Systems Computation Omics
Michigan State University

RNA–Seq Data Analysis Psychiatry Genetics

Statistical Learning Comparative pathogenomics Systems Medicine

Molecular networks Precision Medicine Algorithms Single Cell RNA–Seq

Penalized Regressions Molecular drug/vaccine discovery Individualized Medicine

Transcriptional Analysis Complex Networks Computational Genetics

Phylogenetics Quantitative Genetics Development

Boolean Models

Deep Learning Statistical Genetics Metabolomics

Data integration

Text–mining Transcriptomics Epigenetics

Epigenomics Phenomics

Proteomics Metabolism

Genomics

Brain R Julia

Bioinformatics

Data Visualization Systems Biology Metastatic cancer

Neural Networks

Signaling Pathways Leukemia and Myeloma Computational Biology

Molecular Evolution Multi–Omics Integration Chromatin Structure

Translational bioinformatics Machine learning Computational Toxicology

Drug Repositioning Bioinformatics Transcriptomics Single cell transcriptomics

Statistics Personalized cancer therapy Bayesian Methods

Stem Cell Therapy Network Biology ER stress

Prepared By: George I. Mias (gmias@msu.edu)

Mission Statement

Systems approaches are now facilitated with developments in computational statistical methods, and the availability of multiple omics data as indispensable parts of modern biological research. Michigan State University has multiple faculty across colleges and departments involved in numerous ground-breaking research projects in the field ranging from systems biology in basic science to systems medicine. Our common goal is to assemble an interdisciplinary group of experts, based on our research synergies, shared mathematical approaches and collaborative projects that can collaborate and can lead MSU to becoming a leader in Systems Computational Omics.

Mission:

The goal of the Systems Computational Omics working group at Michigan State University is to utilize computational and mathematical methods to:

- Develop state-of-the-art methodology for bioinformatics and statistical omics analyses.
- Employ systems levels analyses to describe biological systems at all scales
- Create a platform for research collaboration not only between computational but also experimental groups
- Develop a robust training program for our students and postdocs

Vision:

To utilize the interdisciplinary computational and mathematical expertise across Michigan State University's campuses, to enhance collaboration, development of novel methodology and provide an interactive environment making MSU a leader in computational approaches, both for research as well as training of the next generation of computational scientists.

Faculty Membership
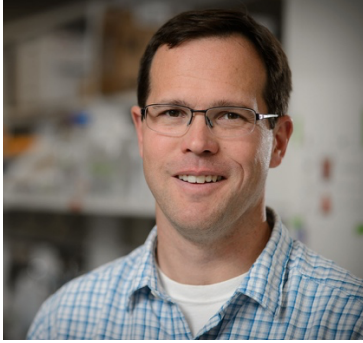
Eran Andrechek, PhD
McMaster University, Biology, PhD 2003

Associate Professor in Physiology Department

- *Research Interests*: Working on breast cancer with a particular focus is on metastasis.

- *Research Methods:*
  - Transcriptome Analysis
  - Whole genome sequencing
  - Mouse models (knockouts, transgenics, conditional activation etc.)
  - CRISPR modification of cell lines

Keywords: Genomics; Bioinformatics; Transcriptomics; Mouse models; breast cancer

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Sudin Bhattacharya, PhD
University of Michigan, Mechanical Engineering, PhD 2006

Assistant Professor in Departments of Biomedical Engineering and Pharmacology & Toxicology
http://sbhattac.msu.domains

- *Research Interests*: The Bhattacharya Lab uses various computational methods to understand the signaling and transcriptional regulatory networks that underlie the determination of cell fate, and these networks' perturbation by environmental pollutants. We are integrating diverse genomic data sets to map and model transcriptional regulatory networks and their environmental perturbation in the immune system and the liver.
- *Research Methods:*
  - Transcriptome Analysis
  - Regulatory Network Reconstruction
  - Single-cell Analysis

Keywords: Genomics; Bioinformatics; Transcriptomics; Systems Biology; Computational Toxicology.

Systems Computational Omics, Michigan State University

Gustavo de los Campos, PhD
University of Wisconsin-Madison, Quantitative Genetics and Agricultural &
Applied Economics, PhD 1997

Professor Departments of Epidemiology & Biostatistics and Statistics &
Probability
https://quantgen.github.io

- *Research Interests*: Quantitative, Statistical and Computational Genetics.
Prediction of Complex Traits using DNA information and other omics.

