic potential.
Conclusions: These results indicate that there are some distinct differences in nephrotoxicity as compared to DILI, such as the reabsorption, secretion, or passive filtering of drugs by the kidney. DIRIL will be a relevant and invaluable resource for the improvement of nephrotoxic research in areas such as the discovery of new methodologies to access the severity and better classify nephrotoxicity earlier within the drug development process.

Keywords: Drug-Induced Renal Injury, Drug-Induced Kidney Injury, Nephrotoxicity, New Approach Methods, Drug Safety, Organ Toxicity

Poster Number: 22

Global Proteomics of *Dictyostelium discoideum* Resistance to Death Mechanism on Exposure to Zinc Oxide Nanoparticles

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Background: Cell death mechanisms are integral to various diseases, including cancer and infectious diseases. Understanding the diverse pathways leading to cell demise is essential for unfolding the complex landscape of these conditions. Apoptosis, known for its crucial role in programmed cell death, serves as a key defense mechanism against deadly diseases. The emergence of alternative cell death pathways, such as autophagy, pyroptosis, necroptosis, autosis, and ferroptosis, introduces a range of cellular responses to invading pathogens or cancer, each with unique molecular signatures and implications for disease outcomes.
Method: *Dictyostelium discoideum*, which is an NIH-approved model organism, was employed, providing an opportunity to examine orthologs of cancer-associated genes. We conducted global proteomics, in the presence and absence of nanomaterials, to elucidate the pathway and understand how the organism intelligently employs deceptive mechanisms during exposure.
Results: While extensively researched nanoparticles are known to exhibit toxicity against cells, our findings reveal that *Dictyostelium* demonstrates resistance and adapts to such materials. We identified multiple pathways directly linked to cancer that showed upregulation, and notably, the Detoxification of Reactive Oxygen Species pathway exhibited significant upregulation both biologically and statistically. This pathway plays a critical role in cellular well-being by countering oxidative stress induced by reactive oxygen species (ROS), which can otherwise lead to cell damage and death. The effectiveness of detoxification mechanisms is crucial for shielding cells against ROS-induced cell death.
Conclusion: Our proteomic analysis pinpointed two genes, namely, Probable copper chaperone for superoxide dismutase and Thioredoxin domain-containing protein, as key contributors to this protective response.

Keywords: nanoparticles, cancer, *Dictyostelium discoideum*, proteomics

Poster Number: 23

Up-Regulation of Osh6 Reveals the Route of DNA Trafficking During Transformation

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Background: Transformation is a routine technique used in biotechnology, although the underlying mechanism is not clear. In yeast cells, foreign DNA enters cells through endocytosis. However, the major destiny of endocytosis is the degradative organelle vacuole.
Methods: Here we tested the impacts of different endocytosis mutants on transformation. We did this by the generation of novel strains using a mating protocol, and then the new strains were compared using a novel transformation procedure to test for differences in frequency.
Results: While blocking endocytosis blocks transformation as reported, mutants with increased endocytosis (inp54delta) did not affect transformation. We previously constructed a mutant (Perg6-OSH6) that accumulates phosphatidylinositol-4-phosphate (PI4P) on the trans-Golgi network (TGN) and enhances the TGN to late endosome (LE) (then vacuole) traffic. Interestingly, this mutant had lower transformation frequency but had accelerated endocytosis from the plasma membrane to TGN. Blocking the TGN-LE traffic or altering the PI4P transport greatly increases the transformation frequency of Perg6-OSH6.
Conclusions: Thus, the TGN is one station where endocytosed DNA stops after endocytosis and vesicle traffic derived from the TGN determines whether the endocytosed DNA goes to the vacuole through TGN-LE or to the nucleus via retrograde traffic from the TGN.

Keywords: Yeast, Cellular Biology, Transformation, Microbiology, Mutant Generation

Poster Number: 24

Drug-UGT interactions as Predictors of Drug-Induced Liver Injury

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Background: Drug-induced liver injury (DILI) is a leading cause of acute liver failure and a common reason for the withdrawal of approved drugs from the market. Drug metabolism can play a significant role in the induction of DILI. While some studies have been conducted to investigate how drug interaction with cytochrome P450 (non-CYP) enzymes can be associated with DILI, there has been no comprehensive investigation to associate several non-CYP enzymes with DILI.

Methods: For 42 non-CYP enzymes, we gathered data on how 317 drugs interacted with the enzymes as substrates, inhibitors and/or inducers from the Pharmapendium database. The drugs' propensity for DILI was obtained from the LTKB database. We performed multivariate logistic regression on the dataset to investigate associations between the drugs' DILI outcomes and enzyme families, individual enzymes, types of drug-enzyme interaction.

Results: Generally, inhibitors of non-CYP enzymes were associated with severe DILI. Drug interaction with UDP-glucuronosyltransferase (UGT) enzymes increased the potential of a drug having severe DILI outcomes. UGT inhibitors were found to be significantly associated with an increased likelihood of having severe DILI. Drugs that are UGT substrates were also found to increase likelihood of possessing severe DILI outcomes, but only when they as dual substrate-inhibitors of UGT enzymes.

Conclusions: This shows that drug interaction with UGT enzymes can serve as a valuable predictor of severe DILI, expanding the tools that are available to predict DILI.

Keywords: Drug-induced liver injury (DILI), UDP-glucuronosyltransferase (UGT) enzymes, drug metabolism

Poster Number: 25

Therapeutic Efficiency and Uptake of AuNSs-GE-11 peptide loaded with Rapamycin on Cell Proliferation and Apoptosis in Pancreatic Cancer

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Background: Pancreatic cancer (PC) is the 4th leading cause of cancer related deaths in the USA due to its severe aggressiveness. Epidermal Growth Factor Receptor (EGFR) is over expressed in more than 95% of PC patients. GE-11 peptide containing EGF sequence has been demonstrated to have high affinity for EGFR. Rapamycin is a specific mammalian target of cell proliferative pathway where it complexes with the FK-binding protein-12 (FKBP-12) andbinds to mTOR-complex 1, inhibiting its activity and thus, cell proliferation. However, extreme toxicity has largely restricted its therapeutic applications. To overcome these limitations, Rapamycin loaded GE-11 peptide conjugated gold nanoparticles (AuNPs) were formulated, characterized, and tested against pancreatic cancer (Panc-1 cells).
Methodology: Thiol moiety modified GE-11 peptide was covalently bonded to Rapamycin loaded carboxyl gold nanoparticles. The conjugate was characterized using Fourier transform infrared spectroscopy (FTIR), UV-Vis Spectrophotometry and Dynamic Light Scattering (DLS). Panc-1 cells were then treated with AuNPs-Ge-11-Rap. ICP-MS confirmed cellular uptake. Cytotoxicity, Reactive Oxygen Species, Flow Cytometry, Caspase-3/7, Lactate dehydrogenase, Mitochondria Membrane Potential, proliferation assay, and DNA Fragmentation studies were done to test the effects of formulated nanodrug. . Statistical analysis was performed using GraphPad Prism. P value ≤ 0.005 was considered statistically significant.
Results: FTIR, UV-VIS Spectra and DLS showed a shift between AuNPs, AuNPs-Ge-11 and AuNPs-Ge 11-Rap confirmed successful conjugation. ICP-MS shows that the peptide conjugated nanoparticles were consistently taken up by Panc-1 cells. Rapamycin encapsulation efficiency was 42%. The IC_{50} for Au, Au-GE-11 and AU-Ge-11-Rap were 370.58ug/ml, 10.4ug/ml and 10ug/ml, respectively. MTT and LDH assays show dose dependent (7.8–62.4 μg ml−1) inhibition of cell viability. Flow Cytometry demonstrated a significant increase in apoptosis at 31.23ug/ml Au-Ge-11-Rap as compared to control (P< 0.001).
Conclusion: Our findings suggest that AuNPs- Ge-11-Rap conjugate has potential as a therapeutic candidate drug for pancreatic cancer due to its selective toxicity to cancer cells only.

Keywords: AuNPs, Ge-11, -Rapamycin, Pancreatic cancer, Apoptosis, Caspase 3/7

Poster Number: 26

Ionic materials as Combination Nanomedicines: Synthesis, Characterization, and in vitro studies

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Background: Doxorubicin (DOX) is a widely used FDA approved chemotherapy drug. However, it is known to enhance cardiotoxicity. Therefore, it is essential to enhance its selective toxicity towards tumor cells by minimizing its side effect. The use of combination nanomedicines (CNMs) is a promising approach to treat tumors using two or more different mechanisms.[1] Moreover, nanoparticle-based drugs exhibit increased intracellular concentration in cancer cells and lower toxicity in normal cells.[2]

Methods: Herein, we report the synthesis and characterization of combination ionic material from FDA approved chemotherapeutic drug (chemo), Doxorubicin (DOX) and NIR dyes (NaICG, NaIR820 and NaIR783) as a photothermal therapeutic drug. Carrier-free CNMs were derived via a facile reprecipitation. Photophysical properties including the Forster resonance energy transfer (FRET) mechanism were studied in detail. The phototherapeutic efficiency of the combination drugs was evaluated by measuring photothermal conversion efficiency and singlet oxygen quantum yield. Cellular uptake, dark and light toxicity studies, and cell death mechanism of the chemo-PTT nanoparticles were also studied in vitro.

