

# MCBIOS 2025

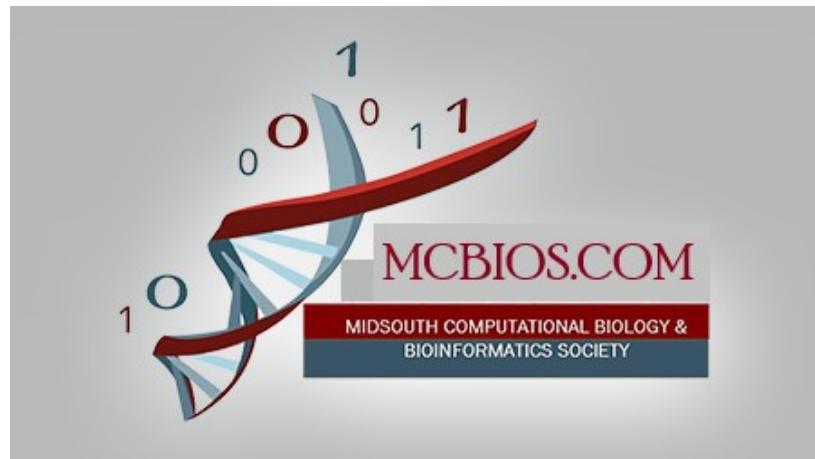
## PROGRAM BOOK



**Data-Driven Discovery:**  
*Harnessing the power of AI to transform health*

The 21st Annual Meeting of the MidSouth Computational Biology and Bioinformatics Society (MCBIOS)

University of Utah  
March 27-29, 2025



# MCBIOS 2025 Organizing Committees

## Conference Chairs

**Aik Choon Tan, Ph.D.**  
**Jincheng Shen, Ph.D.**

*Huntsman Cancer Institute, University of Utah  
University of Utah*

## Local Organizing Chair

**January Day, MSIS**

*Huntsman Cancer Institute, University of Utah*

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**Rakesh Kaundal, Ph.D.** *Utah State University*  
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**Samuel Payne, Ph.D.** *Brigham Young University*  
**Sha Cao, Ph.D.** *Oregon Health and Science University*  
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**Zaki Wilmot, Ph.D.** *University of Utah*  
**Zhaohui Qin, Ph.D.** *Emory University*  
**Zongliang Yue, Ph.D.** *Auburn University*

## Local Organizing Committees (Volunteers)

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**Amelia Nelson** *University of Utah*  
**Ching-Nung Lin, Ph.D.** *Huntsman Cancer Institute, University of Utah*  
**David Stone** *Huntsman Cancer Institute, University of Utah*  
**Emily Tan** *Skyline High School*  
**Griffin Caryotakis** *Huntsman Cancer Institute, University of Utah*

|                                     |  |
|-------------------------------------|--|
| <b>Li Li, Ph.D.</b>                 | <i>Huntsman Cancer Institute, University of Utah</i> |
| <b>Luke Boland</b>                  | <i>Huntsman Cancer Institute, University of Utah</i> |
| <b>Jacob Tye</b>                    | <i>University of Utah</i>                            |
| <b>Jake Reed, Ph.D.</b>             | <i>Huntsman Cancer Institute, University of Utah</i> |
| <b>Jax Lubkowitz</b>                | <i>University of Utah</i>                            |
| <b>Min Hu</b>                       | <i>Huntsman Cancer Institute, University of Utah</i> |
| <b>Olivia Cheng, Ph.D.</b>          | <i>Huntsman Cancer Institute, University of Utah</i> |
| <b>Samuel Coleman</b>               | <i>University of Utah</i>                            |
| <b>Veronika Romero, Ph.D., M.D.</b> | <i>University of Utah</i>                            |
| <b>Zaki Wilmot, Ph.D.</b>           | <i>Huntsman Cancer Institute, University of Utah</i> |

**Web Designer**

**Samuel Adetunji**

## Acknowledgements to MCBIOS 2025 Sponsors



Division of Biostatistics  
Department of Population Health Sciences



## MCBIOS 2025 Program At A Glance

| DAY 1 March 27, 2025 (Thursday) |  |                                |            |                 |  |
|---------------------------------|--|--------------------------------|------------|-----------------|--|
| 11:00 am - 1:00 pm              | REGISTRATION (Ballroom Lobby)                |                                |            |                 |  |
|                                 | Ballroom A                                   | Ballroom B                     | Ballroom C | Henrickson Room |  |
| 1:00 - 1:15 pm                  | Welcome Remarks                              |                                |            | POSTER VIEWING  |  |
| 1:15 - 2:15 pm                  | KEYNOTE 1<br>Jill Barnholtz - Sloan          |                                |            |                 |  |
| 2:15 - 2:30 pm                  | Break  |                                |            |                 |  |
| 2:30 - 3:30 pm                  | TUTORIAL 1<br><br>Rebecca Barter             |                                |            |                 |  |
| 3:30 - 3:45 pm                  | Break  |                                |            |                 |  |
| 3:45 - 4:30 pm                  | YSEA<br>(Grad Student)                       | YSEA<br>(Post-doc / Undergrad) |            |                 |  |
| 5:00 - 7:00 pm                  | RECEPTION & POSTER SESSION                   |                                |            |                 |  |
| 7:00 PM                         | MCBIOS Business Session (By Invitation Only) |                                |            |                 |  |

| DAY 2 March 28, 2025 (Friday) |   |  |  |   |
|-------------------------------|---|--|--|---|
| 7:30 - 8:30 am                | BREAKFAST   |  |  |   |
|                               | Ballroom A  | Ballroom B   | Ballroom C   | Henrickson Room   |
| 8:30 - 9:30 am                | KEYNOTE 2<br>Jessica Li   |  |  |   |
| 9:30 - 9:45 am                | Break   |  |  |   |
| 9:45 - 11:00 am               | <b>SESSION 101</b><br>Chair<br>Hao Chen<br>Wei Chen<br><br>AI methods and applications in single cell spatial omics               | <b>SESSION 102</b><br>Chair<br>Inimary Toby<br>Ogundehi<br><br>AI in Computational Sciences: Shaping the Future of Research, Education, and Biomolecular Discovery | <b>SESSION 103</b><br>Chair<br>Xi Qiao<br><br>Innovative Approaches to Orchestrating the Microbial Symphony    | <b>TUTORIAL 2</b><br>Devin Lange  |
| 11:00 - 11:15 am              | Break   |  |  |   |
| 11:15 - 12:30 pm              | <b>SESSION 201</b><br>Chair<br>Sha Cao<br><br>Innovative integrations of omics and computational approaches in biological systems | <b>SESSION 202</b><br>Chair<br>Yan Sun<br><br>Recent Advances in Biostatistical Research   | <b>SESSION 203</b><br>Chair<br>Tim Shaw<br>Riyue Bao<br><br>Leveraging AI to reconcile barriers in IO Research | <b>SESSION 204</b><br>Chair<br>Rakesh Kaundal<br><br>Harnessing Integrative Multi-Omics and AI to Decipher Host-Pathogen Interactions |
| 12:30 - 1:30 pm               | LUNCH   |  |  |   |
| 1:30 - 2:45 pm                | <b>SESSION 301</b><br>Chair<br>Zongliang Yue<br><br>From Omics to Network Pharmacology and Systems Medicine (Zoom)                | <b>SESSION 302</b><br>Chair<br>Yuehua Cui<br><br>Advancing Statistical and Machine Learning Models for Single-Cell and Spatial Omics                               | <b>SESSION 303</b><br>Chair<br>AC Tan<br><br>Oncological Data Science  | <b>SESSION 304</b><br>Chair<br>Zaki Wilmot<br><br>Lighting Talk 1   |

