

MCBIOS 2025

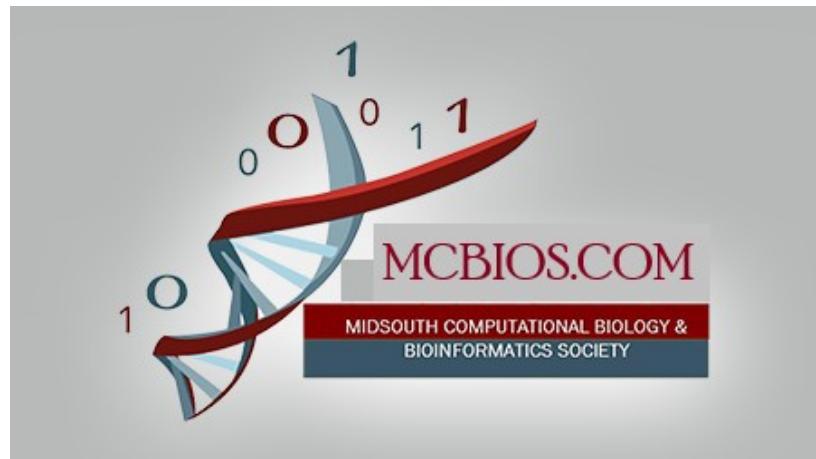
PROGRAM BOOK



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

Program Committees

Aik Choon Tan, Ph.D. *University of Utah*
Ann Chen, Ph.D. *University of Utah*
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Chang Su, Ph.D. *Emory University*
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Inimary Toby Ogundehi, PhD *University of Dallas*
Jincheng Shen, Ph.D. *University of Utah*
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Mary Davis, Ph.D. *Brigham Young University*
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Riyue Bao, Ph.D. *University of Pittsburgh Medical Center*
Robert J. Doerksen *University of Mississippi*
Samuel Payne, Ph.D. *Brigham Young University*
Sha Cao, Ph.D. *Oregon Health and Science University*
Timothy Shaw, Ph.D. *Moffitt Cancer Center*
Vinay Raj, Ph.D. *University of Arkansas at Pine Bluff*
Wei Chen, Ph.D. *University of Pittsburgh*
Xi Qiao, Ph.D. *University of Utah*
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Xuefeng Wang, Ph.D. *Moffitt Cancer Center*
Yan Sun, Ph.D. *Utah State University*
Yuehua Cui, Ph.D. *Michigan State University*
Zaki Wilmot, Ph.D. *University of Utah*
Zhaohui Qin, Ph.D. *Emory University*
Zongliang Yue, Ph.D. *Auburn University*

Local Organizing Committees (Volunteers)

Abhay Rastogi *University of Utah*
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*

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

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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 Jill Barnholtz - Sloan | | | | |
| 2:15 - 2:30 pm | Break | | | | |
| 2:30 - 3:30 pm | TUTORIAL 1 Rebecca Barter | | | | |
| 3:30 - 3:45 pm | Break | | | | |
| 3:45 - 4:30 pm | YSEA (Grad Student) | YSEA (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 Jessica Li | | | |
| 9:30 - 9:45 am | Break | | | |
| 9:45 - 11:00 am | SESSION 101 Chair Hao Chen Wei Chen AI methods and applications in single cell spatial omics | SESSION 102 Chair Inimary Toby Ogundehi AI in Computational Sciences: Shaping the Future of Research, Education, and Biomolecular Discovery | SESSION 103 Chair Xi Qiao Innovative Approaches to Orchestrating the Microbial Symphony | TUTORIAL 2 Devin Lange |
| 11:00 - 11:15 am | Break | | | |
| 11:15 - 12:30 pm | SESSION 201 Chair Sha Cao Innovative integrations of omics and computational approaches in biological systems | SESSION 202 Chair Yan Sun Recent Advances in Biostatistical Research | SESSION 203 Chair Tim Shaw Riyue Bao Leveraging AI to reconcile barriers in IO Research | SESSION 204 Chair Rakesh Kaundal Harnessing Integrative Multi-Omics and AI to Decipher Host-Pathogen Interactions |
| 12:30 - 1:30 pm | LUNCH | | | |
| 1:30 - 2:45 pm | SESSION 301 Chair Zongliang Yue From Omics to Network Pharmacology and Systems Medicine (Zoom) | SESSION 302 Chair Yuehua Cui Advancing Statistical and Machine Learning Models for Single-Cell and Spatial Omics | SESSION 303 Chair AC Tan Oncological Data Science | SESSION 304 Chair Zaki Wilmot Lighting Talk 1 |