Results: *In vitro* dark and light cellular study showed an increased cytotoxicity (lowered IC_{50}) as opposed to DOX, revealing the significance of nanoparticle modification and improved photophysical properties. The CNM exhibited enhanced cytotoxicity as compared to their respective parent compounds. Moreover, the apoptosis cell death mechanism was almost doubled for CNM than the free DOX which is attributed to enhanced cellular uptake and accumulation within key organelles. Examination of the combination index and improved *in vitro* cytotoxicity results revealed a great synergy between chemo and PTT drugs in the newly developed CNMs.

Conclusions: The CNMs exhibited improved phototherapeutic activities. These CNMs exhibited enhanced cellular uptake and significantly increased the toxicity due to synergy between DOX and NIR dye.

Keywords: Combination therapy, Ionic nanomaterial, Doxorubicin, Photothermal therapy, Cytotoxicity, Cell death mechanism

Poster Number: 27

Development of QSAR Models for Prediction of Drug-induced Cardiotoxicity Using DICTrank

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Background: Drug-induced Cardiotoxicity (DICT) is the most frequently reported cause of safety-related withdrawal of marketed drugs. Identifying potential DICT risks during the early stages of drug development is imperative. A large dataset containing a large number of drugs with reliable DICT annotation is critical for the development of new approach methods, including AI models for early identification of DICT risk during drug development and beyond.

Methods: The FDA's DICTrank evaluated 1318 drugs for their likelihood of causing DICT in humans, of which over 900 drugs were classified into three categories (Most-DICT-Concern, Less-DICT-Concern, and No-DICT-Concern). Utilizing this dataset, we developed and evaluated several Quantitative Structure-Activity Relationship (QSAR) machine learning (ML) models. Five ML methods with varying computational complexity were employed to assess their impact on model outcomes.

Results: Our findings underscore the robustness of DICTrank drug lists, demonstrating their effectiveness in achieving good model performance during cross-validation and on the test set. We observed that these methods yielded comparable results, indicating that the choice of ML method had minimal impact on model outcomes. Furthermore, we found that the models have more discrimination power to identify the DICT potential of drugs belonging to the World Health Organization therapeutic category of 'alimentary tract and metabolism' compared to other categories. Caution is advised when applying these models to therapeutic categories with less reliable data. Moreover, through informative molecular feature importance analysis, certain features such as 'Topological Structure Autocorrelation' and 'Eigenvalues from Burden Matrix' were identified as strongly associated with specific drug properties. This aligns with existing literature on the mechanisms of cardiotoxicity.

Conclusions: The developed DICTrank and QSAR models could serve as a valuable resource for the early identification of drug-induced cardiotoxicity risks and contribute to the advancement of AI predictive modeling in drug development.

Keywords: Drug-induced cardiotoxicity (DICT), QSAR, Machine learning, DICTrank, Drug safety

Poster Number: 28

Identifying Vulnerabilities to NSAID Adverse Events in the US Population: An Analysis of Pre-Existing Conditions and Gender

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Background: In 2005, the Food and Drug Administration (FDA) issued a decision memorandum regarding nonsteroidal anti-inflammatory drugs (NSAIDs). The memorandum recommended the withdrawal of certain NSAIDs due to potential cardiovascular adverse effects. It highlighted the issue of cardiovascular risk associated with NSAIDs as a class.

The NSAID medication guide includes a wide range of adverse drug reactions (ADRs), such as increased blood pressure, liver failure, allergic reactions, heart attack, and intestinal bleeding. Although both sexes have an increased risk of ADRs with NSAID use, females have a greater risk than males due to differences in pharmacodynamics and higher medication concentrations (mg/kg).

The prevalence of NSAIDs and the disparity in risk of ADR) by sex within this class of medications make this a significant public health issue. This study quantifies sex-specific differences associated with prescription NSAID use.

Methods: The data for this study was obtained from the National Health and Nutrition Examination Survey (NHANES), a complex survey conducted by the Centers for Disease Control and Prevention in two-year cycles. NHANES is designed to make inferences about the health of the US civilian noninstitutionalized population.

A survey-weighted logistic regression model investigated potential sex differences in the relationship between NSAIDs, kidney disease, hypertension, liver disease, insurance status, coronary heart disease, and age within the 2011-2018 NHANES cycles.

Results: Females reported a slightly higher percentage of high blood pressure and kidney disease than males, while males reported a slightly higher percentage of coronary heart and liver disease. Furthermore, a larger percentage of females reported having health insurance coverage than males. Last, the model indicated that females were 58% more likely to have used a prescription NSAID than males.

Conclusions: The results confirm that women and people with medical conditions, who would potentially suffer greater harm from NSAIDs, are at higher risk of experiencing ADRs.

Keywords: NSAIDS; Gender; Adverse Drug Reaction; Complex Survey; Women's Health.

Poster Number: 29

Assessment of Challenges Towards Implementing New Approach Methods (NAMs) for Predicting Drug Induced Liver Injury

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Background: Conventional animal toxicity tests have been used in the past for human health hazard and risk assessment; however, animal studies can be expensive, time consuming and have limited extrapolation to humans. New approach methods (NAMs) serve as an alternative to animal studies for prediction of human response to drugs. Drug-induced liver injury (DILI) has been a leading cause of safety-related drug withdrawals. Various NAMs have been used to predict DILI; however, discrepancies have been observed DILI annotation. Our investigation was aimed at addressing the similarities and distinctions exist among various NAMs for DILI.
Method: We established inclusion and exclusion criteria ensuring the relevance and quality of studies for our analysis. The prediction data from the models in the selected studies were converted into binary classification based on their respective thresholds. We assessed the DILI prediction agreement among studies by examining drug overlap and annotation concordance. Additionally, using DILIst and Garside datasets, we assessed the impact of the DILI annotation reference on the models' performance. Furthermore, an analysis of Anatomical Therapeutic Chemical (ATC) categories was conducted to identify patterns relevant for regulatory decision-making.
Results: Analysis of the six selected studies revealed a lack of common drugs, minimal concordance in DILI classification, and a neglect of drug pair analysis among models. Notably, model performance exhibited inconsistency with varied reference lists, with specificity showing more significant changes than sensitivity. Additionally, the limited number of drugs hindered the identification of therapeutic-category-specific patterns.
Conclusion: Consensus in the drug list and DILI reference among different NAMs is critical and needed to enable a meaningful evaluation of NAMs for DILI prediction.

Keywords: DILI, new approach methods, drug safety

Poster Number: 30

Tocotrienols Are Uniquely Efficacious Whole-Body Radioprotectors Through a Synergistic Combination of Antioxidant Properties and Signaling Mechanisms

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Background: Tocotrienols have shown a remarkable ability to protect the hematopoietic, gastrointestinal, vascular endothelial, and other systems against lethal doses of radiation. Thus, tocotrienols are promising candidates for developing as radiation countermeasures due to their powerful whole-body radioprotective properties in multiple organ systems. To facilitate their development as radiation countermeasures, it is crucial to better understand the mechanisms behind their radioprotective properties.

Methods: We performed an extensive literature review on all relevant tocotrienol radioprotection research, investigating both therapeutic and mechanistic studies. Our goal was to integrate these findings into a comprehensive pharmacological framework that explains how tocotrienols are such effective whole-body radioprotectors.

Results: The antioxidant effects of tocotrienols have long been recognized as the free radical scavenging directly prevents oxidative damage to cellular biomolecules from ionizing radiation. However, there is a growing body of evidence indicating that the radioprotective mechanism of action for tocotrienols extends far beyond their antioxidant properties. In this regard, tocotrienols also appear to modulate a wide array of critical signaling factors involved in radiation injury. These signaling effects are becoming increasingly implicated in their radioprotective efficacy in each organ system, including the hematopoietic, gastrointestinal, and vascular endothelial systems. The antioxidant properties and other signaling effects of tocotrienols appear to be mechanistically intertwined in the context of radioprotection. Furthermore, a systems biology perspective indicates that tocotrienols may be providing multi-organ radioprotection through interdependent physiological mechanisms between key organ systems.

Conclusions: This raises a new pharmacological paradigm that tocotrienols are uniquely efficacious radioprotectors due to a synergistic combination of antioxidant and other signaling effects in multiple key organ systems.