- *Research Methods:*
  o High-Dimensional Regression
  o Bayesian and Penalized Methods
  o Multivariate Analysis
  o Multi-Omic methods

Keywords: Genomics; Computational Genetics, Statistical Genetics, Quantitative Genetics, Bayesian Methods, Penalized Regressions, R, Julia

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Christina Chan, PhD
University of Pennsylvania, Chemical and Biochemical Engineering, PhD
1990

George W. Bissell Professor in Department of Chemical Engineering and
Materials Science (and Biochemistry and Molecular Biology)
https://www.egr.msu.edu/changroup/

- *Research Interests*: Her laboratory focuses on understanding the signaling
and regulatory mechanisms that are altered in diseases, such as obesity,
Alzheimer's disease and cancer. They develop and apply metabolic
engineering, bioinformatics, and systems biology approaches in combination
with biochemical, biophysical, and molecular biology measurements and animal studies to identify targets
and disease biomarkers. Her group also is developing polymeric-based drug delivery and tissue
engineering platforms to modulate these pathways for treating these diseases.
- *Research Methods:*
  o CRISPR, RT-PCR, Western blot analysis, protein purification
  o Cell culture
  o Network Analysis
  o Regulatory Network Reconstruction

Keywords: ER stress; Transcriptional analysis; Signaling pathways; Stem cell therapy

Systems Computational Omics, Michigan State University

Bin Chen, PhD
Indiana University at Bloomington, 2012, Informatics

Assistant Professor in Departments of Pediatrics and Human Development, Pharmacology and Toxicology
http://binchenlab.org

- *Research Interests*: Rapidly decreasing costs of molecular measurement technologies not only enable profiling of disease sample molecular features (e.g., transcriptome, proteome, metabolome) at different levels (e.g., tissues, single cells), but also enable measuring of molecular signatures of individual drugs in clinically relevant models. My lab is interested in developing computational methods to relate diseases to potentially efficacious drugs through various molecular features. The lab is also interested in using deep learning and single cell data to discover new therapeutics.
- *Research Methods:*
  - Large-scale disease and drug molecular data integration and mining
  - RNA-Seq data analysis
  - Deep learning
  - Genomic data analysis

Keywords: RNA-Seq, Single cell RNA-Seq, Drug repositioning, Deep learning, Personalized cancer therapy, Metastatic cancer, Translational bioinformatics

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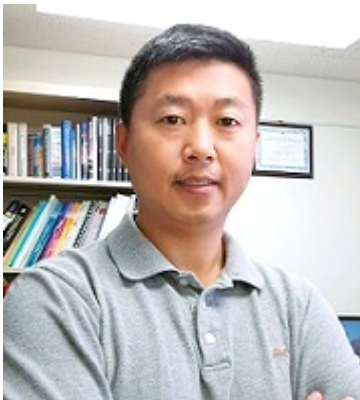
Yuehua Cui, PhD
University of Florida, Statistics, PhD 2005

Professor in Department of Statistics and Probability
https://www.stt.msu.edu/~cui/

- *Research Interests*: Statistical genetics/genomics, statistical machine learning, longitudinal/functional data analysis, statistical applications in applied science.

- *Research Methods:*
  - Gene-gene and gene-environment interactions
  - Casual mediation analysis
  - Multi-level omics data integration
  - Gene network inference

**Keywords*: Genetics, Genomics; Bioinformatics; Epigenetics; Statistics*

Erich Grotewold, PhD
University of Buenos Aires, Argentina, Chemistry & Biochemistry, PhD 1988

Professor in Department of Biochemistry & Molecular Biology
https://eglab.osu.edu

- *Research Interests*: Gene regulatory networks, mechanisms of gene regulation, plant metabolic engineering, trafficking of specialized metabolites

- *Research Methods:*
  - Transcriptome Analysis
  - Chromatin immunoprecipitation – High Throughput Sequencing (ChIP-Seq)
  - DNA-Affinity Purification - High Throughput Sequencing (DAP-Seq)
  - Cap Analysis Gene Expression (CAGE)
  - Regulatory Network Reconstruction
  - Metabolic Profiling
  - Analysis of Protein-Protein and Protein-DNA Interactions