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

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

MCBIOS 2025 Program

DAY 1 : Thursday 3/27/25

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



DAY 2 : Friday 3/28/25

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

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| | <p>4. The tumor microbiome affects the microenvironment as a function of the microbe and cancer type Daniel J Spakowicz, The Ohio State University</p> <p>5. Cross-Platform Concordance in Microbiome Analysis: 16S rRNA vs. Metagenomic Shotgun Sequencing Xi Qiao, Huntsman Cancer Institute</p> |
| TUTORIAL 2: Devin Lange, Ph.D. | |
| Topic: Visualization of Complex Data |  |
| 9:45 - 11:00am | |
| Room: Henrickson Room | |
| 11:00 – 11:15am Ballroom Lobby | BREAK |
| Session 201: Innovative integrations of omics and computational approaches in biological systems | |
| Session Chair: Sha Cao | |
| Room: Ballroom A | |
| 11:15 - 12:30pm | <p>1. Context-specific spatial genomics reveals insights into the functional impacts of genetic variants Jianrong Wang, Michigan State University</p> <p>2. Error-controlled hypothesis generation in generic machine learning models Yang Lu, University of Waterloo</p> <p>3. Quantitative 3D reconstruction and multi-omic mapping of human pancreas tissue reveals shocking heterogeneity in precancer development Ashley Lynn Kiemen, Johns Hopkins</p> <p>4. Metabolomic Profiles for Biomarker Discovery Oana A. Zelezniak, Harvard University</p> <p>5. Accurate Imputation of Pathway-Specific Gene Expression in Spatial Transcriptomics with PASTA Ziyi Li, MD Anderson Cancer Center</p> |
| Session 202: Recent Advances in Biostatistical Research | |
| Session Chair: Yan Sun | |
| Room: Ballroom 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 Brinley Zabriskie, 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 Chunyang Li, University of Utah</p> <p>3. Mediation Analysis of Multiple Mediators with Incomplete Omics Data John Kidd, 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 Tom Jensen, Utah State University</p> <p>5. Deep MAGIC: Enhancing Data Imputation through Manifold Learning and Autoencoders Devin Eddington, Utah State University</p> |
| Session 203: Leveraging AI to reconcile barriers in IO Research | |
| Session Chair: Tim Shaw/Riyue Bao | |
| Room: Ballroom C | |
| 11:15 - 12:30pm | <p>1. Digital Twin: Harmonizing patient data Aik-Choon Tan, Huntsman Cancer Institute, University of Utah</p> <p>2. Integrating OMICS technologies Linghua Wang, MD Anderson Cancer Center</p> <p>3. Harmonizing patient and cancer models Xuefeng Wang, H Lee Moffitt Cancer Center</p> |
| Session 204: Harnessing Integrative Multi-Omics and AI to Decipher Host-Pathogen Interactions | |
| Session Chair: Rakesh Kaundal | |
| Room: Henrickson Room | |
| 11:15 - 12:30pm | <p>1. Profiling Host-Microbe Interactions in Pulmonary Diseases W. Evan Johnson, Rutgers University</p> <p>2. APInet: A Multi-Method Database for Predicting and Visualizing Animal-Pathogen Protein Interactions David Guevara, Utah State University</p> <p>3. Leveraging AI to Advance Image and Cell-Based Drug Discovery Qianqian Song, University of Florida</p> <p>4. HPIpy: A Multi-Model Python-based Toolbox for Predicting Host-Pathogen Protein-Protein Interactions using Diverse Computational Models Raghav Kataria, 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. Rousselene B. Larson, Utah State University</p> |
| 12:30 – 1:30 pm Ballroom Lobby | Lunch |
| Session 301: From Omics to Network Pharmacology and Systems Medicine | |
| Session Chair: Zongliang Yue | |
| Room: Ballroom A | |
| 1:30 - 2:45pm | <p>1. Decoding Cancer: Mapping Protein-Protein Interaction Networks to Identify Drug Targets Ece (Gamsiz) Uzun, Brown University</p> <p>2. Single-cell Network Biology and Medicine Daifeng Wang, 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 Qi Li, Fisk University</p> |