|                       |  |  |   |   |
|-----------------------|--|--|---|---|
| <b>2:45 - 3:00 pm</b> | <b>Break</b>   |  |   |   |
| <b>3:00 - 4:15 pm</b> | <b>SESSION 401</b><br>Chair<br>Jun Ding<br>Xiaowei Zhan<br><br>AI meets genetics<br>and genomics | <b>SESSION 402</b><br>Chairs<br>AC Tan<br>Samuel Payne<br><br>Frontiers in<br>Computational<br>Biology and<br>Bioinformatics | <b>SESSION 403</b><br>Chair<br>Jincheng Shi<br><br>Innovative Data-<br>Driven Strategies<br>for Precision<br>Cancer Treatment | <b>SESSION 404</b><br>Chair<br>Bernie Daigle<br><br>Lighting Talk 2 |
| <b>4:15 - 4:30 pm</b> | <b>Break</b>   |  |   |   |
| <b>4:30 - 5:30 pm</b> | <b>KEYNOTE 3</b><br>Xihong Lin   |  |   |   |
| <b>5:30 - 7:00 pm</b> | <b>BANQUET</b>   |  |   |   |

| <b>DAY 3 March 29, 2025 (Saturday)</b> |  |   |  |   |
|--|--|---|--|---|
| <b>7:30 - 8:30 am</b>                  | <b>BREAKFAST</b>   |   |  |   |
| <b>7:30 - 8:30 am</b>                  | <b>MCBIOS Board Meeting (By Invitation Only) Patel Room</b>  |   |  |   |
|  | <b>Ballroom A</b>  | <b>Ballroom B</b>   | <b>Ballroom C</b>  | <b>Henrickson Room</b>  |
| <b>8:30 - 9:30 am</b>                  | <b>KEYNOTE 4</b><br>Berton Earnshaw  |   |  |   |
| <b>9:30 - 9:45 am</b>                  | <b>Break</b>   |   |  |   |
| <b>9:45 - 11:00 am</b>                 | <b>SESSION 501</b><br>Chair<br>Zhaohui "Steve" Qin<br>Chang Su<br><br>Advances in<br>statistical methods<br>applied to genomics<br>and biomedicine | <b>SESSION 502</b><br>Chair<br>Xuefeng Wang<br><br>Emerging<br>methods in<br>single-cell<br>analysis and AI-<br>driven biomarker<br>discovery | <b>SESSION 503</b><br>Chair<br>Chi Wang<br><br>Recent advances<br>in statistical and<br>computational<br>methods for<br>omics data | <b>SESSION 504</b><br>Chairs<br>Mary Davis<br>Samuel Payne<br><br>Lighting Talk 3 |
| <b>11:00 - 11:15 am</b>                | <b>Break</b>   |   |  |   |
| <b>11:15 - 12:30 pm</b>                | <b>SESSION 601</b><br>Chairs<br>Paul Stewart<br>Ann Chen<br><br>Computational Mass<br>Spec   | <b>SESSION 602</b><br>Chair<br>Qi Zheng<br><br>Statistical<br>analysis for<br>integrated<br>biomedical data                                   | <b>SESSION 603</b><br>Chair<br>Jincheng Shen<br><br>Lighting Talk 4  | <b>SESSION 604</b><br>Chair<br>Robert Doerksen<br><br>Lighting Talk 5             |
| <b>12:30 - 1:00 pm</b>                 | <b>AWARDS and CLOSING CEREMONY</b>   |   |  |   |

# MCBIOS 2025 Program

DAY 1 : Thursday 3/27/25

|  |   |
|--|---|
| <b>Room: Ballroom A &amp; Ballroom B</b>   |   |
| <b>Welcome Remarks</b>   |   |
| Aik Choon Tan, Ph.D.<br>Jincheng Shen, Ph.D.<br><b>MCBIOS 2025 Co-Chairs</b>   |   |
| 1:00 – 1:15pm  |   |
| <b>KEYNOTE 1: Jill S. Barnholtz-Sloan, Ph.D.</b><br>Acting Director - Center for Biomedical Informatics & Information Technology<br><b>Title: Utilizing Data and Technology for Advancing Cancer Discoveries</b> |   |
| 1:15 – 2:15pm  |  |
| 2:15 – 2:30pm  | <b>BREAK</b>  |
| <b>TUTORIAL 1: Rebecca Barter, Ph.D.</b>   |   |
| <b>Topic: Using AI to Code</b>   |   |
| 2:30 – 3:30pm  |  |
| 3:30 – 3:45pm  | <b>BREAK</b>  |
| <b>YSEA – Graduate Student Session</b>   |   |
| <b>Session Chair: Su Chang</b>   |   |
| <b>Room: Ballroom A</b>  |   |
| 3:45 - 4:30pm  | YSEA – Graduate Student   |
| <b>YSEA – Post-Doctoral Research Fellows and Undergraduate Student Session</b>   |   |
| <b>Session Chair: Vinay Raj</b>  |   |
| <b>Room: Ballroom B</b>  |   |
| 3:45 - 4:30pm  | YSEA – Post-Doc Research Fellows<br><br>YSEA – Undergraduate Students               |
| <b>Room: Ballroom C</b>  |   |
| 1:00 - 4:30pm  | Poster Viewing  |
| <b>Poster Session and Reception</b>  |   |
| <b>Room: Ballroom A, B, C</b>  |   |
| 5:00 – 7:00pm  | Poster Sessions   |

## DAY 2 : Friday 3/28/25

|   |  |
|---|--|
| 7:30 – 8:30am<br><b>Ballroom Lobby</b>  | <b>BREAKFAST</b>   |
| <b>Room: Ballroom A, B, C</b>   |  |
| <b>KEYNOTE 2: Jingyi Jessica Li, Ph.D.</b><br><b>Professor, University of California, Los Angeles (UCLA)</b><br><b>Title: Semi-synthetic Negative &amp; Positive Control Enhancing the Reliability and Power in Omics Data Analysis</b> |   |
| 8:30 – 9:30am<br><b>Ballroom Lobby</b>  | <b>BREAK</b>   |
| <b>Session 101: AI methods and applications in single cell spatial omics</b><br><b>Session Chair: Hao Chen/Wei Chen</b>   |  |
| <b>Room: Ballroom A</b>   |  |
| 9:45 - 11:00am  | <ol style="list-style-type: none"> <li>1. Decoding spatial transcriptomics at any resolution<br/><b>Wei Chen</b>, University of Pittsburgh</li> <li>2. Generative Modeling of Single-Cell Multiomics Data with Latent Diffusion Models<br/><b>Qiao Liu</b>, Yale University</li> <li>3. Graph signal processing is a bridge connecting spatial omics technologies and applications<br/><b>Yuzhou Chang</b>, The Ohio State University</li> <li>4. Advancing spatial transcriptomics analysis to single-cell resolution with scResolve<br/><b>Hao Chen</b>, Department of Computer Science, University of Illinois Chicago</li> </ol> |
| <b>Session 102: AI in Computational Sciences: Shaping the Future of Research, Education, and Biomolecular Discovery</b><br><b>Session Chair: Inimary Toby Ogundesi</b>  |  |
| <b>Room: Ballroom B</b>   |  |
| 9:45 - 11:00am  | Panelist #1, Ricardo Avila-Sanchez, Biology student, University of Dallas, Biology Department<br>Panelist #2, Vinay Raj, PhD, University of Arkansas, Pine Bluff, Department of Biology<br>Panelist #3, Nisha Pillai, PhD, Mississippi State University, Computer Science and Engineering  |
| <b>Session 103: Innovative Approaches to Orchestrating the Microbial Symphony</b><br><b>Session Chair: Xi Qiao</b>  |  |
| <b>Room: Ballroom C</b>   |  |
| 9:45 - 11:00am  | <ol style="list-style-type: none"> <li>1. The Intratumor Microbiome as a Biomarker for Gemcitabine Response in Pancreatic Cancer<br/><b>Youngchul Kim</b>, Moffitt Cancer Center</li> <li>2. Open-source microbiome and multi-omic data science with scikit-bio<br/><b>Qiyun Zhu</b>, Arizona State University</li> <li>3. Enhancing Microbiome Analysis with Semisynthetic Data<br/><b>Kris Sankaran</b>, University of Wisconsin-Madison</li> </ol>  |