Keywords: Radiation, radioprotectors, tocotrienols, mechanism of action, signaling effects

Topic Area D:

Environmental and Agricultural Research

Poster Number: 31

CRISPR/Cas9-RNP Mediated Gene Editing of Rice (*Oryza sativa* SPP. *Japonica* CV. Nipponbare)

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CRISPR/Cas9 is a natural defense mechanism in bacteria against invading viruses. This mechanism is used as gene-editing technology. CRISPR/Cas9 system comprises two components: guide RNA (gRNA) and Cas9 (a CRISPR-associated protein). Guide RNA drags Cas9 to target sequence, and Cas9 breaks the DNA sequences 3-5 base pair upstream of Protospacer Adjacent Motif (PAM). gRNA binds with Cas9 nuclease to form gRNA-Cas9 complex or Ribonucleoprotein (RNP), the ultimate molecule responsible for CRISPR/Cas9 gene editing. Delivering CRISPR reagents as RNP into cells is faster and minimizes the off-target effects. The objective of this study is the direct delivery of preassembled RNP into cells using the PDS-1000/He Particle Delivery System for candidate gene editing. The first exon of the candidate gene was selected for editing, and two target sites were identified and sequenced along with their PAM at the UAMS DNA Core Facility. Based on target sites, two gRNAs were designed and synthesized. Externally synthesized gRNAs and Cas9 were combined at room temperature to form an RNP complex. Segment of length 597 base pair, which includes target sites with their PAM, was amplified and subjected to *in-vitro* cleavage assay to confirm activity of Cas9 nuclease. pCAMBIA1301 vector carrying Hygromycin-resistant marker gene was also co-delivered along with RNP for plant selection. One micro-meter gold particle coated with RNP/Vector were bombarded over 4-7 days old rice calluses under an 1100 psi rupture disk at a 9-centimeter target distance. Bombarded calluses were passed through selection process and, eventually, regenerated into rice plants. The transformation of regenerated rice plant was confirmed by the presence of a hygromycin-resistant gene through Polymerase Chain Reaction (PCR) with regeneration and transformation efficiency of 24% and 4% respectively. T_0 plants are growing and will be sequenced to analyze editing.

Keywords: CRISPR/Cas9, Ribonuceloprotein (RNP), Gene editing, Biolistic Delivery

Poster Number: 32

Differential Analysis of Gut Microbial Composition and its Importance for Plastic-Degrading Waxworm Larvae

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Background: One of the primary challenges of modern society is plastic waste management. In particular, low-density polyethylene (LDPE) accounts for more than 30% of all plastic produced. Low quality of recycled products and associated energy costs make current plastic management strategies less feasible. There is an urgent need for fast, efficient, and energetically sustainable alternatives. Larvae of the waxworm Galleria mellonella have shown the ability to rapidly biodegrade LDPE at room temperature. Our laboratory has made similar observations in microgravity conditions on the International Space Station. Multiple studies suggest that microbes within the waxworm's gut, together with its salivary enzymes, are responsible for biodegrading plastic. However, while some bacterial species have been identified, the literature lacks systematic assessment. We hypothesize that microbial composition and abundance in the waxworm's gut will change according to diet, thus allowing us to identify key species important for plastic degradation. Before evaluating the microbiome from larvae exposed to microgravity stress, it is imperative to establish a microbial community under plastic diet conditions. Therefore, our current study evaluates the waxworm microbiome under a restricted beeswax diet (natural feed source) versus beeswax and plastic.

Methods: Before the experiment, larvae were starved for 48 hours and exposed to these diets for 12 and 24 days. Sequencing was performed for a marker gene associated with bacteria (16S rRNA hypervariable region 4) to determine microbial community composition and differential abundance of bacterial species across different treatments.

Results: Initial results show that composition and species abundance are significantly different between pre and post-diet microbiomes, with no significant difference between dietary treatments. However, further research is needed to confirm our findings.

Conclusions: This study will help understand the microbial community in the waxworm's gut, which may give further insight into utilizing waxworms as a potential solution for managing plastic waste on Earth and in space.

Keywords: microbiome, plastic, biodegradation, waxworm

Poster Number: 33

Time Series Analysis of Long-Term Agricultural Biometeorological Trends to Explore Sustainable Crop Production in Arkansas USA

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Background: Climate change may be impacting key weather metrics that influence horticultural production. However, long-term analyses of climate trends relevant to agriculture are lacking in Arkansas, USA.
Methods: Daily temperature, precipitation, and derived biometeorological indices for 10 stations in Arkansas spanning 120 years were compiled. Missing data were initially handled via mean imputation (MI) to enable preliminary analysis.
Results: Initial time series analyses suggested potential changes in some indicators like growing season length and extreme heat days over the study period. However, additional time series modeling utilizing more appropriate and improved missing data imputation methods are required to confirm these preliminary climate trends.
Conclusions: Current findings point to possible climate-related changes in agricultural biometeorological indices in Arkansas during the 20th century. However, continued time series analyses using appropriate techniques for missing data are needed to quantify climate change impacts on fruit and vegetable production suitability in the region.

Keywords: Climate change, Time series analysis, Missing data, Crop suitability, Agricultural adaptation

Poster Number: 34

Peptidoglycan Hydrolases as Alternatives to Antibiotics to Treat *Staphylococcus aureus* Infections

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Background: *Staphylococcus aureus* is a highly pathogenic, gram-positive bacterium that is multidrug-resistant and virulent, causing infections in animals and humans. It can colonize fish and persist in the environment, raising concerns about potential transmission between animals and humans. The prevalence of antibiotic resistance in *S. aureus*, particularly the emergence of methicillin-resistant *S. aureus* (MRSA), poses a significant challenge to treatment. MRSA has been identified in fish and shrimp from aquaculture sources, significantly impacting animal health and imposing economic impact globally. In humans, *S. aureus* causes osteomyelitis, leading to bone degeneration. New therapeutic strategies are needed, either alone or in combination with conventional antibiotics.

Methods: Using bioinformatics, four peptidoglycan hydrolases (PGHs) were identified, recombinant PGH-6x His tag were cloned in pET21a (+) vector, overexpressed in competent *E. coli*, purified over a nickel column, and tested against 20 clinical *S. aureus isolates*.

Results: In our study, we identified two PGHs that showed promising results against 20 clinical isolates of *S. aureus* via plate lysis, MIC, and zymogram analysis.

Conclusion: Our findings suggest PGHs are potential new therapeutics in treating *S. aureus* infections, offering a promising direction in addressing antibiotic resistance issues.

Keywords: osteomyelitis, peptidoglycan hydrolases, zymogram

Poster Number: 35

Artemia as Growth and Immunostimulant Live Feed in Aquaculture

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Background: The aquaculture industry is a significant contributor to global food protein, with an annual production of 87.5 million tons, effectively meeting the ever-increasing demands of the world's population. Arkansas serves as the hub for warm water aquaculture and the baitfish industry. Losses attributed to fish diseases and high production costs necessitate the development of sustainable, immunostimulant, and nutritious diets. Artemia, commonly known as brine shrimp, has garnered immense significance owing to its exceptional nutritional value and suitability for feeding a broad spectrum of aquatic organisms, especially during their early life stages. Its small size, high nutritional content, and adaptability render it an ideal live feed for various aquatic species, particularly fish and shrimp larvae, fish fry, and fingerlings.

Methods: This study aims to evaluate the impact of varying doses of artemia on growth, immunity, and disease resistance in fat head minnows and gold fish.

health and growth benefits of artemia in the early life stages of ornamental and baitfish, as well as to evaluate its cost-effectiveness.

Results: Our studies indicate that artemia also fosters faster growth and higher survival rates in shrimp post-larvae (PL). With its rich protein, lipid, and essential fatty acid content, artemia potentially fulfills the dietary requirements of most larvae. We have developed an artemia culture system at UAPB, controlling temperature, oxygen supply, and light. Incubating artemia cysts at 30°C and 25 parts per thousand (ppt) for 20 to 22 hours resulted in an 80 to 90% hatch rate. We plan to conduct artemia feed trials during larval stages and Flavobacterium challenge studies to determine growth and disease resistance.

Conclusion: Ability to hatch and grow artemia will enable us to do conduct bacterial challenge studies to test disease resistance and growth effects to benefit aquaculture industry.

Keywords: Artemia, bait and ornamental fish, *flavobacterium*

Poster Number: 36

The Comparative Analysis of Microbiome and Reproductive Performance of Longevity Sow's Groups through 4 Parities

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Background: The parity of sows is one of the important indicators affecting reproductive performance. Furthermore, gut and vaginal microbes appear to be related to reproductive performance. However, the correlations between microbiome and multiple parities of sows remain unclear.
Methods: To investigate the characteristics of microbiome in multiple parities, sows which went through 4 parities were followed. A parity lasted approximately 135 days, and the vaginal and fecal swabs were collected respectively in day0 and day 110 in each parity. 16S sequencing of the V4 region via the Illumina MiSeq platform was applied to all samples.
Results: Only 9 out of 48 sows which went through 4 parities were regarded as longevity groups in this study. For focused sows (n=9), the reproductive performance including average alive born piglets and weaned piglets weight demonstrated significant differences between 4 parities. For microbiome analysis, alpha and beta diversity proved the significant differences of bacteria within and between 4 parities. Furthermore, LEfSe analysis help to find the biomarker bacteria in each parity. Importantly, we listed the vaginal and fecal top 10 ASVs and observed their dynamic changes. For the correlation analysis between bacteria and reproductive performance, we found that the alive born piglets' number was positively associated with ASV3 *Lactobacillus* in day0 feces and ASV25 *Streptococcus* in day0 vagina showed a strong correlation with total born weight.
Conclusions: In total, this study showed the dynamic characteristics of longevity sows fecal and vaginal bacteria through 4 parities and laid the foundation for the study of microbes and sow parity.