Keywords: Metabolism; Genomics; Bioinformatics; Transcriptomics; Systems Biology

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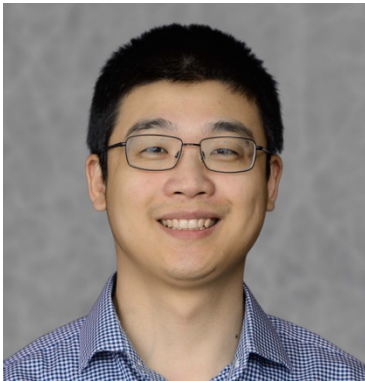
Wen Huang, PhD
University of Wisconsin-Madison, Dairy Science, PhD 2011

Assistant Professor in Department of Animal Science
https://msu.edu/~huangw53/index.html

- *Research Interests*: Genetic basis of complex quantitative traits, context dependent genetic effects, genetic networks

- *Research Methods:*
  - Statistical genetics
  - Bioinformatics
  - Next generation sequencing
  - Molecular genetics

Keywords: Quantitative Genetics; Statistical Genetics; Genomics; Bioinformatics

Arjun Krishnan, PhD
Virginia Tech, Genetics, Bioinformatics, and Computational Biology, PhD 2010

Assistant Professor in the Department of Computational Mathematics, Science and Engineering, and the Department of Biochemistry and Molecular Biology
https://www.thekrishnanlab.org

- *Research Interests*: We develop computational data-driven approaches to build predictive models that help us link genes and cellular mechanisms to various aspects of health and disease.

- *Research Methods:*
  - *Genomics & computational biology*
  - *Applied statistical/machine learning*
  - *Integrative analysis of large-scale genomics and biomedical data*
  - *Genome-wide molecular networks*
  - *Age-specificity and sexual dimorphism in health and disease*
  - *Cross-species models for human traits and diseases*
  - *Genetic heterogeneity of complex disease and precision medicine*

Keywords: Transcriptomics; Text-mining; Machine learning; Molecular networks; Data integration

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George I. Mias, PhD
Yale University, Physics, PhD 2007

Associate Professor of Biochemistry and Molecular Biology
Division Chief, Systems Biology, Institute for Quantitative Health Science and Engineering.
https://georgemias.org

- *Research Interests*: *Using interdisciplinary computational and experimental methods to explore the integration of existing and developing omics technologies and their application in systems precision medicine. We monitor individuals transitioning through various physiological states, from health to disease (asthma, leukemia, immune disorders, etc), towards universal individualized medicine. A key aspect is the study of longitudinal dynamics from omics data, using complex networks and geometric methods.*

- *Research Methods:*
  - Individualized multi-omics profiling
  - Time series Analysis
  - Combinatorial optimization of drug combinations
  - Algorithms for Data Analysis and Integration
  - Machine Learning

Keywords: Systems Medicine; Systems Biology; Individualized Medicine; Genomics; Bioinformatics; Transcriptomics; Metabolomics; Proteomics; Complex Networks; Leukemia; Multi-Omics Integration

Carlo Piermarocchi, PhD
Swiss Federal Institute of Technology Lausanne, Switzerland, Physics, PhD
1998
Professor in the Department of Physics and Astronomy

- *Research Interests*: *My research focuses on developing novel mathematical models to describe cellular processes in normal and hematological cancer cells, and predict their response to drugs and drug combinations. Our systems biology models integrate different types of omics with in vitro drug screening data and use concepts from the theory of complex networks and nonlinear dynamics*

- *Research Methods:*
    - Regulatory network reconstruction
    - Neural network models of cell dynamics
    - Time series analysis
    - Combinatorial optimization of drug combinations
    - Algorithms for the analysis of single cell transcriptomics

Keywords: Genomics; Bioinformatics; Transcriptomics; Precision Medicine Algorithms; Neural Networks, Machine Learning, Complex Networks, Boolean Models; Leukemia and Myeloma; Single cell transcriptomics.

Jeremy W Prokop, PhD
The University of Akron, Integrative Biosciences, PhD 2014

Assistant Professor in Department of Pediatrics and Human Development with second appointment in Pharmacology and Toxicology

- *Research Interests*: The Prokop lab focuses on integrative biosciences for understanding genes and genetic variants, utilizing computational tools to generate testable hypotheses for genomic variants (coding and noncoding) and protein function that are then used to guide wet lab experiments into disease mechanisms and pharmacological intervention.

