

## EDUCATION

2010	Ph. D. Genetics, Bioinformatics & Computational Biology Virginia Bioinformatics Institute	Virginia Tech Blacksburg, VA, USA
2006	B. Tech. Industrial Biotechnology Centre for Biotechnology, AC College of Technology	Anna University Chennai, India

## PROFESSIONAL APPOINTMENTS

2022–Present	Associate Professor Dept. of Biomedical Informatics Center for Health Artificial Intelligence	University of Colorado Anschutz Medical Campus Aurora, CO, USA
2017–2022	Assistant Professor Dept. of Computational Math, Science, and Engineering Dept. of Biochemistry and Molecular Biology	Michigan State University East Lansing, MI, USA
2013–2016	Associate Research Scholar	Princeton University
2011–2013	Postdoctoral Research Associate Lewis-Sigler Institute for Integrative Genomics	Princeton, NJ, USA
2010–2011	Postdoctoral Research Associate	Virginia Tech
2006–2010	Graduate Research Assistant Virginia Bioinformatics Institute	Blacksburg, VA, USA

## PUBLICATIONS

[ ● Co-primary authors ] [ \*\* Co-corresponding authors ]

### Preprints

1. PyGenePlexus: A Python package for gene discovery using network-based machine learning.  
Mancuso CA, Liu R, Krishnan A  
*bioRxiv* (2022) [10.1101/2022.07.02.498552](https://doi.org/10.1101/2022.07.02.498552). Under revision at *Bioinformatics* [Software: [PyGenePlexus](#)]
2. Accurately modeling biased random walks on weighted graphs using *node2vec+*.  
Liu R, Hirn M\*\*, Krishnan A\*\*  
*bioRxiv* (2022) [10.1101/2022.08.14.503926](https://doi.org/10.1101/2022.08.14.503926). Under revision at *Bioinformatics* [Software: [PecanPy 2.0](#)]
3. Co-expression signatures of combinatorial gene regulation.  
Gomez-Cano F, Xu Q, Shiu SH, Krishnan A, Grotewold E  
*bioRxiv* (2020) [10.1101/2020.05.19.104935](https://doi.org/10.1101/2020.05.19.104935).
4. SANe: The Seed Active Network For Mining Transcriptional Regulatory Programs of Seed Development.  
Gupta C, Krishnan A, Collakova E, Wolinski P, Pereira A  
*bioRxiv* (2017) [10.1101/165894](https://doi.org/10.1101/165894).

### Peer-reviewed Journal Articles

1. A network-based approach for isolating the chronic inflammation gene signatures underlying complex diseases towards finding new treatment opportunities.  
Hickey SL●, McKim A●, Mancuso CA, Krishnan A  
*Frontiers in Pharmacology* (2022) [Preprint] [Code: [chronic-inflammation](#)]
2. GenePlexus: A web-server for network-based machine learning for human gene classification.  
Mancuso CA, Bills P, Newsted J, Krum D, Liu R, Krishnan A  
*Nucleic Acids Research* (2022) [Web-server: [geneplexus.net](#)]
3. Systematic tissue annotations of genomics samples by modeling unstructured metadata.  
Hawkins NT, Maldaver M, Yannakopoulos A, Guare LA, Krishnan A  
Accepted in *Nature Communications* (2022). [Preprint] [Software: [Txt2Onto](#)]