Key words: Sows, microbiota, parity, reproductive performance

Poster Number: 37

Functionalizing Chitosan Nanoparticles against A. hydrophila in catfish, a Potential Antibiotic Alternative

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Background: *Aeromonas hydrophila*, a gram-negative bacterium, causes Motile Aeromonas Septicemia (MAS) across many important fish species, resulting in substantial global economic ramifications. The inefficacy of vaccines and increased antibiotic resistance poses a formidable challenge in combatting bacterial infections in fish. This necessitates exploring alternative treatment methods. Plants house a plethora of bioactive compounds, including phenols, flavonoids, and carotenoids, having antioxidative, antifungal, bactericidal, and bacteriostatic properties. Certain spices such as garlic, clove, cumin, coriander, onion, and dill weed have demonstrated antibacterial properties.
Methods: We have extracted bioactive compounds from spices and herbs and synthesized chitosan nanoparticles harboring Eugenol.
Results: Our earlier investigations unveiled that extracts from clove (*Syzygium aromaticum*) possess remarkable bactericidal and bacteriostatic effects against *A. hydrophila*, with no cytotoxic, genotoxic, or growth effects in channel catfish ovary cells (CCO). Eugenol, the primary constituent of clove extract, exhibited substantial antimicrobial activity. However, its volatile nature impedes its practical application. Nanoparticles, being small and with a larger surface area, have demonstrated notable efficacy in drug delivery in human medicine and are increasingly being explored in fish medicine. Chitosan is a natural polymer with no cytotoxicity but is an immunostimulant, antimicrobial, and biodegradable. Our approach involves functionalizing chitosan-TPP nanoparticles to deliver Eugenol to treat *A. hydrophila* in catfish.
Conclusion: To verify and quantify the combination of eugenol with chitosan-TPP nanoparticles, we will employ Fourier Transform Infrared Spectroscopy (FTIR), Nuclear Magnetic Resonance Spectroscopy (NMR), and Scanning Electron Microscopy (SEM). Eugenol has been functionalized on the chitosan nanoparticles. Our initial results on FTIR indicated the functionalization.

Keywords: *Aeromonas hydrophila*, Eugenol, chitosan-TPP nanoparticles

Poster Number: 38

Advancing Soybean Disease Detection: Implementing Convolutional Neural Networks for Enhanced Laboratory Analysis

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Background: Soybean plants face numerous biotic stresses, with their survival hinging on effective adaptation strategies. Accurate diagnosis of these stresses is crucial to minimize crop loss and implement timely treatments. Traditional diagnostic methods, based primarily on human observation, often fall short due to the subtlety of early-stage symptoms. This study aims to address these challenges by developing a more reliable, technology-driven approach for disease detection in soybeans.
Methods: The core of our approach is a mobile application powered by a Convolutional Neural Network (CNN), chosen for its superior automatic feature extraction and scalability compared to the previously used Support Vector Machines (SVM). We utilized a pre-existing, annotated dataset, enhancing it with two new categories: “not soybean, healthy” and “not soybean, unhealthy,” to facilitate more detailed classification. The app captures images for analysis, processed on a dedicated server to manage the computational demands of the CNN.
Results: The application demonstrated a significant improvement in accurately diagnosing and assessing the severity of soybean diseases. The enhanced dataset, enriched with real-time, app-captured images and subsequent manual verifications, contributed to the continuous refinement of the model's accuracy.
Conclusions: The deployment of this mobile application marks a substantial advancement in soybean disease management. By leveraging advanced machine learning algorithms, it offers a more accurate, efficient, and scalable solution for disease detection and severity estimation in soybean cultivation. This tool not only aids in reducing crop loss but also serves as an educational resource for agricultural professionals.

Keywords: Soybean Disease Detection, Convolutional Neural Networks, Machine Learning in Agriculture, Crop Disease Management, Automated Plant Diagnosis.

Poster Number: 39

Green synthesis and characterization of Ultra high specific surface area of biomass-Porous carbon

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Background: Porous carbon derived from renewable resources, has been the most used precursor for biomedical and portable energy applications due to their economically friendly and environmentally abundant characteristics. The chemical activation methodology has been used in the past to enhance porosity as well as surface area characteristics. In this project, we present a physical freeze pore strategy to attain the high surface area carbon with improved mesoporous characteristics.

Methods: Herein, we report the synthesis and characterization of carbon materials derived from ligonosol renewable resource. A green microwave method was utilized to carbonize the carbon. A very economical and ecofriendly physical approach, freeze pore method was utilized to enhance the porosity as well as surface area of the carbon materials. The resulting carbon materials were characterized using SEM-EDS, Raman spectroscopy, XPS and BET to investigate their surface morphology, elemental composition, porosity as well as surface area. The characteristics of the physically activated sample were compared with the chemically activated carbon sample as well. We also studied the electrochemical properties to investigate their use for supercapacitor and battery applications.

Results: The freeze pore approach significantly enhanced the specific surface area of the carbon. The resultant surface area values are comparable with chemically activated samples. We also observed the changes in the elemental composition of the resultant samples. The detailed analysis of electrochemical characterization revealed their significance for energy storage and lithium-sulfur battery. The drug delivery application of these carbon materials will be investigated in future.

Conclusions: The physically activated freeze pore method produces carbon with high porosity as well as with high surface area that are comparable with the sample prepared using harsh chemical activation approach. Biomass derived carbon materials exhibited tremendous potential for energy storage and drug delivery applications.

Keywords: Renewable resources, carbon, porosity, surface area, microwave, freeze pore method.

Poster Number: 40

Peptidoglycan Hydrolases to Treat *Streptococcus iniae Infections*

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Background: *Streptococcus iniae*, a significant aquatic pathogen causing Streptococcosis, rapidly spreads through the bloodstream, affecting around 30 species and resulting in substantial annual economic losses in aquaculture, reaching billions of dollars. Antibiotics, commonly used for treatment, face scrutiny due to emerging multi-drug-resistant strains and the potential spread of resistance from farms to clinical settings. There's an urgent need to develop alternative antimicrobials with refractory resistance development and positive economic impact. One such alternative is bacteriophage therapy, limited by phage specificity. This study aims to study phage endolysins, enzymatic antimicrobials targeting bacterial cell wall peptidoglycans that offer potential against intracellular *S. iniae*.
Methods: Using bioinformatics, ten peptidoglycan hydrolases (PGHs) were identified, recombinant PGH-6x His tag were cloned in pET21a (+) vector, overexpressed in competent *E. coli*, purified over a nickel column, and tested against *S. iniae strains*.
Results: Two PGHs showed high lytic activity against *S. iniae strains* via several plate lysis and zymograms. The PGHs showed specific activity against *S.iniae* at 24 to 96 hours. Zymogram results indicate that the PGHs are stable and active at room temperature for more than 96 hrs.
Conclusion: Our findings indicate that PGHs are potential antibiotic alternatives for treating *S. iniae* infections that benefit the aquaculture industry.

Key Words: Streptococcosis, peptidoglycan hydrolases, zymogram

Topic Area E:

Machine Learning and AI in Health

Poster Number: 41

Developing a Transformer-Based Model for Regulatory Article Classification

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Background: Because of the sheer volume of said publications produced by the FDA, as well as more coming in the future, it is infeasible to have them all manually label. This, it was decided that AI could be best utilized for the task of document classification. In this particular case, a model was created using a pretrained transformer-based model as the backbone and finetuning it to existing dataset of regulatory and non-regulatory publications. This serves a test case for using such AI models for this task throughout the FDA

Methods: The dataset consists of a collection of 260 publications, each of which have a regulatory label assigned as well as 1000 non-regulatory publications sampled randomly from the NCTR database. We chose this ratio in order to create a representative sample of what the model will encounter once it is live. From these, the abstract and the label was kept, using the abstract as input. Because of the small size of the dataset, a simple train-test split of 80/20 was made, stratifying to ensure consistent ratios across both sets. To compensate, we decided to go with a stratified K-Fold cross validation when training and evaluating the model. This gives a better sense of the model's performance, though admittedly, it is likely still optimistic. The model chosen was the DistilBERT model from the huggingface transformers library. It was chosen due to having similar performance to BERT while only being 60% of the size. This also help head off against overfitting.

Results: Early results suggest high performance on the cross-validated dataset, with an AUC score of 0.9. The precision, recall, and f1 scores were similar, all being at 0.9.*

*However these may not be representative of the final results.

Conclusion: This model shows high potential for being used to automate the process of classify documents within the FDA. It likely can also be extended to account for more labels should the need arise.

Poster Number: 42

Tackling Vaccine Hesitancy Via Analytical Models

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Background: The COVID-19 pandemic posed significant challenges in allocating critical healthcare resources. These challenges were due to the virus's fast transmission rate, high demand for critical healthcare resources, and vaccine hesitancy (VH). Compartmental epidemiological models developed to estimate the spread of the COVID-19 virus and its impacts on the population failed to capture the influence of VH and the availability of healthcare resources on disease dynamics, the expected number of hospitalizations, and the expected number of fatalities. This study proposes enhancements of the compartmental models by incorporating specific characteristics of COVID-19 and the influence of vaccination, VH, and resource availability on the dynamics of the disease.