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

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| | <p>3. A Multi-Omics Computational Approach to Predict Novel Drug Combinations for Glioblastoma Yuxin Zhao, Huntsman Cancer Institute, University of Utah</p> <p>4. AI-Driven Combination Drug Discovery: Addressing the Heterogeneity of Amyotrophic Lateral Sclerosis Victoria Xu, Dougherty Valley High School</p> <p>5. Integrating Chemical Language Model and Machine Learning for Dual mTOR/PI3K-α Inhibition in Breast Cancer Fuad Al Abir, University of Alabama at Birmingham</p> <p>6. Novel Mitochondrial Haplogroups Associated with Alzheimer's Disease Brianna B. Greenwood, Brigham Young University</p> <p>7. Longitudinal PTSD Biomarker Discovery from Multi-omic Biotypes Mazen Istambouli, University of Memphis</p> <p>8. A Platform for Developing AI-Powered Smartphone Medical Applications Deepa Reghu, Mississippi Valley State University</p> |
| 2:45 – 3:00 pm Ballroom Lobby | BREAK |
| Session 401: AI meets genetics and genomics | |
| Session Chair: Jun Ding/Xiaowei Zhan | |
| Room: Ballroom A | |
| 3:00 - 4:15pm | <p>1. Innovating the fight against antibiotic resistance with machine learning Xiaowei Zhan, University of Texas Southwestern Medical Center</p> <p>2. Harnessing tumor microenvironment depicted by histological images to improve cancer prognosis through a deep learning system Zhangsheng Yu, Shanghai Jiao Tong University</p> <p>3. Scaling up spatial transcriptomics for large-sized tissues Amelia Schroeder, University of Pennsylvania</p> |
| Session 402: Frontiers in Computational Biology and Bioinformatics (BYU Capstone I) | |
| Session Chair: AC Tan / Samuel Payne | |
| Room: Ballroom B | |
| 3:00 - 4:15pm | <p>1. Uncovering Patterns in Cancer Treatment Timelines MaKenna Hardy, Brigham Young University Megan Knight, Luke Squires, Abby Chen</p> <p>2. PTM Disrupting Mutational Hotspots & Potential Cancer Drug discovery Hailey Johnson, Brigham Young University Tessa Bass, Darian Ferry, Eric Upton-Rowley</p> <p>3. Identifying distance as a disparity through GIS mapping of care for rural patients Gage Bowman, Brigham Young University Maddie Brammer, Clark Roylance, Kirsten Kerksiek</p> |

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| | <p>4. Identifying diet and persistent organic pollution patterns that drive metabolic disease Rebecca Kreutz, Brigham Young University Amulek Brenes Sandoval, Merek Helmer, Griffin Cropper</p> <p>5. An informatic tool to align post-translational modification sites between species Zachary Everton, Brigham Young University Camille Krieger, Brandon Lewis</p> |
| Session 403: Innovative Data-Driven Strategies for Precision Cancer Treatment | |
| Session Chair: Jincheng Shen | |
| Room: Ballroom C | |
| 3:00 - 4:15pm | <ol style="list-style-type: none"> 1. Scalable AI Solutions for Adaptive Cancer Care Chris Gregg, University of Utah 2. Multi-Gene Risk-Score for Prediction of Clinical Outcomes in Treatment-Naïve Metastatic Castrate Resistant Prostate Cancer Zaki Wilmot, Huntsman Cancer Institute, University of Utah 3. Harnessing Tumor Microenvironment Dynamics to Predict Rational Therapy Combinations using single cell RNA-seq data Chloe Tran, Huntsman Cancer Institute, University of Utah 4. Reinforcement Learning for Adaptive Treatment Strategies in Advanced Non-Small Cell Lung Cancer Using EHR Data Jincheng Shen, University of Utah |
| Session 404: Lighting Talk 2 | |
| Session Chair: Bernie Daigle | |
| Room: Henrickson Room | |
| 3:00 - 4:15pm | <ol style="list-style-type: none"> 1. Unsupervised Clustering of Protein Language Model Embeddings for Homology Detection Priscilla Udomprasert, Auburn University at Montgomery 2. An Integrated Mouse Spinal Cord Atlas Revealing Microglia Heterogeneity in Health and Injury Conditions Qi Guo, The Ohio State University Wexner Medical Center 3. Repulsive scaling replica exchange molecular dynamics: Sea cucumber fucosylated glycosaminoglycan inhibition of heparan-6-O-endosulfatase 2 Robert J. Doerksen, University of Mississippi 4. Longitudinal Multi-Omics PTSD Biotype Discovery: A Similarity Network Fusion Approach Serena Zhao, University of Memphis 5. Transformer-Based Foundation Model for Peptide Elution Order Prediction Jose Humberto Giraldez Chavez, Brigham Young University 6. Development of Super-PAG in Functional Genomics using PAG Network and Large Language Model Zongliang Yue, Auburn University |