4. Robust normalization & transformation techniques for constructing gene coexpression networks from RNA-seq data.  
Johnson KA, Krishnan A  
*Genome Biology* (2022) doi.org/10.1186/s13059-021-02568-9. [Code: [RNAseq\\_coexpression](#)]
5. Combinatorial patterns of gene expression changes contribute to variable expressivity of the developmental delay-associated 16p12.1 deletion.  
Jensen M, Tyryshkina A, Pizzo L, Smolen C, Das M, Huber E, Krishnan A, Girirajan S  
*Genome Medicine* (2021) doi.org/10.1186/s13073-021-00982-z.
6. Reconciling multiple connectivity scores for drug repurposing.  
Samart K●, Tuyishime P●, Krishnan A\*\*, Ravi J\*\*  
*Briefings in Bioinformatics* (2021) doi.org/10.1093/bib/bbab161. [Repo + Live document]
7. PecanPy: a fast, efficient, and parallelized Python implementation of *node2vec*.  
Liu R, Krishnan A  
*Bioinformatics* (2021) doi.org/10.1093/bioinformatics/btab202. [Software: PecanPy]
8. A flexible, interpretable, and accurate approach for imputing the expression of unmeasured genes.  
Mancuso CA●, Canfield JL●, Singla D, Krishnan A  
*Nucleic Acids Research* (2020) 48:e125. [Code + data: [Expresto](#)]
9. Supervised-learning is an accurate method for network-based gene classification.  
Liu R●, Mancuso CA●, Yannakopoulos A, Johnson KA, Krishnan A  
*Bioinformatics* (2020) 36:3457–3465. [Code + data: [GenePlexus](#)]
10. Functional assessment of the “two-hit” model for neurodevelopmental defects in *Drosophila* and *X. laevis*.  
Pizzo L●, Lasser M●, Yusuff T, Jensen M, Ingraham P, Huber E, ..., Krishnan A, Rolls M, Lowery LA, Girirajan S  
*PLoS Genetics* (2020) 17(4): e1009112.
11. Rare variants in the genetic background modulate the expressivity of neurodevelopmental disorders.  
Pizzo L, Jensen M, Polyak A, Rosenfeld JA, Mannik K, Krishnan A, ..., Amor DJ, Andrieux J, Girirajan S  
*Genetics in Medicine* (2019) 21:816-825.
12. A computational framework for genome-wide characterization of the human disease landscape.  
Lee Y, Krishnan A, Oughtred R, Rust J, Chang CS, Ryu J, Kristensen VN, Dolinski K, Theesfeld CL, Troyanskaya OG  
*Cell Systems* (2019) 8:152-162. [Web-server: [URSAhd](#)]
13. Pervasive genetic interactions modulate neurodevelopmental defects of the autism-associated *16p11.2* deletion in *Drosophila melanogaster*.  
Iyer J, Singh MD, Jensen M, Patel P, Pizzo L, Huber E, ..., Badano J, Manak JR, Rolls MM, Krishnan A, Girirajan S  
*Nature Communications* (2018) 9:2548.
14. GIANT 2.0: Genome-scale Integrated Analysis of gene Networks in Tissues.  
Wong AK, Krishnan A, Troyanskaya OG  
*Nucleic Acids Research* (2018) 46:W65–W70. [Web-server: [GIANT-v2](#)]
15. A loop-counting method for covariate-corrected low-rank biclustering of gene-expression and genome-wide association study data.  
Rangan AV, McGrouther CC, Kelsoe J, Schork N, Stahl E, Zhu Q, Krishnan A, Yao V, Troyanskaya OG, ..., Raghavan P, Bergen S, Jureus A, Landen M, Bipolar Disorders Working Group of the Psychiatric Genomics Consortium  
*PLoS Computational Biology* (2018) 14: e1006105.
16. RECoN: Rice Environment Coexpression Network for systems-level analysis of abiotic-stress response.  
Krishnan A, Gupta C, Ambavaram MMR, Pereira A  
*Frontiers in Plant Science* (2017) 8:1640. [Web-server: [RECoN](#)]
17. Integrative networks illuminate biological factors underlying gene-disease associations.  
Krishnan A\*\*, Taroni JN, Greene CS\*\*  
*Current Genetic Medicine Reports* (2016) 4:155-162.
18. Genome-wide prediction and functional characterization of the genetic basis of autism spectrum disorder.  
Krishnan A●, Zhang R●, Yao V, Theesfeld CL, Wong AK, Tadych A, Volfovsky N, Packer A, Lash A, Troyanskaya OG  
*Nature Neuroscience* (2016) 19:1454-1462. [Web-server: [ASD](#)]
19. IMP 2.0: A multi-species functional genomics portal for integration, visualization and prediction of protein functions and networks.