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|   | <p>4. The tumor microbiome affects the microenvironment as a function of the microbe and cancer type<br/> <b>Daniel J Spakowicz</b>, The Ohio State University</p> <p>5. Cross-Platform Concordance in Microbiome Analysis: 16S rRNA vs. Metagenomic Shotgun Sequencing<br/> <b>Xi Qiao</b>, Huntsman Cancer Institute</p>   |
| <b>TUTORIAL 2: Devin Lange, Ph.D.</b>   |  |
| <b>Topic: Visualization of Complex Data</b>   |   |
| 9:45 - 11:00am  |  |
| <b>Room: Henrickson Room</b>  |  |
| 11:00 – 11:15am<br><b>Ballroom Lobby</b>  | <b>BREAK</b>   |
| <b>Session 201: Innovative integrations of omics and computational approaches in biological systems</b> |  |
| <b>Session Chair: Sha Cao</b>   |  |
| <b>Room: Ballroom A</b>   |  |
| 11:15 - 12:30pm   | <p>1. Context-specific spatial genomics reveals insights into the functional impacts of genetic variants<br/> <b>Jianrong Wang</b>, Michigan State University</p> <p>2. Error-controlled hypothesis generation in generic machine learning models<br/> <b>Yang Lu</b>, University of Waterloo</p> <p>3. Quantitative 3D reconstruction and multi-omic mapping of human pancreas tissue reveals shocking heterogeneity in precancer development<br/> <b>Ashley Lynn Kiemen</b>, Johns Hopkins</p> <p>4. Metabolomic Profiles for Biomarker Discovery<br/> <b>Oana A. Zelezniak</b>, Harvard University</p> <p>5. Accurate Imputation of Pathway-Specific Gene Expression in Spatial Transcriptomics with PASTA<br/> <b>Ziyi Li</b>, MD Anderson Cancer Center</p> |
| <b>Session 202: Recent Advances in Biostatistical Research</b>  |  |
| <b>Session Chair: Yan Sun</b>   |  |
| <b>Room: Ballroom B</b>   |  |
| 11:15 - 12:30pm   | <p>1. Rare but Important: Statistical Advances in Meta-Analysis of Low-Frequency Events in Clinical and Public Health Research<br/> <b>Brinley Zabriskie</b>, Utah State University</p> <p>2. Deep Learning Treatment Recommendations for Patients Diagnosed with Non-Metastatic Castration-Resistant Prostate Cancer Treated with Androgen Deprivation Treatment<br/> <b>Chunyang Li</b>, University of Utah</p> <p>3. Mediation Analysis of Multiple Mediators with Incomplete Omics Data<br/> <b>John Kidd</b>, Utah Valley University</p>  |

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|  | <p>4. Informative Missingness: A Strategy for Proper Handling of Data Missingness in Longitudinal Models of Repeated Measures<br/> <b>Tom Jensen</b>, Utah State University</p> <p>5. Deep MAGIC: Enhancing Data Imputation through Manifold Learning and Autoencoders<br/> <b>Devin Eddington</b>, Utah State University</p>  |
| <b>Session 203: Leveraging AI to reconcile barriers in IO Research</b>                               |  |
| <b>Session Chair: Tim Shaw/Riyue Bao</b>   |  |
| <b>Room: Ballroom C</b>  |  |
| 11:15 - 12:30pm  | <p>1. Digital Twin: Harmonizing patient data<br/> <b>Aik-Choon Tan</b>, Huntsman Cancer Institute, University of Utah</p> <p>2. Integrating OMICS technologies<br/> <b>Linghua Wang</b>, MD Anderson Cancer Center</p> <p>3. Harmonizing patient and cancer models<br/> <b>Xuefeng Wang</b>, H Lee Moffitt Cancer Center</p>   |
| <b>Session 204: Harnessing Integrative Multi-Omics and AI to Decipher Host-Pathogen Interactions</b> |  |
| <b>Session Chair: Rakesh Kaundal</b>   |  |
| <b>Room: Henrickson Room</b>   |  |
| 11:15 - 12:30pm  | <p>1. Profiling Host-Microbe Interactions in Pulmonary Diseases<br/> <b>W. Evan Johnson</b>, Rutgers University</p> <p>2. APInet: A Multi-Method Database for Predicting and Visualizing Animal-Pathogen Protein Interactions<br/> <b>David Guevara</b>, Utah State University</p> <p>3. Leveraging AI to Advance Image and Cell-Based Drug Discovery<br/> <b>Qianqian Song</b>, University of Florida</p> <p>4. HPIpy: A Multi-Model Python-based Toolbox for Predicting Host-Pathogen Protein-Protein Interactions using Diverse Computational Models<br/> <b>Raghav Kataria</b>, Utah State University</p> <p>5. Exploring potential treatment for Multiple Myeloma: a large-scale docking and simulation study to identify natural compounds, and developing a database, myDockDB.<br/> <b>Rousselene B. Larson</b>, Utah State University</p> |
| 12:30 – 1:30 pm<br><b>Ballroom Lobby</b>   | <b>Lunch</b>   |
| <b>Session 301: From Omics to Network Pharmacology and Systems Medicine</b>                          |  |
| <b>Session Chair: Zongliang Yue</b>  |  |
| <b>Room: Ballroom A</b>  |  |
| 1:30 - 2:45pm  | <p>1. Decoding Cancer: Mapping Protein-Protein Interaction Networks to Identify Drug Targets<br/> <b>Ece (Gamsiz) Uzun</b>, Brown University</p> <p>2. Single-cell Network Biology and Medicine<br/> <b>Daifeng Wang</b>, University of Wisconsin-Madison</p> <p>3. TodenE 2.0: An upgrade of TodenE for Super-PAG Mining in Functional Genomics using Unsupervised Few-shot Learning<br/> <b>Qi Li</b>, Fisk University</p>   |