Methods: Historical VH data from the COVID-19 Trends and Impact Survey (CTIS) are used to model the changes in VH over time. We use the results of this analysis to develop scenario paths for VH. We simulate the proposed compartmental model for each scenario path to explain the impacts of public attitudes towards vaccination and epidemic outcomes, the impacts of healthcare resources on patient outcomes, and the timing of vaccine rollout on the progression and severity of the epidemic.

Results: Findings demonstrate that reducing VH improves health outcomes, reinforcing the importance of addressing VH to curb infectious diseases. Ensuring adequate levels of critical healthcare resources is crucial for minimizing fatalities. Additionally, the results highlight the life-saving impact of timely and effective vaccination programs.

Conclusions: Our analysis highlights the significant influence of vaccination, VH, and the availability of critical resources on public health outcomes during a pandemic. Our next steps will focus on extending this work by developing multi-stage stochastic optimization models that support dynamic resource allocation decisions under uncertainty. Such models mimic reality since decision-makers continually refine their decisions as new data emerges to ensure a proactive and adaptive response to pandemics.

Keywords: compartmental model, COVID-19, data analytics, vaccine hesitancy

Poster Number: 43

A Comparative Analysis of GAN-based and Conventional Machine Learning Models for Predicting Compound-Induced Responses in Rat Serum Liver Enzymes

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Background: Predictive toxicology is vital for drug and chemical safety assessment. As this field progresses, the integration of Artificial Intelligence (AI) methodologies becomes increasingly important. While conventional Machine Learning (ML) models have been instrumental, Generative Adversarial Network (GAN)-based approaches offer novel perspective by synthesizing realistic data. This poster aims to compare these two methods in predictive toxicology.
Methods: Using clinical pathology data from the TG-GATEs database, we compared AnimalGAN, our previously developed GAN-based model, with conventional ML models in predicting rat serum liver enzymes under specific treatment conditions. Conventional ML models typically provide deterministic predictions, whereas AnimalGAN, learning from animal-level data, provides probabilistic results that reflect population variability. For a fair comparison, consistent inputs and study designs were used for both AnimalGAN and conventional ML models. During comparisons, we developed 12 different regression models for each of the 7 enzymes, learning from detailed animal-level data, which are exactly same training data with AnimalGAN. The average of 100 valid profiles generated by AnimalGAN for each treatment condition was used to representing AnimalGAN results.
Results: AnimalGAN significantly outperformed conventional ML models in predicting all seven liver enzymes, evaluated using a test set of 28 compounds across 332 treatment conditions. It notably reduced Root Mean Squared Errors (RMSEs) for enzymes critical in Drug-Induced Liver Injury (DILI) risk assessment – alanine aminotransferase (ALT), aspartate aminotransferase (AST) and total bilirubin (TBIL) – with reductions of 26.22%, 24.12%, and 23.57%, respectively. An analysis of the important features used by each model revealed minimal overlap between AnimalGAN and ML models. Notably, AnimalGAN showed less sensitivity to the applicability domain, highlighting its robustness and adaptability.
Conclusions: This study demonstrates AnimalGAN's superior predictive performance and its simulation capability in complex animal experiments, underscoring the value of integrating advanced GAN-based models in toxicological research.

Keywords: Generative Adversarial Network; Machine Learning; Predictive Toxicology

Poster Number: 44

Heart Failure Prediction using an Integrated Mechanistic + Machine Learning Model

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Background: Cardiac fibrosis is a significant contributor to heart failure (HF) progression, which is exceedingly difficult to control or predict. Developing systems biology-based mechanistic models offers potential for improving patient-specific prognoses given fibrosis-related biomarkers, but such system biology models depend on many unknown parameters with is insufficient experimental data to calculate critical rate constants. We hypothesized that integrating mechanistic kinetic models with neural network machine learning models would improve the accuracy of patient-specific HF predictions.
Methods: Here, we developed mechanistic models for cardiac fibrosis by capturing mass-action reaction kinetics between matrix, protease, and protease inhibitor concentrations as a dynamic system of ordinary differential equations. This ODE system was coupled with neural network algorithms and trained using a clinical dataset encompassing protein biomarker levels and echocardiography-based cardiac function metrics across hundreds of healthy and HF patients. We then tested the coupled model's ability to perform regression tasks (quantiatively predict echocardiography parameters) and classification tasks (group each patient into HF vs. control).
Results: The machine learning algorithm classified the HF and control patients to 72% accuracy with limited datasets and 82% accuracy with expanded datasets with AUROC equalling 78% for limited datasets and 88% for expanded datasets. For the regression analysis, we obtained an r-squared score of up to 92% for the expanded datasets, and the MSE is 0.0003.
Conclusions: We have developed a functional method to incorporate mechanistic, systems biology models with machine learning frameworks. Although more work will be done from the results obtained, the results show that these integrated "chemistry-informed" neural networks show improved performance for clinical predictions.

Keywords: mechanistic model, machine learning, cardiac fibrosis, heart failure.

Poster Number: 45

A Comparative Sentiment Analysis of Stigmatized and Non-Stigmatized Disease on Social Media

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Background: Cancer and heart disease elicit different societal reactions and perceptions. Cancer is often associated with death, fear, and stigma. Heart disease and certain stigmatized cancers such as lung cancer may be perceived more as lifestyle diseases. This study aimed to compare societal perceptions of non-stigmatized cancers, stigmatized cancers, and heart diseases.
Methods: A mixed methods study analyzed 1,000 tweets for each of 3 disease categories: non-stigmatized cancers, stigmatized cancers, and heart diseases. Tweets were in English and extracted from personal accounts discussing their own or loved ones' illnesses. Quantitative analysis focused on employing sentiment analysis to compare the attitudes, perceptions, and overall impressions of individuals in the three study groups. Topic Clustering, a form of Latent Dirichlet Allocation (LDA), is then used to form clusters of related words/terms within the Twitter data for each study group. Qualitative analysis was also employed to examine themes in the tweets.
Results: Preliminary quantitative analyses suggest potential differences in the perceptions the public may have of non-stigmatized cancers, stigmatized cancers, and heart diseases. Qualitative analyses of the extracted tweets and the resulting topic clusters within each study group reveal differing themes related to stigma, emotion, and lifestyle factors between the groups.
Conclusions: Initial findings suggest possible differences in societal perceptions, including stigma and emotion, towards stigmatized and non-stigmatized disease on social media. Further quantitative analyses and qualitative theme development are needed as the study continues. Follow-up studies could further explore reasons behind societal reactions to these diseases.

Keywords: Disease Perceptions, Cancers, Heart Disease, Twitter, Sentiment Analysis

Poster Number: 46

SD-WEAT: Towards Robustly Measuring Bias in Input Embeddings

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Background: Artificial intelligence (AI) is rapidly being adopted to build products and aid in the decision-making process across industries. However, AI systems have been shown to exhibit and even amplify biases, causing a growing concern among people world-wide. Thus, investigating methods of measuring and mitigating bias within these AI-powered tools is necessary.

Methods: In this study, we introduce SD-WEAT, which is a modified version of the Word Embedding Association Test (WEAT) that utilizes the standard deviation (SD) of multiple permutations of the WEAT tests in order to calculate bias in input embeddings, a common area of measuring and mitigating bias in AI.

Results: This method produces results comparable to that of WEAT, while addressing some of its largest limitations. More specifically, SD-WEAT is more accessible as it removes the need to pre-define attribute groups, and because SD-WEAT measures bias over multiple runs rather than one, it reduces the impact of outliers and sample size.

Conclusion: Thus, SD-WEAT shows promise for robustly measuring bias in the input embeddings fed to AI language models.

Keywords: bias in artificial intelligence, bias measurement, natural language processing, input embeddings, language models

Poster Number: 47

Sequential Patterning of Dynamic Brain States Distinguishes Individuals with Parkinson's Disease

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Background: Abnormalities in the dynamic organization of neural-network activity are believed to subserve cognitive and motor impairments among people with Parkinson's disease (PwPD). The purpose of the current project was to evaluate two machine-learning methods of characterizing the sequential organization of derived brain states to determine whether these features can accurately distinguish PwPD from healthy aging individuals (HAI).

Methods: Electroencephalography (EEG) and functional magnetic resonance imaging (fMRI) data were separately collected from 32 PwPD and 26 HAI following IRB approval and informed consent. Seven EEG microstates were derived using the EEGLab Microstates Toolbox from resting, eyes-closed EEG recorded using a 256-channel system (Magstim-EGI), following removal of artifacts using Brainstorm. Four states of dynamic functional connectivity (dFC-states) among resting-state networks were derived using the Group Independent Component Analyses for fMRI Toolbox (GIFT) from resting, eyes-closed fMRI data collected on a Siemens 3T TRIO scanner and pre-processed using FSL. Sequences of letters indicating transitions across states for each modality were separately used as input to two Python-based methods of sequential pattern mining: 1) Sqn2vec, which utilizes the Paragraph Vector-Distributed Bag-of-Words approach to learn embedding vectors for sequential patterns, and 2) Seq2pat, which was developed to analyze click-stream data using a multi-valued decision diagram approach. The sequential patterning features derived from each method were then used to train a Support Vector Machine (SVM) classifier to distinguish PwPD from HAI using 80/20 training/testing splits.