- Wong AK, Krishnan A, Yao V, Tadych A, Troyanskaya OG  
*Nucleic Acids Research* (2015) 43:W128-133.
20. FNTM: a server for predicting Functional Networks of Tissues in Mouse.  
Goya J●, Wong AK●, Yao V●, Krishnan A, Homilius M, Troyanskaya OG  
*Nucleic Acids Research* (2015) 43:W182-W187.
  21. Low variance RNAs identify Parkinson's disease molecular signature in blood.  
Chikina MD, Gerald CP, Li X, Ge Y, Pincas H, Nair VD, Wong AK, Krishnan A, ..., Bressman SB, Yue Z, Sealfon SC  
*Movement Disorders* (2015) 30:813-821.
  22. Understanding multicellular function and disease with human tissue-specific gene interaction networks.  
Greene C●, Krishnan A●, Wong AK●, Ricciotti E, Zelaya R, Himmelstein DS, Zhang R, Hartmann BM, Zaslavsky E, Sealfon SC, Chasman D, FitzGerald G, Dolinski K, Grosser T, Troyanskaya OG  
*Nature Genetics* (2015) 47:569-576. [Web-server: [GIANT](#)]
  23. Targeted exploration and analysis of large cross-platform human transcriptomic compendia.  
Zhu Q, Wong AK, Krishnan A, ..., Charikar M, Li K, Troyanskaya OG  
*Nature Methods* (2015) 12:211-214. [Web-server: [SEEK](#)]
  24. Tissue-aware data integration approach for the inference of pathway interactions in metazoan organisms.  
Park C, Krishnan A, Zhu Q, Wong AK, Lee Y, Troyanskaya OG  
*Bioinformatics* (2015) 31:1093-1101. [Web-server: [PathwayNet](#)]
  25. Rice GROWTH UNDER DROUGHT KINASE is required for drought tolerance and grain yield under normal and drought stress conditions.  
Venkategowda R, Basu S, Krishnan A, Pereira A  
*Plant Physiology* (2014) 166:1634-1645.
  26. Drought responsive genes and their functional terms identified by GS FLX Pyro sequencing in maize.  
Batlang U, Ambavaram MMR, Krishnan A, Pereira A  
*Maydica* (2014) 59: 306-314.
  27. Coordinate regulation of photosynthetic carbon metabolism for yield and environmental stress response in rice.  
Ambavaram MM, Basu S, Krishnan A, Venkategowda R, Batlang U, Rahman L, Baisakh N, Pereira A  
*Nature Communications* (2014) 5:5302.
  28. Reconciling differential gene expression data with molecular interaction networks.  
Poirel CL, Rahman A, Rodrigues RR, Krishnan A, Addesa JR, Murali TM  
*Bioinformatics* (2013) 29:622-629.
  29. Ontology-aware classification of tissue and cell-type signals in gene expression profiles across platforms and technologies.  
Lee Y, Krishnan A, Zhu Q, Troyanskaya OG  
*Bioinformatics* (2013) 29:3036-3044. [Web-server: [URSA](#)]
  30. Stochastic modeling of dwell-time distributions during transcriptional pausing and initiation.  
Xu X, Kumar N, Krishnan A, Kulkarni R  
*52nd IEEE Conference on Decision and Control* (2013) 4068-4073.
  31. Effects of drought on gene expression in maize reproductive and leaf meristem tissue revealed by RNA-Seq.  
Kakumanu A, Ambavaram MM, ..., Krishnan A, ..., Myers E, Grene R, Pereira A  
*Plant Physiology* (2012) 160:846-867.
  32. Coordinated activation of cellulose and repression of lignin biosynthesis pathways in rice.  
Ambavaram MM●, Krishnan A●, Trijatmiko KR, Pereira A  
*Plant Physiology* (2011) 155:916-931.
  33. Molecular and physiological analysis of drought stress in Arabidopsis reveals early responses leading to acclimation in plant growth.  
Harb A, Krishnan A, Pereira A  
*Plant Physiology* (2010) 154:1254-1271.
  34. Mechanisms of action and medicinal applications of abscisic acid.  
Bassaganya-Riera J, Skoneczka J, Kingston DG, Krishnan A, ..., Pereira A, Guri AJ, Tumarkin R, Hontecillas R  
*Current Medicinal Chemistry* (2009) 17:467-478.