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

DAY 3 : Saturday 3/29/25

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

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| Session 502: Emerging methods in single-cell analysis and AI-driven biomarker discovery | |
| Session Chair: Xuefeng Wang | |
| Room: Ballroom B | |
| 9:45 - 11:00am | <ol style="list-style-type: none"> Comparative single cell analysis reveals cellular architecture of tumor bone metastasis Shenglin Mei, Virginia Tech HapCNV: A Comparative Framework for CNV Detection in Low-input DNA sequencing data Feifei Xiao, University of Florida Artificial Intelligence for Biomarker Development and Drug Discovery Qianqian Song, University of Florida Generalizing Transfer Learning: A Flexible Doubly Robust Estimation Approach for Missing Data Tianying Wang, Colorado State University |
| Session 503: Recent advances in statistical and computational methods for omics data | |
| Session Chair: Chi Wang | |
| Room: Ballroom C | |
| 9:45 - 11:00am | <ol style="list-style-type: none"> SDePER: a hybrid machine learning and regression method for cell-type deconvolution of spatial barcoding-based transcriptomic data Xiting Yan, Yale University Bayesian Edge Regression: Characterizing Observation-Specific Heterogeneity in Estimating Undirected Graphical Models Zeya Wang, University of Kentucky A Bayesian informative shrinkage approach for large-scale multiple hypothesis testing: with applications in transcriptomic differential expression analysis Ya Su, Virginia Commonwealth University Leveraging Large Language Models for Integrative Analysis of Cancer Omics Data Jinpeng Liu, University of Kentucky |
| Session 504: Lightning Talk 3 (BYU Capstone II) | |
| Session Chair: Mary Davis / Samuel Payne | |
| Room: Henrickson Room | |
| 9:45 - 11:00am | <ol style="list-style-type: none"> HLA typing the All of Us dataset Rebecca Caylor, Brigham Young University Jacqui Durney, Parker Reyes Biomarker-Based Stratification of Cancer Patients for ASMase-Targeted Therapy Spencer Gardner, Brigham Young University Spencer Boris, Catherine Clive Identifying functionally essential amino acids in phage proteins Caz Cullimore, Brigham Young University Benjamin Driggs, Teancum Hoopes, Britton Stanley |

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



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| | <ol style="list-style-type: none"> 3. Genotype and phenotype risk score analyses of genetically admixed multiple sclerosis patients in All of Us Will Brugger, Brigham Young University 4. Convolutions Accelerate mRNA Ramp Sequence Research in ExtRamp 2.0 Matthew Cloward, Brigham Young University 5. Improving B-Cell receptor prediction with a Single-Cell Long-Read VAE approach David Redd, Brigham Young University 6. Clinician-Derived Phenotypic Risk Scores (PheRS): Removing time to diagnosis for multiple sclerosis patients Hailey Whittier, Brigham Young University 7. Investigating increased risk of postpartum depression (PPD) in inflammatory autoimmune disease Alyks Odell, Brigham Young University |
| Session 604: Lightning Talk 5 | |
| Session Chair: Robert Doerkson | |
| Room: Henrickson Room | |
| 11:15 - 12:30pm | <ol style="list-style-type: none"> 1. Statistical methods for handling cellular heterogeneity in quantitative single-cell experiments: review simulations and recommendations Hannah Boekweg, Brigham Young University 2. CUB Hub: an Interactive Web Tool for Visualizing Codon Usage Bias Across Diverse Species Jac Taylor, Brigham Young University 3. SKAT Analysis Testing Reveals Novel Nuclear-Mitochondrial Genes Associated with Alzheimer's Disease Jared G. Gibson, Brigham Young University 4. A Bayesian Hierarchical Model for Asymmetric Spatial Interactions in the Tumor Microenvironment Joel N Eliason, University of Michigan 5. Improved Prediction of Dehydrated Patients using IPFM-Synthesized PVP Waveforms Jeremiah Wimer, University of Arkansas 6. An Introduction to Peptide Embedding for Machine Learning in Proteomics Luke Squires, Brigham Young University 7. GRACKLE: An interpretable matrix factorization approach for clinical subtyping Lucas Gillenwater, University of Colorado Anschutz Medical Campus 8. Enabling Transcriptome Classification in Micro-Cohorts with MLOps Madi Shabanian, University of Utah 9. Association of Antibiotic Therapy and Immune-related Adverse Events for Immune Checkpoint Inhibitors Treated Cancer Patients |