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|   | <p>4. Inter- and intra-tumoral heterogeneity of TNBC determined by spatial gene transcriptomics<br/> <b>Fengyuan Huang</b>, Tuskegee University</p>   |
| <b>Session 302: Advancing Statistical and Machine Learning Models for Single-Cell and Spatial Omics</b> |   |
| <b>Session Chair: Jianrong Wang</b>   |   |
| <b>Room: Ballroom B</b>   |   |
| 1:30 - 2:45pm   | <ol style="list-style-type: none"> <li>1. Improving single-cell data analysis with statistical inference and machine learning<br/> <b>Hui Jiang</b>, University of Michigan</li> <li>2. Advancing systems biology approaches to study metabolic variations in diseases<br/> <b>Chi Zhang</b>, Oregon Health &amp; Science University</li> <li>3. A spatially informed model for gene co-expression network analysis<br/> <b>Ying Ma</b>, Brown University</li> <li>4. Empower functional annotation of noncoding variants using single-cell epigenomic data<br/> <b>Hongbo Liu</b>, University of Rochester Medical Center</li> <li>5. A unified model for cell-type-specific spatially variable gene detection in spatial transcriptomics<br/> <b>Yuehua Cui</b>, Michigan State University</li> </ol> |
| <b>Session 303: Oncological Data Science</b>  |   |
| <b>Session Chair: AC Tan</b>  |   |
| <b>Room: Ballroom C</b>   |   |
| 1:30 - 2:45pm   | <ol style="list-style-type: none"> <li>1. A robust statistical approach for finding informative spatially associated pathways, with application in cancer<br/> <b>Tianwei Yu</b>, The Chinese University of Hong Kong – Shenzhen</li> <li>2. Harnessing cellular imaging modalities in spatial transcriptomic profiling of tumor tissues<br/> <b>Xiaofei Song</b>, Moffitt Cancer Center</li> <li>3. Analytical methods and tools to understand the spatial architecture of the tumor microenvironment<br/> <b>Brooke Fridley</b>, Children's Mercy Research Institute</li> <li>4. Learning the balancing act of immunotherapy and immune-related adverse events from real-world data<br/> <b>Aik Choon Tan</b>, Huntsman Cancer Institute, University of Utah</li> </ol>                               |
| <b>Session 304: Lighting Talk 1</b>   |   |
| <b>Session Chair: Zaki Wilmot</b>   |   |
| <b>Room: Henrickson Room</b>  |   |
| 1:30 - 2:45pm   | <ol style="list-style-type: none"> <li>1. Human protein atlas: a resource for target expression across 19 human tissues<br/> <b>Lida Vadakumchery</b>, Biognosys</li> <li>2. gwSPADE: reference-free deconvolution in spatial transcriptomics with gene weighting<br/> <b>Aoqi Xie</b>, Michigan State University</li> </ol>  |

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|  | <ul style="list-style-type: none"> <li>3. A Multi-Omics Computational Approach to Predict Novel Drug Combinations for Glioblastoma<br/><b>Yuxin Zhao</b>, Huntsman Cancer Institute, University of Utah</li> <li>4. AI-Driven Combination Drug Discovery: Addressing the Heterogeneity of Amyotrophic Lateral Sclerosis<br/><b>Victoria Xu</b>, Dougherty Valley High School</li> <li>5. Integrating Chemical Language Model and Machine Learning for Dual mTOR/PI3K-α Inhibition in Breast Cancer<br/><b>Fuad Al Abir</b>, University of Alabama at Birmingham</li> <li>6. Novel Mitochondrial Haplogroups Associated with Alzheimer's Disease<br/><b>Brianna B. Greenwood</b>, Brigham Young University</li> <li>7. Longitudinal PTSD Biomarker Discovery from Multi-omic Biotypes<br/><b>Mazen Istambouli</b>, University of Memphis</li> <li>8. A Platform for Developing AI-Powered Smartphone Medical Applications<br/><b>Deepa Reghu</b>, Mississippi Valley State University</li> </ul> |
| 2:45 – 3:00 pm<br><b>Ballroom Lobby</b>  | <b>BREAK</b>  |
| <b>Session 401: AI meets genetics and genomics</b>   |   |
| <b>Session Chair: Jun Ding/Xiaowei Zhan</b>  |   |
| <b>Room: Ballroom A</b>  |   |
| 3:00 - 4:15pm  | <ul style="list-style-type: none"> <li>1. Machine learning applied to DNA methylation data<br/><b>Zhaohui Steve Qin</b>, Emory University</li> <li>2. Innovating the fight against antibiotic resistance with machine learning<br/><b>Xiaowei Zhan</b>, University of Texas Southwestern Medical Center</li> <li>3. Scaling up spatial transcriptomics for large-sized tissues<br/><b>Amelia Schroeder</b>, University of Pennsylvania</li> <li>4. Harnessing tumor microenvironment depicted by histological images to improve cancer prognosis through a deep learning system<br/><b>Zhangsheng Yu</b>, Shanghai Jiao Tong University</li> </ul>  |
| <b>Session 402: Frontiers in Computational Biology and Bioinformatics (BYU Capstone I)</b> |   |
| <b>Session Chair: AC Tan / Samuel Payne</b>  |   |
| <b>Room: Ballroom B</b>  |   |
| 3:00 - 4:15pm  | <ul style="list-style-type: none"> <li>1. Uncovering Patterns in Cancer Treatment Timelines<br/><b>MaKenna Hardy</b>, Brigham Young University<br/><b>Megan Knight, Luke Squires, Abby Chen</b></li> <li>2. PTM Disrupting Mutational Hotspots &amp; Potential Cancer Drug discovery<br/><b>Hailey Johnson</b>, Brigham Young University<br/><b>Tessa Bass, Darian Ferry, Eric Upton-Rowley</b></li> </ul>  |

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|  | <p>3. Identifying distance as a disparity through GIS mapping of care for rural patients<br/> <b>Gage Bowman</b>, Brigham Young University<br/> <b>Maddie Brammer, Clark Roylance, Kirsten Kerksiek</b></p> <p>4. Identifying diet and persistent organic pollution patterns that drive metabolic disease<br/> <b>Rebecca Kreutz</b>, Brigham Young University<br/> <b>Amulek Brenes Sandoval, Merek Helmer, Griffin Cropper</b></p> <p>5. An informatic tool to align post-translational modification sites between species<br/> <b>Zachary Everton</b>, Brigham Young University<br/> <b>Camille Krieger, Brandon Lewis</b></p>   |
| <b>Session 403: Innovative Data-Driven Strategies for Precision Cancer Treatment</b> |   |
| <b>Session Chair: Jincheng Shen</b>  |   |
| <b>Room: Ballroom C</b>  |   |
| 3:00 - 4:15pm  | <p>1. Scalable AI Solutions for Adaptive Cancer Care<br/> <b>Chris Gregg</b>, University of Utah</p> <p>2. Multi-Gene Risk-Score for Prediction of Clinical Outcomes in Treatment-Naïve Metastatic Castrate Resistant Prostate Cancer<br/> <b>Zaki Wilmot</b>, Huntsman Cancer Institute, University of Utah</p> <p>3. Harnessing Tumor Microenvironment Dynamics to Predict Rational Therapy Combinations using single cell RNA-seq data<br/> <b>Chloe Tran</b>, Huntsman Cancer Institute, University of Utah</p> <p>4. Reinforcement Learning for Adaptive Treatment Strategies in Advanced Non-Small Cell Lung Cancer Using EHR Data<br/> <b>Jincheng Shen</b>, University of Utah</p>  |
| <b>Session 404: Lighting Talk 2</b>  |   |
| <b>Session Chair: Bernie Daigle</b>  |   |
| <b>Room: Henrickson Room</b>   |   |
| 3:00 - 4:15pm  | <p>1. Unsupervised Clustering of Protein Language Model Embeddings for Homology Detection<br/> <b>Priscilla Udomprasert</b>, Auburn University at Montgomery</p> <p>2. An Integrated Mouse Spinal Cord Atlas Revealing Microglia Heterogeneity in Health and Injury Conditions<br/> <b>Qi Guo</b>, The Ohio State University Wexner Medical Center</p> <p>3. Repulsive scaling replica exchange molecular dynamics: Sea cucumber fucosylated glycosaminoglycan inhibition of heparan-6-O-endosulfatase 2<br/> <b>Robert J. Doerksen</b>, University of Mississippi</p> <p>4. Longitudinal Multi-Omics PTSD Biotype Discovery: A Similarity Network Fusion Approach<br/> <b>Serena Zhao</b>, University of Memphis</p> <p>5. Transformer-Based Foundation Model for Peptide Elution Order Prediction<br/> <b>Jose Humberto Giraldez Chavez</b>, Brigham Young University</p> |