35. Diversity of En/Spm transposons in maize and rice.  
Krishnan A, Greco R, Pereira A  
*Maydica* (2009) 53:181-187.
36. Mutant resources in rice for functional genomics of the grasses.  
Krishnan A, Guiderdoni E, An G, ..., Ramachandran S, Zhang Q, Sundaresan V, Hirochika H, Leung H, Pereira A  
*Plant Physiology* (2009) 149:165-170.
37. Integrative approaches for mining transcriptional regulatory programs in Arabidopsis.  
Krishnan A, Pereira A  
*Briefings in Functional Genomics and Proteomics* (2008) 7:264-274.
38. Improvement of water use efficiency in rice by expression of HARDY, an Arabidopsis drought & salt tolerance gene.  
Karaba A, Dixit S, Greco R, Aharoni A, Trijatmiko KR, Marsch-Martinez N, Krishnan A, ..., Udayakumar M, Pereira A  
*Proceedings of the National Academy of Sciences USA* (2017) 104:15270-15275.

## Book Chapters

1. Microarray data analysis.  
Mohapatra SK, Krishnan A  
*Plant Reverse Genetics. Methods in Molecular Biology* (2009) vol 678. Humana Press, Totowa, NJ.
2. Genetic networks underlying plant abiotic stress responses.  
Krishnan A, Ambavaram MMR, Harb A, Batlang U, Wittich PE, Pereira A  
*Genes for Plant Abiotic Stress* (2009) John Wiley & Sons, Inc., Ames IA, USA.

## SOFTWARE, DATABASES, AND WEB-SERVERS

1. Text-based omics sample annotation using NLP
  - [Txt2Onto](#): A Python tool for tissue classification using natural language processing and machine learning  
Designed to infer tissue annotations to a million human -omics samples based on their unstructured metadata.
2. Network-based gene classification with GenePlexus
  - [GenePlexus\\_benchmark](#): Benchmarking framework for network-based gene classification  
Code and data for supervised learning to classify genes to functions, traits, and diseases based on their molecular network patterns.
  - [GenePlexus.net](#): A webserver for network-based machine learning for human gene classification  
An interactive web-interface for researchers to leverage human genome-scale gene networks to expand their gene sets of interest.
  - [PyGenePlexus](#): A Python package of the GenePlexus analysis pipeline.  
A streamlined codebase for computational researchers to incorporate geneplexus into their workflows.
3. [RNAseq\\_coexpression](#): Code to build genome-scale coexpression networks from RNA-seq datasets  
Also contains data and scripts to perform a systematic evaluation of methods for coexpression network construction.
4. [PecanPy](#): Parallelized, efficient, and accelerated *node2vec* software written in Python  
The current best implementation of *node2vec* that can create numerical embeddings for nodes in very large and dense graphs.  
Also, contains an implementation of *node2vec+*, an improved version that better leverages weighted graphs.
5. [Expresto](#): Software for flexible sparse-regression methods to impute the expression of unmeasured genes  
Implements *SampleLASSO*, a method to complete partially measured human transcriptomes from various platforms and technologies.
6. [ASD](#): A webserver for gene candidates associated with autism spectrum disorder  
Genome-wide prediction of autism-associated genes in the context of a human brain-specific gene interaction network.
7. [GIANT](#): A webserver for human tissue-specific genome-scale gene interaction networks  
Gene functional interaction networks specific to hundreds of human tissues and cell types.

## FUNDING

### Active External Research Awards

NIH NIAID R21 AI169301

Krishnan (PI)

05/22 – 04/24

Mechanism-guided drug repurposing for host-directed therapy of infectious diseases using interpretable, integrative ML

**Role:** PI; **Funding:** \$414,047 (total)

This project aims to develop interpretable machine learning methods that integrate drug gene signatures, disease-gene associations, and gene interaction network models to predict host-directed therapies for infectious diseases.

NSF BIO DBI CAREER 2045651 Krishnan (PI) 05/21 – 04/26  
 Assigning comprehensive, standardized sample annotations to enhance the ability to discover, use, and interpret millions of –omics profiles  
Role: PI; Funding: \$704,889 (total)

This project aims to develop new machine learning methods that use both text and molecular data to assign comprehensive, standardized annotations to nearly 2 million publicly-available –omics samples.