Results: The highest mean accuracy across 100 cross-validation runs was 66% for the EEG microstates and 71% for the dFC states, using the Seq2pat features.

Conclusions: While the classifiers show only modest accuracy, the fact that all were above chance level does indicate that the sequential patterning of derived brain states warrants further investigation as possible indicators of abnormality in the dynamic, temporal organization of neural network activity among PwPD.

Keywords: Neuroimaging, Parkinson's disease, Machine Learning, Pattern Mining

Poster Number: 48

Elevating Pharmacovigilance with Advanced AI: A Study on LLM-Based Literature Screening

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Background: Pharmacovigilance plays a crucial role in ensuring the safety of pharmaceutical products. It involves the systematic monitoring of adverse events and the detection of potential safety concerns related to drugs. Manual literature screening for pharmacovigilance related articles is a labor-intensive and time-consuming task, requiring streamlined solutions to cope with the continuous growth of literature. This study explores the application of Large Language Models (LLMs) to automate literature screening, aiming to expedite the process and pinpoint articles relevant to the focused area of pharmacovigilance. The overarching objective is to enhance the efficiency and accuracy of article identification, contributing to the ongoing efforts to ensure drug safety.
Methods: In this research, we assess the performance of leading LLMs, including GPT-3.5, GPT-4, and Anthropic's Claude2, in automating the categorization of medical publications as relevant or irrelevant for safety signal reviews. We employ a pre-labeled dataset to evaluate the effectiveness of these models. Our analysis encompasses the assessment of N-shot learning, the elucidation of chain-of-thought reasoning, the determination of sensitivity and specificity, and the exploration of factors impacting accuracy.
Results: The findings highlight the promising potential of LLMs in literature screening, showcasing notable strengths in terms of reproducibility and sensitivity, although demonstrating a moderate specificity. Notably, when provided with a few examples of abstracts, labels, and corresponding reasoning explanations, we observed an improvement in categorization performance. Moreover, our exploration identified several potential contributing factors influencing prediction outcomes. These factors encompassed the choice of key words and prompt formats, the balance within the training data, and variations in reasoning explanations.
Conclusions: By configuring advanced LLMs for swift screening of extensive literature databases, the potential for transformative impact in drug safety monitoring becomes evident. Furthermore, this innovative approach holds promise for extension to various other pharmacovigilance tasks that entail processing large volumes of text data.

Keywords: Large Language Models, LLMs, Literature Screening.

Poster Number: 49

Early Detection of Tuberculosis with Machine Learning-Based Cough Audio Analysis: Towards More Accessible Diagnostics for Global Triaging Usage

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Background: Tuberculosis (TB), a bacterial disease mainly affecting the lungs, is the leading infectious cause of mortality worldwide after COVID-19. To prevent TB from spreading within the body, which can cause life-threatening complications, timely and effective anti-TB treatment is crucial. Cough is a standard symptom of active TB. Current gold standards for TB diagnosis are slow or inaccessible, especially in rural areas where TB is most prevalent. In addition, TB diagnostics with machine learning (ML) like utilizing chest radiographs still poses high costs and access barriers for low/middle income countries where accessible diagnostics are needed.
Methods: To enable effective diagnosis, a multi-input ensemble model was developed that uses a novel ML architecture to analyze coughs' acoustic epidemiologies from smartphones' microphones to detect TB. The architecture includes a 2D-CNN that was trained on almost 10,000 cough audio samples and demographics from 7 countries. After exploring various feature extractions (Mel-spectrograms and MFCCs) and data augmentations (White-noise and IR-convolution), the final model uses Kaiming initialization, consisting of six convolutional layers with ReLu activation and batch normalization, followed by an AdaptiveAvgPool2d layer.
Results: The multi-input model achieved an AUROC (area under the receiving operator characteristic) of 86%, surpassing WHO's recommended requirements for a TB screening test. The results are available within 15 seconds and can easily be accessible via web or mobile app that was created.
Conclusions: This research showcases a promising AI-powered tool to improve TB diagnosis through an accurate, quick, and accessible tool. By easily gleaning TB status information from periodic cough sounds as treatment progresses, a high risk of treatment or dosage irregularity can also be predicted. Furthermore, this enables better diagnostics for populations (i.e. children and individuals with HIV) that don’t produce sputum (needed for smear microscopy tests).

Keywords: Tuberculosis, Machine Learning, Cough, AI Diagnostics

Poster Number: 50

Confirmatory Factor Analysis of the 42-Item Sexual Minority Identity Emotion Scale for Sexual Minority Adolescents

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Background: Previous exploratory factor analysis (EFA) results using this data suggested items used in this study could be grouped into 4 subscales. The aim of this study was to use Confirmatory factor analysis (CFA) to investigate the results from the EFA.

Methods: This study included a total of 232 adolescents between the ages of 14 and 17 years who identified as cisgender male or female, resided in the USA, and identified as not 100% heterosexual. The data used in this study was collected using the 42-item Sexual Minority Identity Emotion Scale (SMIES), which was originally collected as part of a longitudinal study measuring the stress of sexual minority adolescents over time in a national sample. CFA was performed in R using the Lavaan (v. 0.6.16) package to evaluate the model with maximum likelihood estimation.

Results: CFA was conducted with two models (unidimensional and single-order multidimensional). The comparative fit index (CFI), root mean square error of approximation (RMSEA) and the standardized root mean squared (SRMR) for the unidimensional model were 0.597, 0.133 and 0.137 respectively. The CFI, RMSEA and SRMR for the single-order multidimensional model were 0.902, 0.066 and 0.073 respectively. The fit statistics measured suggested a poor fit for the unidimensional model yet a good fit for the single-order multidimensional model.

Conclusion: The results from the CFA indicate that the items used for this study can be grouped into four subscales as previously indicated by the EFA results.

Keywords: Exploratory Factor Analysis, Confirmatory Factor Analysis, Scale Validation, Psychometrics, LGBTQ+ Youth

Poster Number: 51

Finding the Most Important Features of Colorectal Cancer

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Background: There is a well-established link between social and behavioral determinants of health (SBDOH) and cancer incidence and survival rates. Arkansas, a rural state which has some of the worst reported health outcomes in the country, had the 8th highest incidence rate of colorectal cancer (CRC) in the US, and the 6th highest mortality rate from colorectal cancer (American Cancer Society, 2021). In this study, our primary objectives were to 1) identify key features that are significantly associated with CRC and 2) examine the relationships between those features among CRC patients. This research could provide valuable insights into risk factors specific to CRC in Arkansas, potentially guiding targeted interventions.

Methods: Demographic and medical data were collected from 2,355 patients diagnosed from the University of Arkansas for Medical Science (UAMS) electronic health records (EHR). Individual-level SBDoH were purchased from a third-party source and linked with the EHR. Three different dimension reductions were performed in our study: 1) uniform manifold approximation and projection (UMAP), 2) t-distributed stochastic neighbor embedding (t-SNE), and 3) truncated singular value decomposition (truncatedSVD). After the dimensions were reduced, four clustering algorithms were used including 1) ordering points to identify the clustering structure (OPTICS), 2) KMeans clustering (KMeans), 3) balanced iterative reducing and clustering using hierarchies (BIRCH), and 4) density-based spatial clustering of applications with noise (DBScan). OPTUNA, a machine learning model which compares several different dimension reduction and cluster algorithm techniques, was used to select the optimum models for our data. A machine learning model called CATBOOST was used to identify the most important features, with CRC diagnosis being the outcome.

Results: The best method for dimension shrinking was identified to be UMAP, compared to the other methods TSNE and TruncatedSVD. When looking at the important features identified within each clustering algorithm, we see that health insurance is significant to CRC outcomes, as the variables with the highest relative importance factor were ‘having Medicare Advantage Part C’ (24.18), ‘having Medicare coverage with a Medigap supplement’ (18.76), ‘has medicaid’ (17.25) on average. Additional demographic and social features were identified as important, such as ‘having a government health insurance provider’ (10.23).

Keywords: Colorectal Cancer, Important Features, Machine Learning

Poster Number: 52

Assist4PGx - an AI-enhanced framework for identifying and linking Pharmacogenomics information with minority communities

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Background: Pharmacogenomics (PGx) aims to personalize and optimize medical treatments based on an individual's genetic profile, thereby enhancing the effectiveness and safety of drug therapies. However, current clinical studies for PGx biomarkers and related drug doses reveals a concerning trend of limited representation from diverse ethnic populations. To bridge this gap in PGx knowledge across various minority groups, a comprehensive approach involving data extraction, review, and analysis from diverse sources such as drug labels and research articles is needed. Unfortunately, existing keyword-based methods often result in numerous false negatives, and extracting the PGx knowledge from these documents is usually labor-intensive and time-consuming. To overcome these challenges, we propose the implementation of an AI-enhanced framework using large language models (LLMs) to extract PGx information automatically and accurately from text documents.