- *Research Methods:*
    - Transcriptome Analysis
    - Linkage Disequilibrium
    - Genome Wide Association Studies
    - Whole Genome Sequencing
    - Codon Selection
    - Induced pluripotent stem cells (iPSC)

Systems Computational Omics, Michigan State University

- o CRISPR
- o CETCh-Seq
- o Molecular Dynamics Simulations
- o Protein Modeling

Keywords: Genotype-phenotype; rare variant analysis; Transcription; GWAS; Clinical Genomics

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Janani Ravi, PhD
Virginia Tech, Genetics, Bioinformatics & Computational Biology, PhD 2006

Assistant Professor
Pathobiology and Diagnostic Investigation
http://jananiravi.github.io/

- *Research Interests*: *My research focuses on developing novel mathematical models to describe cellular processes in normal and hematological cancer cells, and predict their response to drugs and drug combinations. Our systems biology models integrate different types of omics with in vitro drug screening data and use concepts from the theory of complex networks and nonlinear dynamics.*
  - o *Unraveling molecular mechanisms common between genetic and infectious diseases, to guide targeted drug repurposing*
  - o *Identifying genomic signatures, functions, and mechanisms relevant to host-pathogen interactions, to enable understanding and guide diagnosis*
  - o *Developing tools and resources for seamlessly relating sequence, structure, and function of genes/proteins in poorly characterized pathogens to enable and guide better prevention, diagnostic and treatment regimen*
  - o *Mathematical/statistical modeling of signaling and regulatory networks: host-pathogen interactions, metabolic pathways, and cellular processes.*
- *Research Methods:*
  - o *Programming: R, Unix/Linux (MATLAB, Python, C/C++)*
  - o Data science: data analysis & visualization
  - o Genomic/Transcriptomic analyses: *incl.* transcriptional regulatory networks
  - o Phylogenetics and molecular evolution: *incl.* sequence-structure-function prediction
  - o Dynamical systems and mathematical modeling: *incl.* dynamic Bayesian networks; large quantitative models; deterministic/stochastic modeling with bifurcation analysis

Keywords: **Computational Biology; Bioinformatics; Phylogenetics & Molecular Evolution ; Comparative pathogenomics ; Molecular drug/vaccine discovery; Data Analysis & Visualization ; Genomics/Transcriptomics**

Systems Computational Omics, Michigan State University

Mark Reimers, PhD
University of BC, Mathematics, PhD 1987

Associate Professor in Department of BME and in Neuroscience Program
https://msu.edu/~reimersm/

- *Research Interests*: Working on i) characterizing functional differences reflected in gene expression differences between psychiatric patients and normals; ii) genetic influences on psychiatric disorders; iii) effects of pre-natal infection on mouse brain transcriptome; iv) single cell transcriptome characterizations of key cell types in mouse and human brain; v) simulation of ways genotypes can give rise to behavioral phenotypes.
- *Research Methods:*
  o Transcriptome Analysis
  o GWAS accounting for Linkage Disequilibrium
  o Characterizing PPI Networks of GWAS-implicated sets
  o Simulation of regulatory and behavioral systems

Keywords: Genomics; Bioinformatics; Transcriptomics; Brain; Psychiatry; Development.

Shin-Han Shiu, PhD
University of Wisconsin-Madison, Botany, PhD 2010

Professor of Plant Biology, and Computational Mathematics, Science and Engineering
http://shiulab.plantbiology.msu.edu/index.php

- *Research Interests*: The overall goals for our research program are to elucidate: (1) the molecular evolutionary processes that shape eukaryotic genome content, (2) the distinguishing properties of genomic features, particularly those allowing the classification of functional and non-functional sequences, and (3) the mechanisms that underlie the translation of genomic information to molecular, physiological, and morphological phenotypes.

- *Research Methods:*
  o Evolutionary and population genetics
  o Functional, comparative and phylo- genomics
  o Multi-omics data integration
  o Machine learning
  o Genomic prediction

Keywords: Evolution, Genetics, Bioinformatics, Computational biology, Plant biology.

Juan P. Steibel, PhD
Michigan State University, PhD 2007

Associate Professor in Department of Fisheries and Wildlife
https://www.canr.msu.edu/people/dr_juan_steibel

- *Research Interests*: Working on methods for Genomic prediction and genome-wide association in structured populations. Modeling of social genetic effects. Methods for phenotyping individuals in groups. E.g: group-housed pigs.

- *Research Methods:*
  - Transcriptome Analysis
  - Linkage Disequilibrium
  - Genomic prediction
  - Social genetic effects
  - Image/video analyses

Keywords: Genomics; Quantitative Genetics; Statistical Genetics; Phenomics.