NIH NIGMS R35 GM128765 Maximizing Investigators' Research Award Krishnan (PI) 09/18 – 08/23  
 Resolving and understanding the genomic basis of heterogeneous complex traits and diseases  
Role: PI; Funding: \$1,750,550 (total)

This project aims to develop a suite of computational frameworks that integrate massive collections of genomic and biomedical data to unravel subtypes, age/sex differences, and cross-species analogs of a range of complex disorders.

NIH NIGMS R35 GM128765-04S1 Software Supplement Krishnan (PI) 08/21 – 07/22  
 GenePlexus: a cloud platform for network-based machine learning  
Role: PI; Funding: \$234,750 (total)

This project aims to develop a cloud platform that will enable both biologists and bioinformaticians to easily perform network-based machine learning on massive genome-scale molecular networks and get novel interpretable predictions about gene attributes of interest.

NSF BIO IOS PGRP 1950376 Farre (PI) 05/20 – 04/24  
 MCA-PGR: Cycling below-ground: Circadian regulation in wild and domesticated potato  
Role: Co-PI; Funding: \$13,046 over years 2 & 3 | \$2,206,530 (total)

This project's goal is to understand how circadian rhythms contribute to the development of heterotrophic organs and adaptation to different photoperiods in terms of quantitative loci, functional genomics, and gene regulatory networks.

[Award to mentee] Brain & Behavior Research Foundation's Young Investigator Grant Hickey (PI) 01/22 – 01/24  
 Predicting gene relationships across time and space to identify age- & brain-region-specific treatments for schizophrenia  
Role: Mentor; Funding: \$70,000 (total)

This project aims to develop methods to integrate massive gene expression data collections to build genome-scale gene networks specific to the aging brain and identify druggable targets for schizophrenia.

[Award to mentee] NIH F32 Kirschstein-NRSA Postdoctoral Fellowship, NIGMS Mancuso (PI) 09/19 – 08/22  
 Incorporating molecular network knowledge into predictive data-driven models  
Role: Mentor; Funding: \$190,962 (total)

This project aims to develop methods to infuse prior-knowledge into state-of-the-art data-driven statistical/machine learning models for classifying, interpreting, and translating gene-expression data.

### Active Internal Research Awards

Ecology and Evolutionary Biology Seed Funds Malmstrom, Krishnan, Mauck (Multi-PI) 05/22 – 07/22  
 What makes a virus pathogenic? Using ML to distinguish genomic signatures of virulence in crop and wild viruses  
Role: PI; Funding: \$18,000 (total)

This pilot project is to use machine learning to identify the genomic hallmarks of pathogenicity in RNA viruses.

MSU-DFI Discretionary Funding Initiative Zacharewski (PI) 01/21 – 07/22  
 Does thermoneutrality improve the modeling of toxicant associated fatty liver disease (TAFLD)/toxicant associated steatohepatitis (TASH) in humans?  
Role: Co-PI; Funding: \$50,000 (total)

This pilot project is to study different doses of the persistent environmental contaminant TCDD in mice under thermoneutral temperatures.

BMB Team Research Award 2020 Krishnan, Montgomery, Munch, Chitwood (Multi-PI) 08/20 – 07/22  
 Connecting gene regulatory networks to morphology using topological data analysis and machine learning  
Role: PI (among multiple PIs); Funding: \$109,000 (direct)

This pilot grant is to develop applications of topological data analysis & machine learning to study the molecular basis of plant morphology.

[Awards to mentees] NRT IMPACTS T32 Graduate student (listed below) 01/19 – 12/23  
 Role: Co-advisor (with another MSU faculty member); Funding: 1 year of graduate fellowship (direct)

Nick Moreno (2022): Role of the endogenous circadian clock on potato primary metabolism



Christina Chiu (2021): Transcriptomic and metabolomic network analysis of iron deficiency-induced coumarin secretion pathways

Miles Roberts (2020): Genomic basis of trade-offs in plants with a combination of genome-wide association and simulation

Fabio Gomez-Cano (2019): Characterizing gene regulatory networks in maize

### Active External Education Awards

G-2021-16976 Alfred P Sloan Foundation Stephens (PI) 01/22 – 12/24  
Creating equitable pathways to advanced degrees in data science, a Spelman MSU partnership

Role: Senior Personnel; Funding: \$500,000 (total)

This project will develop a Data Science minor at Spelman at Spelman College, Atlanta (supplementing a 3+2 BS-MS Spelman-MSU program), strengthen and diversify the pipeline of data science students, and train the trainers through faculty development.