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|  | <p>6. Development of Super-PAG in Functional Genomics using PAG Network and Large Language Model<br/> <b>Zongliang Yue</b>, Auburn University</p> <p>7. Are we there yet? Assessing the readiness of single-cell proteomics to answer biological hypotheses<br/> <b>Alyssa A Nitz</b>, Brigham Young University</p> <p>8. scPerb: Predict single-cell perturbation via style transfer-based variational autoencoder<br/> <b>Zijia Tang</b>, Duke University</p> |
| 4:15 – 4:30 pm<br><b>Ballroom Lobby</b>  | <b>BREAK</b>  |
| <b>KEYNOTE 3: Xihong Lin, Ph.D.<br/>Professor, Harvard University</b>                |    |
| <b>Title: Navigate the Crossroad of Statistics, ML/AI and Genomic Health Science</b> |   |
| 4:30 – 5:30am  |   |
| 5:30 – 7:00pm<br><b>Ballroom A, B, C</b>   | <b>BANQUET</b>  |

### DAY 3 : Saturday 3/29/25

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| 7:30 – 8:30am<br><b>Ballroom Lobby</b>  | <b>BREAKFAST</b>  |
| <b>Room: Ballroom A, B, C</b>   |   |
| <b>KEYNOTE 4: Berton Earnshaw, Ph.D.<br/>AI Founding Fellow, Recursion Pharmaceuticals</b>                    |    |
| <b>Title: AI in Drug Discovery</b>  |   |
| 8:30 – 9:30am   |   |
| 9:30 – 9:45am<br><b>Ballroom Lobby</b>  | <b>BREAK</b>  |
| <b>Session 501: Cell-type-specific mapping of enhancers and target genes from single-cell multimodal data</b> |   |
| <b>Session Chair: Zhaohui "Steve" Qin / Chang Su</b>  |   |
| <b>Room: Ballroom A</b>   |   |
| 9:45 - 11:00am  | <ol style="list-style-type: none"> <li>1. Investigating Genetic Regulation of Gene Expression Using Single-Cell Data<br/> <b>Chang Su</b>, Emory University</li> <li>2. Identifying microRNA biomarkers with unequal detection sensitivity in NanoString nCounter<br/> <b>Zhijin Wu</b>, Brown University</li> <li>3. Advancing Precision ALS Treatment through Multiplex Knowledge Graphs Integrating SDOH and Multi-Omics Data<br/> <b>Huanmei Wu</b>, Temple University</li> </ol> |

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|  | <p>4. Extension and Novel Application of the Cross-Entropy Method in Biomedical Data Analysis<br/> <b>Yang Shi</b>, Wayne State University</p>  |
| <b>Session 502: Emerging methods in single-cell analysis and AI-driven biomarker discovery</b> |   |
| <b>Session Chair: Xuefeng Wang</b>   |   |
| <b>Room: Ballroom B</b>  |   |
| 9:45 - 11:00am   | <p>1. Comparative single cell analysis reveals cellular architecture of tumor bone metastasis<br/> <b>Shenglin Mei</b>, Virginia Tech</p> <p>2. HapCNV: A Comparative Framework for CNV Detection in Low-input DNA sequencing data<br/> <b>Feifei Xiao</b>, University of Florida</p> <p>3. Artificial Intelligence for Biomarker Development and Drug Discovery<br/> <b>Qianqian Song</b>, University of Florida</p> <p>4. Generalizing Transfer Learning: A Flexible Doubly Robust Estimation Approach for Missing Data<br/> <b>Tianying Wang</b>, Colorado State University</p>  |
| <b>Session 503: Recent advances in statistical and computational methods for omics data</b>    |   |
| <b>Session Chair: Chi Wang</b>   |   |
| <b>Room: Ballroom C</b>  |   |
| 9:45 - 11:00am   | <p>1. SDePER: a hybrid machine learning and regression method for cell-type deconvolution of spatial barcoding-based transcriptomic data<br/> <b>Xiting Yan</b>, Yale University</p> <p>2. Bayesian Edge Regression: Characterizing Observation-Specific Heterogeneity in Estimating Undirected Graphical Models<br/> <b>Zeya Wang</b>, University of Kentucky</p> <p>3. A Bayesian informative shrinkage approach for large-scale multiple hypothesis testing: with applications in transcriptomic differential expression analysis<br/> <b>Ya Su</b>, Virginia Commonwealth University</p> <p>4. Leveraging Large Language Models for Integrative Analysis of Cancer Omics Data<br/> <b>Jinpeng Liu</b>, University of Kentucky</p> |
| <b>Session 504: Lightning Talk 3 (BYU Capstone II)</b>   |   |
| <b>Session Chair: Mary Davis / Samuel Payne</b>  |   |
| <b>Room: Henrickson Room</b>   |   |
| 9:45 - 11:00am   | <p>1. HLA typing the All of Us dataset<br/> <b>Rebecca Caylor</b>, Brigham Young University<br/> <b>Jacqui Durney</b>, Parker Reyes</p> <p>2. Biomarker-Based Stratification of Cancer Patients for ASMase-Targeted Therapy<br/> <b>Spencer Gardner</b>, Brigham Young University<br/> <b>Spencer Boris</b>, Catherine Clive</p>  |

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|   | <p>3. Identifying functionally essential amino acids in phage proteins<br/> <b>Caz Cullimore</b>, Brigham Young University<br/> <b>Benjamin Driggs, Teancum Hoopes, Britton Stanley</b></p> <p>4. Assessing average nucleotide identities and codon usage biases of bacteriophages and their hosts<br/> <b>Blake McGee</b>, Brigham Young University<br/> <b>Jonah Checketts, James Cheshire, Alex Atkinson</b></p> <p>5. Metabolic Partitioning in Lichens<br/> <b>Rachel Hunter</b>, Brigham Young University</p>  |
| 11:00 – 11:15 am<br><b>Ballroom Lobby</b>                               | <b>BREAK</b>   |
| <b>Session 601: Computational Mass Spec</b>                             |  |
| <b>Session Chair: Paul Stewart / Ann Chen</b>                           |  |
| <b>Room: Ballroom A</b>   |  |
| 11:15 - 12:30pm   | <ol style="list-style-type: none"> <li>1. MODE: high-resolution digital dissociation with deep multimodal autoencoder<br/> <b>Qian Li</b>, St. Jude Children's Research Hospital</li> <li>2. Computational Challenges for Single Cell Proteomics<br/> <b>Samuel H. Payne</b>, Brigham Young University</li> <li>3. Deep Learning Methods for Metabolite Annotation<br/> <b>Habtom W. Ressom</b>, Lombardi Comprehensive Cancer Center</li> <li>4. Developing accessible informatics resources for mass spectrometry-centered multi-omic studies<br/> <b>Tim Griffin</b>, University of Minnesota</li> <li>5. Leveraging Metabolomic Profiles to Reduce the Burden of Ovarian Cancer<br/> <b>Oana A. Zelezniak</b>, Harvard Medical School</li> </ol> |
| <b>Session 602: Statistical analysis for integrated biomedical data</b> |  |
| <b>Session Chair: Qi Zheng</b>  |  |
| <b>Room: Ballroom B</b>   |  |
| 11:15 - 12:30pm   | <ol style="list-style-type: none"> <li>1. Integrating spatial transcriptomics and snRNA-seq data enhances differential gene expression studies of AD<br/> <b>Jingjing Yang</b>, Emory University</li> <li>2. Discriminative Feature Selection for Single-Cell RNAseq Cell Clustering<br/> <b>Chi Wang</b>, University of Kentucky</li> <li>3. Deep Neural Network for Functional Graphical Models Structure Learning<br/> <b>Shuoyang Wang</b>, University of Louisville</li> </ol>  |
| <b>Session 603: Special Presentation &amp; Lightning Talk 4</b>         |  |
| <b>Session Chair: Jincheng Shen</b>                                     |  |
| <b>Room: Ballroom C</b>   |  |