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| | <p>David Stone, Huntsman Cancer Institute, University of Utah</p> <p>10. Automated Weed Detection of Rumex Species using Convolutional Neural Network</p> <p>Ricaria Gordon, Mississippi Valley State University</p> |
| 12:30 – 1:00pm Ballroom A, B, C | AWARDS and CLOSING CEREMONY |

MCBIOS 2025 Posters

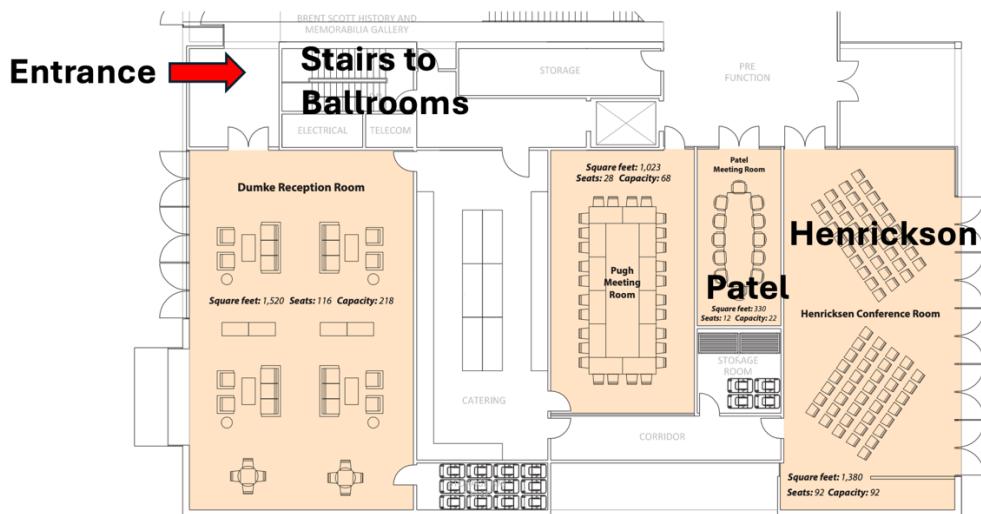
| Poster | Name | Title |
|--------|--------------------------------------|---|
| P001 | Fuad Al Abir | Integrating Chemical Language Model and Machine Learning for Dual mTOR/PI3K-a Inhibition in Breast Cancer |
| P002 | Hannah Boekweg | Statistical methods for handling cellular heterogeneity in quantitative 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 | μEx Splice Code: A Deep Learning Approach to Neuronal Splicing and Disease |
| 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 |

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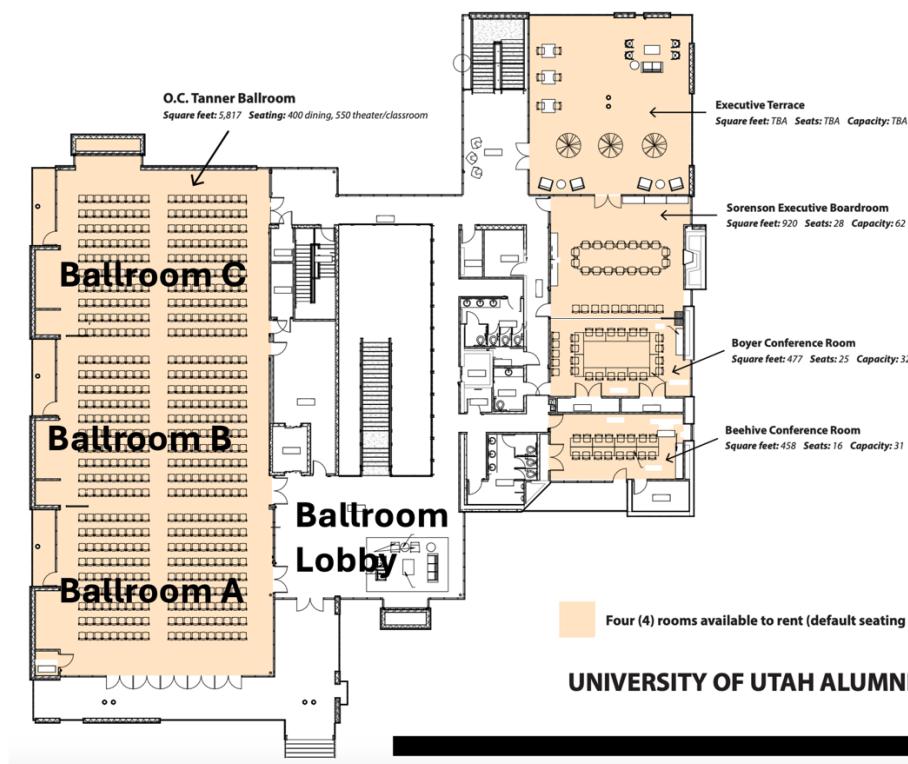
ALUMNI HOUSE LAYOUT