2123260 NSF HDR-Harnessing the Data Revolution Christlieb (PI) 09/21 – 08/24  
Collaborative Research: HDR DSC: Increasing Accessibility through Building Alternative Data Science Pathways

Role: Senior Personnel; Funding: \$1,022,778 (total)

This project will develop a 3+2 program that allows students to complete their BS in a STEM field (e.g., Mathematics, Physics, Biology) at Spelman College, Atlanta and complete a MS in Data Science.

1949912 NSF REU Site O'Shea (PI) 04/20 – 03/23  
ICER Advanced Computational Research Experience for Students

Role: Co-PI; Funding: \$401,234 (total)

This award offers students the opportunity to conduct cutting-edge research in computational and data science under the supervision of faculty who are recognized experts in their disciplines.

### Completed Awards

(External) Google exploreCSR Krishnan, Kerzendorf (Multi-PI) 10/20 – 06/21

MSU Explore Computational Research Experience

Role: PI (among multiple PIs); Funding: \$18,000 (total)

This program provided computing research experiences at MSU for URM students in Michigan community colleges.

(Internal) BMB Team Research Award 2019 Krishnan, He, Arnosti, Ralston (Multi-PI) 06/19 – 05/21

Gene regulation in single cells

Role: PI (among multiple PIs); Funding: \$109,000 (direct)

This pilot grant was to develop methods to analyze and integrate single-cell transcriptome and ATAC-Seq data in multiple model systems.

(External) NIH NCATS OT2 Single Component Research Project Chen (PI) 01/20 – 05/20

Drug biomarker resources for precise translational research

Role: Co-I; Funding: \$133,616 (total)

This project kickstarted a novel knowledge source for biomarker discovery to improve drug-biomarker-disease-patient associations.

(External) Thorek Memorial Foundation Lipton, Vega (Multi-PI) 01/17 – 12/19

A High Throughput Process to Study Interacting Genetic Risk Factors in Disease through Informatics and Gene Modification

Role: Subawardee; Funding: \$4,200 over two years (direct)

This project developed combinatorial gene manipulation and functional screen (COGMAS) using genomic data and network analyses.

(Internal) BEACON Center for the Study of Evolution in Action Thompson (PI) 05/18 – 04/19

Developing methods to detect functional evolutionary change in expression profiles of rapidly evolving killifishes

Role: Co-I; Funding: \$12,000 (direct)

This pilot project was to develop methods to detect functional evolutionary change in expression profiles of rapidly evolving killifishes.

## TALKS, CONFERENCES

### Invited Talks, Panels, Workshops | External

- 2022: Rhetor 3.0, Symposium of Proteus, the Biology Club of IISER Thiruvananthapuram [Upcoming]
- 2022: Aquatic Models of Human Disease Conference
- 2022: Plenary | Complex Trait Community and the Rat Genomics & Models Community, 19th Annual Meeting

- 2022: NCI Data Science Seminar Series
- 2022: Future Directions in Network Biology, University of Notre Dame
- 2022: Systems Biology Club, Dept. Molecular Cell Biology, Weizmann Institute of Science
- 2022: Artificial Intelligence in Pediatrics, Great Lakes Pediatric Research Day
- 2022: Great Lakes Pediatrics Research Day – Panel on artificial intelligence (AI)
- 2022: NSF Data Science Working Group, Chicago
- 2022: Biostatistics Seminar, University of Tennessee Health Science Center
- 2021: Life Science Trainers How I teach Life Scientist Seminar
- 2021: Biochemistry/Chemistry Seminar, Purdue University Fort Wayne
- 2021: Center for Health Artificial Intelligence, University of Colorado
- 2021: Biology Seminar, Hope College, Holland, Michigan
- 2021: NIH Data Sharing and Reuse Seminar Series
- 2021: African Institute for Mathematical Sciences, Rwanda
- 2021: High End Workshop on Computational Biology & Data Science, SASTRA University, India
- 2019: Computer Science Colloquium, Marquette University, Wisconsin
- 2019: Biology on Tap – Public Lecture, Lansing
- 2018: Genetics Seminar, Rutgers University
- 2017: Wartik Genomics Seminar, Pennsylvania State University
- 2016: Cancer Institute of New Jersey, Rutgers University
- 2015: Sanofi Big Data Symposium, Genzyme, Boston
- 2014: Systems Pharmacology and Translational Therapeutics Seminar, University of Pennsylvania
- 2014: Institute for Mathematical Sciences, Chennai, India
- 2014: Indian Institute of Technology Madras, India
- 2014: National Center for Biological Sciences, India
- 2014: Centre for Cell and Molecular Biology, India
- 2014: University of Hyderabad, India