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| <p>11:15 - 12:30pm</p>                | <ol style="list-style-type: none"> <li>1. Harnessing Responsible AI for Science Discovery, Innovation, and Impact<br/><b>Manish Parashar</b>, University of Utah</li> <li>2. Generating Novel Linker Sequences in Antibody-Drug Conjugates with Diffusion Models<br/><b>April Cao</b>, Western Canada High School</li> <li>3. Genotype and phenotype risk score analyses of genetically admixed multiple sclerosis patients in All of Us<br/><b>Will Brugger</b>, Brigham Young University</li> <li>4. Convolutions Accelerate mRNA Ramp Sequence Research in ExtRamp 2.0<br/><b>Matthew Cloward</b>, Brigham Young University</li> <li>5. Improving B-Cell receptor prediction with a Single-Cell Long-Read VAE approach<br/><b>David Redd</b>, Brigham Young University</li> <li>6. Clinician-Derived Phenotypic Risk Scores (PheRS): Removing time to diagnosis for multiple sclerosis patients<br/><b>Hailey Whittier</b>, Brigham Young University</li> <li>7. Investigating increased risk of postpartum depression (PPD) in inflammatory autoimmune disease<br/><b>Alyks Odell</b>, Brigham Young University</li> </ol> |  |
| <b>Session 604: Lightning Talk 5</b>  |  |   |
| <b>Session Chair: Robert Doerkson</b> |  |   |
| <b>Room: Henrickson Room</b>          |  |   |
| <p>11:15 - 12:30pm</p>                | <ol style="list-style-type: none"> <li>1. Statistical methods for handling cellular heterogeneity in quantitative single-cell experiments: review simulations and recommendations<br/><b>Hannah Boekweg</b>, Brigham Young University</li> <li>2. CUB Hub: an Interactive Web Tool for Visualizing Codon Usage Bias Across Diverse Species<br/><b>Jac Taylor</b>, Brigham Young University</li> <li>3. SKAT Analysis Testing Reveals Novel Nuclear-Mitochondrial Genes Associated with Alzheimer's Disease<br/><b>Jared G. Gibson</b>, Brigham Young University</li> <li>4. A Bayesian Hierarchical Model for Asymmetric Spatial Interactions in the Tumor Microenvironment<br/><b>Joel N Eliason</b>, University of Michigan</li> <li>5. Improved Prediction of Dehydrated Patients using IPFM-Synthesized PVP Waveforms<br/><b>Jeremiah Wimer</b>, University of Arkansas</li> <li>6. An Introduction to Peptide Embedding for Machine Learning in Proteomics<br/><b>Luke Squires</b>, Brigham Young University</li> <li>7. GRACKLE: An interpretable matrix factorization approach for clinical subtyping</li> </ol>        |   |

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|   | <p><b>Lucas Gillenwater</b>, University of Colorado Anschutz Medical Campus</p> <p>8. Enabling Transcriptome Classification in Micro-Cohorts with MLOps<br/> <b>Madi Shabanian</b>, University of Utah</p> <p>9. Association of Antibiotic Therapy and Immune-related Adverse Events for Immune Checkpoint Inhibitors Treated Cancer Patients<br/> <b>David Stone</b>, Huntsman Cancer Institute, University of Utah</p> <p>10. Automated Weed Detection of Rumex Species using Convolutional Neural Network<br/> <b>Ricaria Gordon</b>, Mississippi Valley State University</p> |
| 12:30 – 1:00pm<br><b>Ballroom A, B, C</b> | <b>AWARDS and CLOSING CEREMONY</b>   |

## MCBIOS 2025 Posters

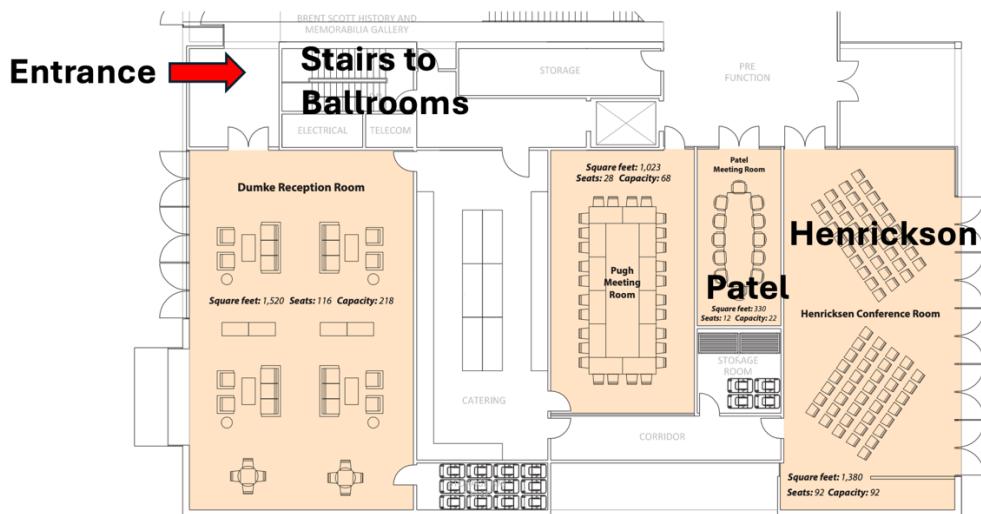
| Poster | Name                                 | Title   |
|--------|--------------------------------------|---|
| P001   | Fuad Al Abir                         | Integrating Chemical Language Model and Machine Learning for Dual mTOR/PI3K-a Inhibition in Breast Cancer                                   |
| P002   | Hannah Boekweg                       | Statistical methods for handling cellular heterogeneity in quantitative single-cell experiments: review simulations and recommendations     |
| P003   | Gage Bowman                          | Identifying distance as a disparity through GIS mapping of care for rural patients  |
| P004   | Will Brugger                         | Genotype and phenotype risk score analyses of genetically admixed multiple sclerosis patients in All of Us                                  |
| P005   | April Cao                            | Generating Novel Linker Sequences in Antibody-Drug Conjugates with Diffusion Models   |
| P006   | Rebecca Caylor                       | HLA typing the All of Us dataset  |
| P007   | James Cheshire                       | Assessing average nucleotide identities and codon usage biases of bacteriophages and their hosts  |
| P008   | Matthew Cloward                      | Convolutions Accelerate mRNA Ramp Sequence Research in ExtRamp 2.0  |
| P009   | Caz Cullimore                        | Identifying functionally essential amino acids in phage proteins  |
| P010   | Robert J. Doerkson                   | Repulsive scaling replica exchange molecular dynamics: Sea cucumber fucosylated glycosaminoglycan inhibition of heparan-6-O-endosulfatase 2 |
| P011   | Benjamin Driggs                      | Identifying metabolic proteins in phage genomes through binding pocket determination  |
| P012   | Jacqui Durney                        | A Consensus-Calling Pipeline for Accurate HLA Genotyping and Disease Risk Identification  |
| P013   | Joel Eliason                         | A Bayesian Hierarchical Model for Asymmetric Spatial Interactions in the Tumor Microenvironment   |
| P014   | Zachary Everton                      | An informatic tool to align post-translational modification sites between species   |
| P015   | Muhammad Zaki Hidayatullah Fadlullah | Multi-Gene Risk-Score for Prediction of Clinical Outcomes in Treatment-Naïve Metastatic Castrate Resistant Prostate Cancer                  |
| P016   | Spencer Gardner                      | Biomarker-Based Stratification of Cancer Patients for ASMase-Targeted Therapy   |
| P017   | Heng Ge                              | A Penalized Kernel Neural Network For Complex Phenotype Prediction  |
| P018   | Jared G. Gibson                      | SKAT Analysis Testing Reveals Novel Nuclear-Mitochondrial Genes Associated with Alzheimer's Disease   |
| P019   | Lucas A Gillenwater                  | GRACKLE: An interpretable matrix factorization approach for clinical subtyping  |
| P020   | Ricaria Gordon                       | Automated Weed Detection of Rumex Species using Convolutional Neural Network  |
| P021   | Brianna B. Greenwood                 | Novel Mitochondrial Haplogroups Associated with Alzheimer's Disease   |
| P022   | David Guevara                        | Enhancing Pathogen Genomics: SNV Profiling and Visualization with SNVGuru   |
| P023   | David Guevara                        | APInet: A Multi-Method Database for Predicting Animal-Pathogen Protein Interactions   |
| P024   | Qi Guo                               | An Integrated Mouse Spinal Cord Atlas Revealing Microglia Heterogeneity in Health and Injury Conditions                                     |
| P025   | MaKenna Hardy                        | Uncovering Patterns in Cancer Treatment Timelines Through Substitution Matrices and Clustering  |
| P026   | Hongbo Liu                           | Integrative genomics and epigenomics reveal convergent coding and regulatory variants   |
| P027   | Michael Huang                        | Characterization of tumor suppressors and oncogenes evaluated from TCGA cancers   |
| P028   | Jose Humberto Giraldez Chavez        | Transformer-Based Foundation Model for Peptide Elution Order Prediction   |
| P029   | Rachel Hunter                        | Metabolic Partitioning in Lichens   |
| P030   | Mazen Istanbouli                     | Longitudinal PTSD Biomarker Discovery from Multi-omic Biotypes  |
| P031   | Anshuman Jaiswal                     | Smartwatch-Based Detection of Parkinson's Disease Using Motion Sensor Data and Machine Learning   |
| P032   | W. Evan Johnson                      | Tools and Methods for Profiling Host-Microbe Interactions in Pulmonary Diseases   |
| P033   | Hailey Johnson                       | PTM Disrupting Mutational Hotspots & Potential Cancer Drug discovery  |
| P034   | Raghav Kataria                       | HPIpy: A Multi-Model Toolbox for Predicting Host-Pathogen Protein-Protein Interactions using Computational Models                           |
| P035   | Kirsten Kerksiek                     | Access to Cancer Care in HCl's Area of Catchment  |