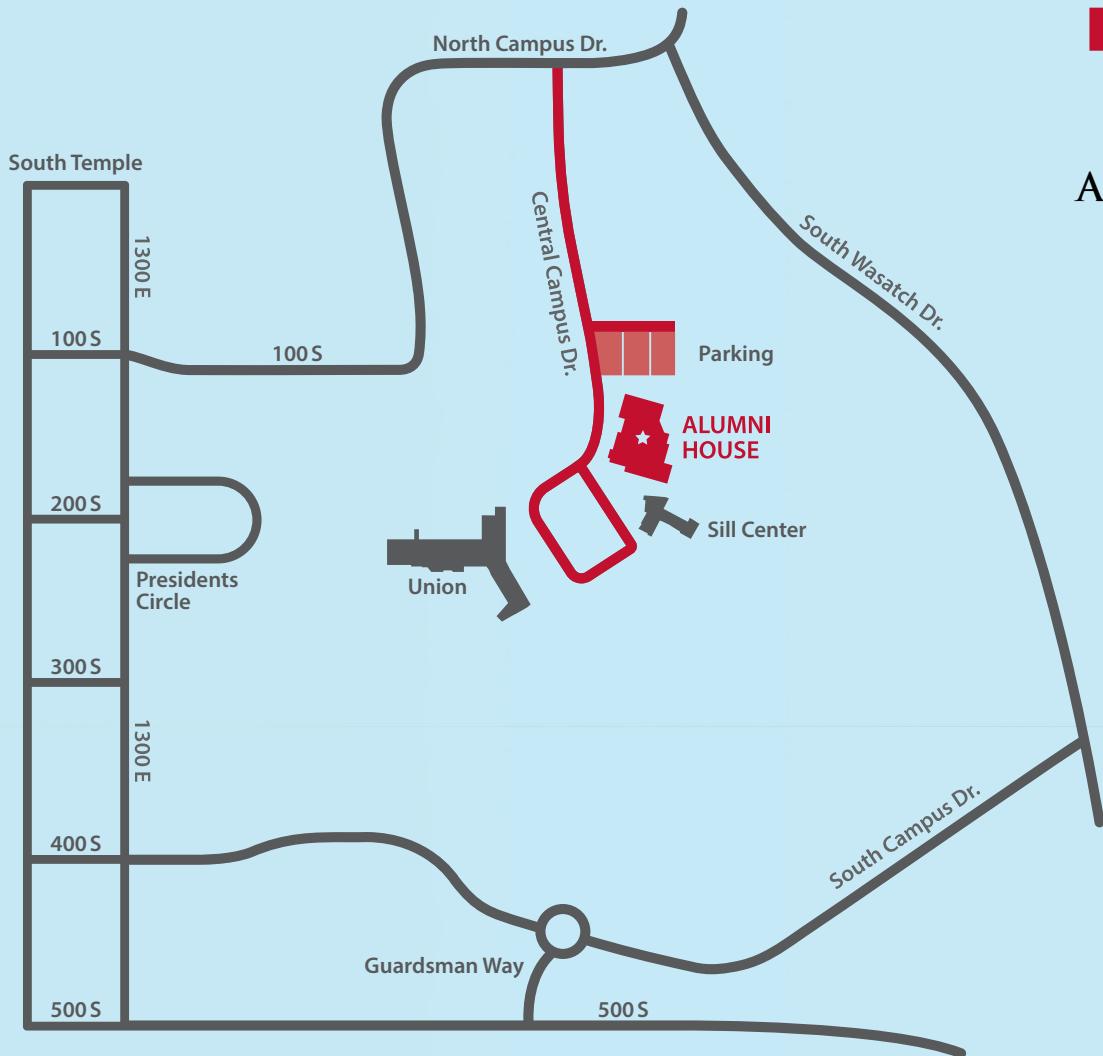


UNIVERSITY OF UTAH ALUMNI HOUSE

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