Ana Vazquez, PhD
University of Wisconsin-Madison, Quantitative Genetics, PhD 2010

Associate Professor of Epidemiology and Biostatistics
https://quantgen.github.io

- *Research Interests*: My research focuses on the development use and implementation of omic-based statistical methods for human health complex traits, including cancer, obesity, exercise and among other health traits. My previous research included studies with generalized linear mixed models (GLMM) with correlated random effects, from which I co-authored an R-package that fits such models.

- *Research Methods:*
  - High-Dimensional Regression
  - Generalized Linear Mixed Models
  - Multivariate Analysis
  - Multi-Omic methods

Keywords: Genomics; Computational Genetics, Statistical Genetics, Quantitative Genetics

Systems Computational Omics, Michigan State University
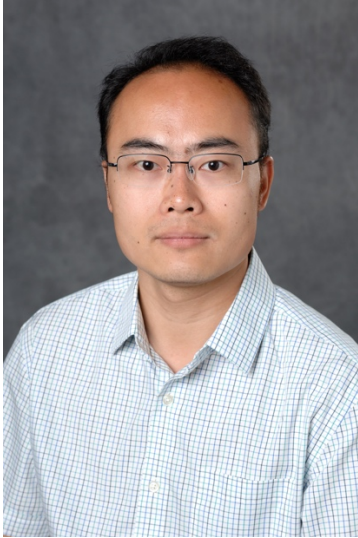
Jianrong Wang, PhD
Georgia Institute of Technology, Bioinformatics, Ph.D. 2012
Assistant Professor in Department of Computational Mathematics, Science and Engineering

- *Research Interests*: Develop machine learning and statistical algorithms to construct context-dependent regulatory networks based on large-scale multi-omics dataset. Leverage the constructed regulatory networks to decode the genetic basis of complex human disease mechanisms. Build integrative models to obtain insights on systems biology of gene regulation, especially on 3D chromatin structures, epigenetics and transcription factors.

- *Research Methods*:
  - Bayesian statistics
  - Machine learning
  - Probabilistic graphical models
  - Network reconstruction
  - Systems genetics
  - Next-generation sequencing (NGS) data processing and analysis
  - Regulatory grammar prediction

Keywords: **Genomics, Network Biology, Bioinformatics, Systems Biology, Epigenomics, Multi-omics integration, Chromatin Structure**
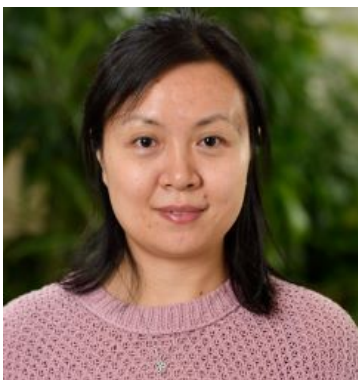
Ling Wang, PhD
University of North Carolina at Chapel Hill, Statistics, PhD 2015

Associate Professor in Department of Medicine
https://medicine.chm.msu.edu/directory/wang-l.html

- *Research Interests*: Statistical genetics, especially Genome-Wide Association Studies (GWAS), neural network and deep learning methods with applications on medical images, identifying genetic markers related with rare diseases.

- *Research Methods:*
  - Bayesian methods
  - Linkage Disequilibrium
  - Gene-environment interactions
  - microRNA analysis
  - Gene network inference

Keywords: Genomics; Bioinformatics; Epigenetics; Statistics; Convolutional Neural Networks

Yuying Xie, PhD
University of North Carolina at Chapel Hill, Statistics, PhD 2015

Assistant Professor in Department of Computational Mathematics, Science and Engineering, and Department of Statistics and Probability
https://cmse.msu.edu/directory/faculty/yuying-xie/

- *Research Interests*: My research mainly focuses on the area of statistical machine learning and consists of two themes: the development of new statistical procedure for high dimensional network models using complex and noisy datasets especially for single cell data, and the inference of association or causal relations among genes, external phenotypes, and intermediate phenotypes, such as gene expression levels and biomarker concentrations.

- *Research Methods:*
    - Neural network models
    - Graphical model
    - Single cell data analyses
    - Cancer immunology

Keywords: Genomics; Bioinformatics; Graphical Model, Cancer Immunology, Single Cell, Graph Neural Network