1) Computational Modeling of Tubulin-Tubulin Interactions
Mahya Hemmat, University of Minnesota Mechanical Engineering.

2) Sequence Handling: A Pipeline to Automate DNA Sequence Aligning and Quality Control Workflows via List-Based Batch Submission and Parallel Processing
Paul Hoffman, University of Minnesota, Agronomy and Plant Genetics; Skylar Wyant, University of Minnesota, Agronomy and Plant Genetics; Thomas Kono, University of Minnesota, Agronomy and Plant Genetics; Peter Morrell, University of Minnesota, Agronomy and Plant Genetics.

3) ANGSD-wraper: Utilities for Analyzing Next Generation Sequencing Data
Chaochih Liu, University of Minnesota, Agronomy & Plant Genetics; Arun Durvasula, University of California, Davis, Plant Sciences; Paul Hoffman, University of Minnesota, Agronomy & Plant Genetics; Tyler Kent, University of California, Davis, Plant Sciences; Thomas Kono, University of Minnesota, Agronomy & Plant Genetics; Peter Morrell, University of Minnesota, Agronomy & Plant Genetics; Jeffrey Ross-Ibarra, University of California, Davis, Plant Sciences; University of California, Davis, Center for Population Biology & Genome Center.

4) Prediction of Drug Response and Resistance in Hematologic Malignancies
Monica Akre, University of Minnesota, Department of Genetics, Cell Biology, and Development; Brian Van Ness, University of Minnesota, Department of Genetics, Cell Biology, and Genetics.

5) Frequent Causal Pattern Mining: An Effective Counterfactual Estimation Framework
Pranjul Yadav, University of Minnesota, Computer Science; Michael Steinbach, University of Minnesota, Computer Science; Alexander Hoff, University of Minnesota, Computer Science; Vipin Kumar, University of Minnesota, Computer Science; Gyorgy Simon, University of Minnesota, Institute of Health Informatics.

6) VC-based Signal Denoising for iEEG Data
Hsiang-Han Chen, University of Minnesota; Han-Tai Shiao, University of Minnesota; Vladimir Cherkassky, University of Minnesota.
7) Information Theory-based Analysis of Classical HLA Genes
Hu Huang, University of Minnesota, BICB; NMDP; Wei Wang, National Marrow Donor Program, Bioinformatics Research; Yung-Tsi Bolon, National Marrow Donor Program, Bioinformatics Research; University of Minnesota, BICB; Craig Malmberg, National Marrow Donor Program; Caleb Kennedy, National Marrow Donor Program, Bioinformatics Research; University of Minnesota, BICB; Martin Maiers, National Marrow Donor Program, Bioinformatics Research.

8) Imputation of Mass Spectrometry-Based Metabolomics Data and the Effect on Classification Outcomes and Metabolite Investigation
LeeAnn Higgins, UMTC Biochemistry, Molecular Biology and Biophysics; Stephen A Brockman, UMTC Horticulture Science; Kevin J Murray, UMTC Biochemistry, Molecular Biology and Biophysics.

9) Behavioral Trait Heritability in Twins
Jasmine Joseph, Brain Sciences Center, Department of Veterans Affairs Health Care System, BICB, University of Minnesota; Peka Christova, Brain Sciences Center, Department of Veterans Affairs Health Care System, Department of Neuroscience, University of Minnesota Medical School; Apostolos G. Georgopoulos, Brain Sciences Center, Department of Veterans Affairs Health Care System, Department of Neuroscience, University of Minnesota Medical School, BICB, University of Minnesota.

10) NGS Informatics Pipeline for Unknown Pathogen Detection, Assembly, and Genome Evaluation
Todd Knutson, Department of Veterinary Population Medicine, Veterinary Diagnostic Laboratory; Matthew Jarvis, Department of Veterinary Population Medicine, Veterinary Diagnostic Laboratory; Douglas Marthaler, Department of Veterinary Population Medicine, Veterinary Diagnostic Laboratory.

11) A Neural Traffic Model of Brain Function
Michelle Chorn, University of Minnesota, Graduate Program in Cognitive Science; Department of Neuroscience; Brain Sciences Center; Arthur C Leuthold, University of Minnesota, Brain Sciences Center; Apostolos Georgopoulos, University of Minnesota, Department of Neuroscience; Brain Sciences Center.

12) Discovering Mode-of-Action for Small Molecules within Saccharomyces cerevisiae and Escherichia Coli
Justin Nelson, Bioinformatics and Computational Biology; Scott Simpson, Bioinformatics and Computational Biology; Hamid Safizadeh, Electrical Engineering, University of Minnesota; Raamesh Deshpande, Paypall Inc; Jeff Piotrowski, Yumanity Therapeutics; Sheena Li, RIKEN Center for Sustainable Resource Science; Jacqueline Barbar; Mami Yoshimura, RIKEN Center for Sustainable Resource Science; Minoru Yoshida. RIKEN Center for Sustainable Resource Science; Charles Boone, Donnelly Centre for Cellular and Biomolecular Research, University of Toronto; Chad Myers, Computer Science and Engineering, University of Minnesota.
13) **Understanding HIV Mutagenesis Using High-Throughput Sequencing Technology**
Morgan Meissner, University of Minnesota, Institute for Molecular Virology; Jonathan Rawson, University of Minnesota, Institute for Molecular Virology; Sean Landman, University of Minnesota, Computer Science; Daryl Gohl, University of Minnesota, Genomics Center; Kenny Beckman, University of Minnesota, Genomics Center; Joshua Baller, University of Minnesota, Supercomputing Institute; Louis M Mansky, University of Minnesota, Institute for Molecular Virology.

14) **Utilizing Co-expression Networks with Phenotypic Data to Discover Candidate Genes in Soybean**
Jean-Michel Michno, University of Minnesota, Agronomy and Plant Genetics; Robert J. Schaefer, University of Minnesota, Veterinary Population Medicine; Joseph R. Jeffers, University of Minnesota, Computer Science; Chad L. Myers, University of Minnesota, Computer Science; Robert M. Stupar, University of Minnesota, Agronomy and Plant Genetics.

15) **Improving the organization of collective data resources using BotBot**
Jack Stanek, University of Minnesota, Computer Science; Rob Schaefer, University of Minnesota, Computer Science.

16) **Scalable Tools for the Quantitative Analysis of Chemical-Genetic Interactions**
Scott Simpkins, University of Minnesota, Bioinformatics and Computational Biology; Justin Nelson, University of Minnesota, Bioinformatics and Computational Biology; Raamesh Deshpande, University of Minnesota, Computer Science and Engineering; Jeffrey S. Piotrowski, Yumanity Therapeutics; Sheena C. Li, RIKEN (Japan), Center for Sustainable Resource Science; Charles M. Boone, University of Toronto, Banting and Best Department of Medical Research; Chad L. Myers, University of Minnesota, Bioinformatics and Computational Biology.

17) **A Robust Pipeline to Predict Deleterious Mutations in Plants**
Li Lei, University of Minnesota; Thomas J. Y. Kono, University of Minnesota, Agronomy and Plant Genetics; Ching-Hua Shih; Paul J. Hoffman, University of Minnesota, Agronomy and Plant Genetics; Peter L. Morrell, University of Minnesota, Agronomy and Plant Genetics; Justin C. Fay.