Methods: In this study, FDA drug labeling contexts and literatures contain drugs, related biomarkers, and certain ethnic keywords were collected. We employed ChatGPT and Claude2, presenting them with well-designed questions (as prompts) to extract information, including drug and biomarker pairs, therapeutic areas, PGx labeling, reasons for PGx, ethnicity statistics, etc.

Results: The findings highlight the promising potential of LLMs in PGx information extraction from text documents. With carefully designed questions (prompts) and given drug labeling sections, both ChatGPT and Claude2 demonstrated the ability to identify the drug-biomarker pairs and related PGx information with high accuracy. Encouragingly, these LLMs also performed well with mixed sections from different drug labeling documents with two drug-biomarker pairs.

Conclusions: In summary, our study underscores the promising role of LLMs in automating the extraction of Pharmacogenomics (PGx) information. Models like ChatGPT and Claude2 demonstrated accuracy in identifying key details related minority groups, offering an efficient solution that minimizes both labor and time costs. Embracing AI-driven approaches can enhance PGx knowledge accessibility and contribute to advancing personalized medicine.

Keywords: Large Language Models, LLMs, Pharmacogenomics, Minority Communities.

Poster Number: 53

A Deep Learning-Based Model for Missing Value Recovery

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Background: The introduction of single-cell RNA sequencing (scRNA-seq) technology has empowered our capacity to investigate cellular diversity and decipher the complexities of intricate diseases. However, the unique challenges of scRNA-seq data analysis, stemming from the inherently low signal-to-noise ratio and a significant number of missing values, necessitate new computational methods.

Methods: We have developed a novel data imputation method, cnnImpute, leveraging convolutional neural networks (CNNs) to address the challenge of prevalent missing data in scRNA-seq. Our approach begins with estimating missing probabilities, followed by constructing a CNN-based model designed to recover expression values with a high likelihood of being missing.

Results: In extensive evaluations, cnnImpute demonstrates its efficacy by accurately imputing missing values while maintaining the integrity of cell clusters in scRNA-seq data analysis. The method exhibits superior performance across various benchmarking experiments, establishing itself as a reliable solution.

Conclusion: With its precision and scalability, cnnImpute stands as a valuable resource for recovering missing values and facilitating scRNA-seq-based analysis and research.

Keywords: single cell RNA sequencing, convolutional neural network, imputation

Topic Area F:

Microbiome and Genetic Research

Poster Number: 54

Comprehensive Characterization of HITI Precision and Off-Target Integration at Genomic and Transcriptomic Levels

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Background: CRISPR-mediated Homology-Independent Targeted Integration (HITI) has demonstrated its potential for transgene integration at specific loci in both post-mitotic and dividing cells. Despite its success, the precision and off-target effects of HITI warrant further investigation to establish its safety for gene integration. Specifically, the post-integration effects at the genomic DNA and mRNA levels remain unclear, both in vitro and in vivo.

Methods: Genomic-level analysis was conducted utilizing a Unique Molecular Identifier (UMI) with transposon-mediated tagmentation (TN5) sequencing. This approach involved the use of primers spanning from the genomic locus to the integrated transgene, ensuring unbiased characterization of editing events. Furthermore, unbiased assessment of post-integration effects in the genome was achieved through the application of nCATS (nanopore CRISPR-Assisted Targeting Sequencing) with adaptive sampling. To complement this, transcriptomic-level data was obtained through 5'RACE-seq and RNA-seq, with a focus on comparing outcomes under in vitro conditions facilitated by non-viral delivery systems.

Results: Our study revealed distinct TN5 NHEJ rearrangement targets, shedding light on the genomic consequences of HITI. Post-integration effects in the transcriptome demonstrated variations between in vitro conditions, with notable differences observed in RNA-seq and 5'RACE seq analyses comparing non-viral treated transcriptomes.

Conclusion: This comprehensive investigation contributes valuable insights into the precision and off-target integration of HITI at both the genomic DNA and mRNA levels. The identified NHEJ rearrangement targets and the divergent transcriptomic effects in different delivery systems underscore the importance of further characterizing HITI for its safe and efficient application in gene integration technologies.

Keywords: sequencing, off-target, integration, transcriptome, unbiased

Poster Number: 55

Comparative Genomic Analysis of Nine Corynebacterium xerosis Genomes

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Background: *Corynebacterium xerosis* is often considered a commensal member of the human and animal microbiota. However, it is beginning to be considered an emerging opportunistic pathogen, as it has been isolated from both human and animal lesions and other clinical cases. Furthermore, it has been proposed that the *Corynebacterium* genus can be divided into nine phylogenetic groups, with Group M encompassing *C. xerosis.* Some members of this phylogenetic group have been considered to be opportunistic pathogens, while others may have potential probiotic properties.
Methods: We analyzed nine (8 publicly available in RefSeq, 1 novel) *C. xerosis* genomes to evaluate *C. xerosis* genomic potential and its potential pathogenic and probiotic functions. All genomes were re-annotated using Prokka, and the *C. xerosis* core and pan-genome were determined using Roary. The Comprehensive Antibiotic Resistance Database, Virulence Factor database, and mobileOG-db database were used to determine potential antimicrobial resistance (AMR) genes, virulence factors, and mobile genetic elements, respectively. PhySpy was used to determine prophages, and antiSMASH was used to determine biosynthetic gene clusters.
Results: Pan-genome analysis found that the *C. xerosis* core genome (present in at least 8/9 genomes) consisted of 1464 genes, and the *C. xerosis* pan-genome consisted of 1704 accessory genes (present in 2-7 genomes) and 2473 unique genes (present in only 1 genome). Differences and similarities in gene content were observed for both AMR genes, virulence factors, mobile genetic elements, prophages, and biosynthetic gene clusters.
Conclusions: While only nine genomes, including all eight publicly available in RefSeq, were included in this analysis, these results shine a light on the potential genetic differences contributing to *C. xerosis'* role as a commensal or pathogenic member of the microbiota.

Keywords: *Corynebacterium xerosis*, microbiota, whole genome sequencing

Poster Number: 56

AA[N]I-miner: A Novel Tool for Measuring a Genome's Paralog Degree and the Ortholog Degree Between Prokaryotic Genomes

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Background: In bacterial genomics, the analysis of genome-to-genome similarity is pivotal for understanding microbial diversity and evolutionary relationships. Average Nucleotide Identity (ANI) and Average Amino Acid Identity (AAI) play a crucial role in evaluating taxonomy, genomic relatedness, and functional potential in bacteria. We present AA[N]I-miner, a novel tool that not only rapidly and accurately computes AAI and ANI, but also measures a genome's paralog degree (PD) and the ortholog degree (OD) between genomes.

Methods: AA[N]I-miner, developed in Python (3.10.0), utilizes the UCLUST algorithm in USEARCH to efficiently process large genome datasets. It offers an adjustable sequence identity for ANI and AAI analysis. AA[N]I-miner calculates a genome's PD as PD(*Gi*) = A[P]I(*Gi*) * R(*Gi*), combining average identity and ratio of paralogs in *Gi*. Furthermore, it determines the OD between genomes (*Gx*, *Gy*) as OD(*Gx*, *Gy*) = AA[N]I(*Gx*, *Gy*) * [(R(*Gx*) + R(*Gy*))/2], considering average identities and ratios of orthologs in *Gx* and *Gy*.

Results: Utilizing a clustering methodology, AA[N]I-miner not only provides accurate ANI and AAI values but also offers an in-depth examination of the functional structure of bacterial genomes. This is achieved by detailed assessments of the degrees of paralogs and orthologs, complemented by visualizations of phylogenetic trees and network structures. Moreover, AA[N]I-miner's robust algorithm ensures faster processing times, making it an invaluable asset for large-scale genomic studies. This marks a considerable improvement over BLAST-based traditional methods, aiding researchers in decoding bacterial genomic complexities. The efficacy of AA[N]I-miner was assessed using three bacterial genome datasets, each varying in taxonomy and genome size.

Conclusions: By offering a more comprehensive analysis, AA[N]I-miner allows researchers to conduct a deeper exploration of microbial genomes, facilitating a better understanding of bacterial taxonomy, phylogeny, and evolution.