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| P036 | Srividya Kottapalli             | <b>μEx Splice Code: A Deep Learning Approach to Neuronal Splicing and Disease</b>  |
| P037 | Rebecca Kreutz                  | Identifying diet and persistent organic pollution patterns that drive metabolic disease  |
| P038 | Rousselene B. Larson            | myDockDB: A Database for Docking Natural Compounds against Multiple Myeloma Proteins   |
| P039 | Jialu Ma                        | A Web-Based Portal for Organizing Single-Cell RNA Sequencing Data on Cancer Transcriptomes   |
| P040 | Blake McGee                     | Assessing average nucleotide identities and codon usage biases of bacteriophages and their hosts   |
| P041 | Alex Mi                         | Revelation of Common Mutation Regions Within the Coding Sequences of MiRNA-Targeted Risk Genes Through Bioinformatic Analysis                    |
| P042 | Zarrin Minuchehr                | What are proteins with the highest number of Chameleon sequences capable of an AI approach   |
| P043 | Alyssa A Nitz                   | Are we there yet? Assessing the readiness of single-cell proteomics to answer biological hypotheses  |
| P044 | Alyks Odell                     | Investigating increased risk of postpartum depression (PPD) in inflammatory autoimmune disease   |
| P045 | Leonardo R. Orozco              | Nota (Network Ontology Transcript Annotation) and Jack: Leveraging Network Inference for Functional Transcript Annotation in Non-Model Organisms |
| P046 | Sai Prashanthi Pallati          | A Deep Learning Framework for Scalable Protein Structural Similarity Search from Sequences   |
| P047 | Sunithya Penumarthy             | Integrative Multi-Omic Analysis of Protein-Metabolite Interactions Using MIDAS   |
| P048 | Latosha Cole and Kylan Williams | Characterization of genes involved in host response of humans to enterotoxigenic Escherichia coli.   |
| P049 | David Redd                      | Improving B-Cell receptor prediction with a Single-Cell Long-Read VAE approach   |
| P050 | Deepa Reghu                     | A Platform for Developing AI-Powered Smartphone Medical Applications   |
| P051 | Ethan Reyes                     | SWEET Pea: Functional Characterization of SWEET1 and SWEET10 Sugar Transporters in Pisum sativum   |
| P052 | Amulek Brenes Sandoval          | Linking dietary patterns to persistent organic pollutants  |
| P053 | Mahdieh Shabanian               | Enabling Transcriptome Classification in Micro-Cohorts with MLOps  |
| P055 | Luke Squires                    | An Introduction to Peptide Embedding for Machine Learning in Proteomics  |
| P056 | David Stone                     | Association of Antibiotic Therapy and Immune-related Adverse Events for Immune Checkpoint Inhibitors Treated Cancer Patients.                    |
| P057 | Mateusz Szczepaniak             | Searching for Disease-Specific Consistency: Using AI for Cross-Platform Integration of Transcriptomic Annotations and Gene Expression            |
| P058 | Zijia Tang                      | scPerb: Predict single-cell perturbation via style transfer-based variational autoencoder  |
| P059 | Jac Taylor                      | CUB Hub: an Interactive Web Tool for Visualizing Codon Usage Bias Across Diverse Species   |
| P060 | Jakobe Thomas                   | Gut and Oral Microbiomes: Diversity, Health, and Disease Implications  |
| P061 | Thuy T. T. Tran                 | Harnessing Tumor Microenvironment Dynamics to Predict Rational Therapy Combinations using single cell RNA-seq data                               |
| P062 | Priscilla Udomprasert           | Unsupervised Clustering of Protein Language Model Embeddings for Homology Detection  |
| P063 | Eric Upton-Rowley               | Identifying Candidate PTM Sites for Cancer Drug Development using Intrinsically Disordered Regions and Phase Separation                          |
| P064 | Lida Vadakumchery               | Human protein atlas: a resource for target expression across 19 human tissues  |
| P065 | Michael van der Veldt           | A Conditional VAE for Interrogable, Compressed Gene Expression Representations   |
| P066 | Hailey Whittier                 | Clinician-Derived Phenotypic Risk Scores (PheRS): Removing time to diagnosis for multiple sclerosis patients                                     |
| P067 | Jeremiah Wimer                  | Improved Prediction of Dehydrated Patients using IPFM-Synthesized PVP Waveforms  |
| P068 | Zongqian Wu                     | Crafting Virtual Patients: Graph-Powered Diffusion Models for Realistic and Privacy-Preserved Synthetic Patient Cohorts                          |