Keywords: Bacterial genome, Ortholog, Paralog, AAI, ANI

Poster Number: 57

Age Related Clonal Expansion of Circulating Mutant Hematopoietic Stem Cells Quantified Using Highly Sensitive DNA Sequencing

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Background: Clonal hematopoiesis (CH) describes the acquisition and clonal expansion of mutant hematopoietic stem cells that results in an increased number of mutant blood cell prodigy in peripheral blood. CH is associated with normal aging, previous exposure to cytotoxic therapies, multiple environmental factors, and increases the risk of hematological cancers, fatal ischemic strokes, myocardial infarctions, and all-cause mortality.
Methods: We developed an error-corrected sequencing (ecNGS) method using unique molecular labelling of target DNA molecules, Q5 polymerase for ultra high-fidelity amplification of targets and of library preparations, and a novel computational workflow, CANcer Variant Allele Sequencing (CANVAS). Using our ecNGS/CANVAS approach, we quantified hotspot mutations with mutant fractions (MFs) $\geq 1 \times 10^{-5}$ in 13 CH-associated genes in genomic DNAs extracted from peripheral blood mononuclear cells (PBMCs) of healthy donors aged 18-81 y.o. (*n*=36).
Results: PBMCs showed 31/36 samples had at least 1 mutant loci with MF $\geq 1 \times 10^{-4}$, with 2 times more mutant loci in older donors (age ≥ 68 y.o.; *n*=12) than younger donors (age ≤ 30 y.o.; *n*=12), correlating positively with age. Greater MFs and number of mutant loci were most evident in *DNMT3A* and *TP53* genes. There were significantly greater MFs in CpG dinucleotide sites, which increased with age and mutation spectra between the young, midage, and older donor DNAs were similar. Notably, the observed mutations correlate positively with pathogenicity prediction scores, suggesting the mutations which are more deleterious have greater propensity to clonally expand.
Conclusions: Collectively, these data show that our ecNGS/CANVAS approach correctly measures DNA mutation, provides a highly sensitive and quantitative measure of induction of new mutation and/or clonal expansion of preexisting mutant cells in human DNA, and that there is an age effect on the tested CH markers.

Key words: clonal hematopoiesis, error-corrected sequencing, mutation, bioinformatics

Poster Number: 58

Impacts of in Utero Antiretrovirals on Offspring Intestinal Microbiome and Metabolites

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Background: Antiretroviral therapies (ART) have helped in the management of the acquired immune deficiency syndrome (AIDS), however their long-term impact on the developing embryo/fetus is unknown. The maternal microbiome is known to influence fetal development. Therefore, objective of this study is to assess whether indirect gestational and lactational antiretroviral exposure has any impact on the offspring gut-microbial population abundance and functions.
Methods: Pregnant Sprague Dawley rats (n=5/group) were exposed via gavage to two different doses of the tricombo-ART (abacavir/dolutegravir/lamivudine) during gestation and lactation (offspring were indirectly exposed via dam during the perinatal period only). The offspring were aged to 12 months and the gut microbiota and short-chain fatty acids (SCFA) in the fecal samples were assessed. Microbiome taxonomic compositions were profiled via shotgun-sequencing and analyzed by relative abundances across groups. The SCFAs were quantified using HPLC analysis.
Results: Dose-related alterations of gut-microbial community structure was seen as shifting proportions of predominant bacterial classifications. Individual SCFA responses diverged widely, in a manner dependent on both dose level and gender. Certain SCFAs (lactic acid) increased to very high concentrations under high exposure conditions compared to basal levels, whereas other SCFAs showed linked trajectories. Gender comparisons further identified complex distinctions, with males and females exhibiting distinct overall SCFA profiles depending on the dose of ART offspring were exposed to during the perinatal period.
Conclusions: Antiviral exposure induced dose and gender-dependent changes in the gut microbiome taxonomy and SCFA production in 12-month-old offspring that were exposed indirectly during gestational and lactational periods. Alterations included subtype specific SCFA stimulation, suppression, and very high elevations. Additional integrated analysis incorporating future correlation testing between compositional and functional datasets is warranted to clarify mechanisms linking microbial changes to physiological health impacts. Determining these connections can guide interventions supporting gut health in the context of early life HIV therapies.

Keywords: Microbiome, Short chain fatty acids, Metabolites, Sequencing, Perinatal exposure.

Poster Number: 59

Probiotics and Immunostimulants Enhance Gut Microbiome and Immune Gene Expression in *Litopenaeus vannamei.*

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Background: The global expansion of shrimp farming, producing approximately five million metric tons annually, is driven by increasing demand for this sought-after seafood. However, suboptimal culture conditions render shrimp vulnerable to diseases. Hence, enhancing immunity and preventing infections in shrimp are crucial. Recent focus in aquaculture has been on leveraging probiotics and immunostimulants to fortify shrimp immune responses. Immunostimulants aid host resistance to infections by modulating the immune system, while probiotics sustain a healthy gut microbiome, thereby improving overall health.
Methods: This study aimed to evaluate the impact of varying doses of probiotics and immunostimulants on immune-related gene expression and gut health in *Litopenaeus vannamei* (white leg shrimp) post-larvae (PL). Over 38 days, PLs were subjected to one of three dietary regimes: a particle diet (control), probiotics, or immunostimulants. We evaluated the gut microbiome composition and assessed the expression of target genes responsible for the host's immune response.
Results: PLs receiving both probiotic and immunostimulant supplementation displayed increased absolute bacterial abundance, relative abundance, and heightened alpha diversity in their gut microbiome. Moreover, the expression of immune-related genes such as Anti-lipopolysaccharide factor (ALF), Glucose Transporter (GLUT 1), and penaeid genes was upregulated in PLs administered higher doses of immunostimulants.
Conclusion: This research provides compelling evidence that the utilization of probiotics and immunostimulants can bolster shrimp immune health by stimulating the expression of immune-related genes and improving gut health.

Key Words: Immunostimulants, Probiotics, *Litopenaeus vannamei*

Poster Number: 60

Transcriptomic Analysis of Aortic Valve Calcification: A Focus on the Renin-Angiotensin System

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Background: The Renin-angiotensin system (RAS) is a fundamental component in cardiovascular physiology, and understanding the classical and counter-regulatory axes of this system has provided robust therapeutic approaches. RAS has been implicated in the development of fibrosis in early aortic valve pathology, but despite this knowledge, there remains a significant gap in research on the counter-regulatory axis of the RAS in aortic valve physiology.

Methods: Bulk Total RNA sequencing reads of 10 noncalcified and 9 calcified tricuspid aortic valve tissue samples from BioProject PRJNA239776 were downloaded from the Sequence Read Archive. Single-cell RNA Sequencing data, consisting of 2 healthy and 4 stenotic valves tissue was retrieved from BioProject PRJNA562645. The Salmon tool (version 1.10) was employed for pseudomapping and counting. DESeq2 was used for differential expression analysis. Clustering was performed using Cluster 3.0, and KEGG Pathways were visualized using PathView. Cell type annotation of single-cell RNA sequencing data will be processed with scGPT, a generative pre-trained transformer for single-cell data.

Results: In our clustering analysis, we observed clear indications of severe inflammation, immune response, and tissue deterioration, which align with expectations for the calcified tissues. For the KEGG pathway analysis, we obtained enrichment for renin secretion, an upstream pathway in RAS. Looking specifically at our genes of interest, we observed significant down-regulation of MAS1 in calcified valves. MAS1 serves as the main receptor in the counter-regulatory RAS.

Conclusions: Our findings suggest the presence of an underlying process that downregulates the expression of counter-regulatory RAS receptors in calcified valves, a result contrary to our initial expectations. Further processing of single-cell data, with the aim of isolating valve endothelial and interstitial cells, the two main cell types within valve tissues, may clarify the process.

Keywords: RAS: Renin-Angiotensin System, KEGG: Kyoto Encyclopedia of Genes and Genomes, MAS1: MAS1 proto-oncogene

Poster Number: 61

The Effects of *Bacillus* Strains Supplementation on Nursery Piglet Gut Microbiome with Multi-Omics

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Background: Weaning is an important phase since the abrupt changes in the diet and environment of piglets lead to reduced feed intake and post-weaning diarrhea. In addition, dysbiosis of the microbiota contributes to the development of diarrhea in weaned piglets. Antibiotic growth promoters have been widely utilized to improve the performance of weaning piglets. However, finding effective antibiotic substitutes is an urgent problem in the livestock industry.

Methods: We aim to evaluate the beneficial effect of *Bacillus* strains with different administration volume and their potential to be an antibiotics alternative. A total of 192 weaning pigs were assigned to one of four treatments including Control (basal diet); *Bacillus* (control diet plus *Bacillus* with 0.0014% of *B. subtilis* and 0.0014% of *B. licheniformis*); Half *Bacillus* (0.0007% of *B. subtilis* and 0.0007% of *B. licheniformis*); Antibiotics (control diet plus antibiotics). Rectal swab samples (n = 8/treatment) were collected from a median body weight pig in each pen at days 0 (weaning), 7, 14, and 40 to do 16S amplicon sequencing. Feces samples (n = 6/treatment) were collected on days 14 and 40 for metagenomic and metabolomic analyses.

Results: Pigs fed with *Bacillus* did not improve their body weight, but the Half *Bacillus* group showed higher feed efficiency during day 7 to 14. The microbial profile changed especially on day 7 and 14 with several potential beneficial ASVs belonging to *Christensenellaceae_R_7_group*, *Olsenella*, and Oscillospiraceae family increased in *Bacillus* treated groups. Moreover, metagenomic data confirmed the beneficial bacteria change and showed vitamin related pathway and coenzyme A biosynthesis pathway upregulated. These findings aligned with the metabolites profile showing increased vitamin and cofactors, and long-chain fatty acids.

Conclusions: This study provided evidence that *Bacillus* supplementation served as an effective alternative to antibiotics in weaned piglets. Multi-omics analysis revealed shifts in gut microbiome composition and metabolic processes.

Key words: *Bacillus*, weaning pigs, multi-omics, gut microbiome