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|------|----------------|---|
| P069 | Fnu Wulijibuhe | ACT-Attention: A Revolutionary AI Model for Deciphering Cellular Populations and Genetic Interactions in Systemic Lupus Erythematosus |
| P070 | Aoqi Xie       | gwSPADE: reference-free deconvolution in spatial transcriptomics with gene weighting  |
| P071 | Victoria Xu    | AI-Driven Combination Drug Discovery: Addressing the Heterogeneity of Amyotrophic Lateral Sclerosis                                   |
| P072 | Huiyi Yang     | Potential Impact of Pharmacogenomic Variability in Prostate Cancer Patients   |
| P073 | Zongliang Yue  | Development of Super-PAG in Functional Genomics using PAG Network and Large Language Model  |
| P074 | Serena Zhao    | Longitudinal Multi-Omics PTSD Biotype Discovery: A Similarity Network Fusion Approach   |
| P075 | Yuxin Zhao     | A Multi-Omics Computational Approach to Predict Novel Drug Combinations for Glioblastoma  |

# MCBIOS 2025

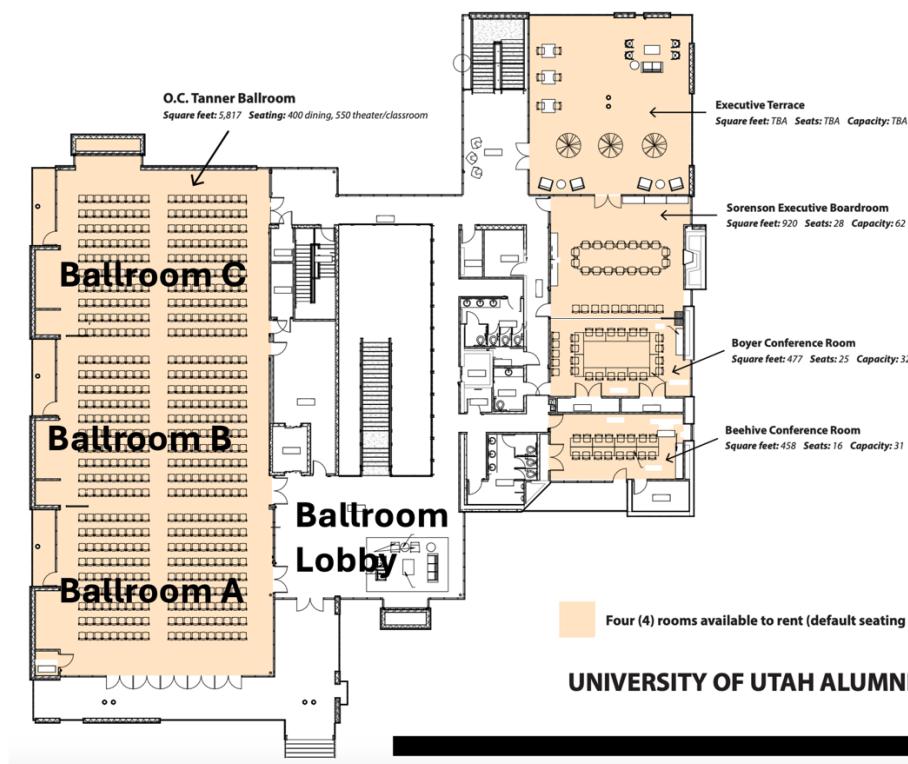
## ALUMNI HOUSE LAYOUT

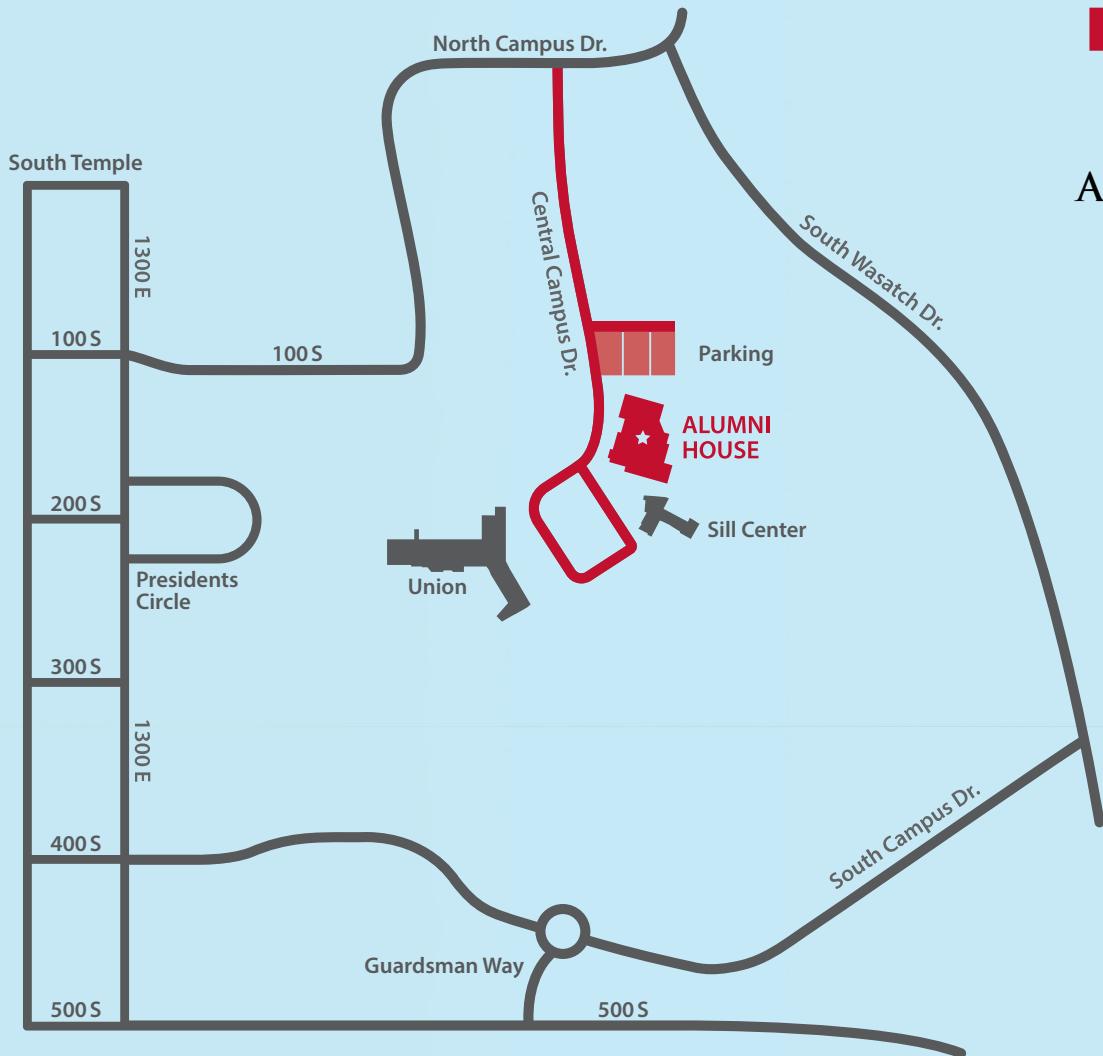


### UNIVERSITY OF UTAH ALUMNI HOUSE

Level 1 event rooms

Four (4) rooms available to rent (default seating arrangement)





## THE CLEONE PETERSON ECCLES ALUMNI HOUSE



**Questions?**  
(801) 581-6995

# PARKING MAP

Cleone Peterson Eycles  
**ALUMNI HOUSE**