### Invited Talks, Panels | Internal

- 2022: Computational Biosciences Seminar
- 2022: GGS Symposium: Precision Genomics: Beating Big Data Bottlenecks
- 2020: Translational Science Seminar, MSU College of Medicine
- 2019: Board of Trustees Meeting, Michigan State University
- 2015: Princeton Area Yeast Meeting, Princeton University
- 2014: Postdoctoral Seminar Series, Princeton University
- 2013: Integrated Science Shorts, Princeton University

### Conference & Workshop Talks

- 2022: Intelligent Systems for Molecular Biology (ISMB), ISCB
- 2022: Organization for the Study of Sex Differences (OSSD), California
- 2022: NSF workshop: Leveraging AI and Data Science for Predicting Mechanisms
- 2021: Intelligent Systems for Molecular Biology (ISMB), ISCB
- 2021: Teaching Science with Big Data, ASBMB
- 2021: Great Lakes Bioinformatics Conference, Minnesota
- 2020: Biological Data Science Meeting, Cold Spring Harbor Laboratories
- 2020: Gateways2020, Science Gateways Community Institute
- 2019: Great Lakes Bioinformatics Conference, Madison
- 2019: Conference in Computational Health, Grand Rapids
- 2019: ASBMB Symposium on Evolution and Core Processes in Gene Expression, Michigan State University
- 2018: Big Data Ignite Conference, Grand Rapids
- 2015: RECOMB/ICSB Conference on Regulatory and Systems Genomics, Philadelphia
- 2015: Complex Systems Digital Campus World e-Conference

- 2015: Leveraging Big Data and Predictive Knowledge to Fight Disease, New York Academy of Sciences
- 2014: ICSB-RECOMB Systems Genomics Conference, San Diego

## Posters

- 2022: Sex Differences Across the Lifespan, Colorado Springs
- 2015: Genome Informatics, Cold-Spring Harbor Laboratories [*Best Poster Award; out of 167 posters*]
- 2014: CIFAR: Genetic Networks Meeting, University of Washington
- 2014: CIFAR: Genetic Networks Meeting, Dana-Farber Cancer Institute, Harvard Medical School
- 2011: Systems Biology, Networks, Cold-Spring Harbor Laboratories
- 2010: Networks Biology Workshop, Mathematical Biosciences Institute, Ohio State University

## TEACHING

### Bioinformatics and Computational Biology | CMSE 410 & 890-005

Spring 2018–Present | Introduction to the inner-workings of analytical techniques, algorithms, and statistical/machine-learning approaches to address questions in biology and medicine. Students also learn how to formulate computational problems, design projects, critically think about data and methods, conduct reproducible research, and effectively communicate findings.

### Gaps, Missteps, and Errors in Data Analysis | BMB 961-301, CMSE 890-310

Fall 2018–Present | A short course on common misunderstandings and typical errors in the practice of statistical data analysis, and providing a mental toolkit for critically thinking about statistical methods and results. Involves lectures, discussions, and hands-on coding-based statistics/data-analysis exercises.

### Introduction to Computational Modeling & Data Analysis | CMSE 201

Fall 2019 | Flipped-class introduction to computational science, computational skills, and application-driven modeling of various systems, with applications to the physical, life, and social sciences, and to engineering and mathematics.

### University-wide Bioinformatics Workshops @ MSU

Summer 2017 | Intensive hands-on training in Linux/R/Python programming, Statistical data analysis and visualization, and Analysis of various types of genomic data (e.g., RNA-seq) to undergraduates, PhD students, and faculty members. The course materials form the basis of the 1-credit Bioinformatics modular courses, which I and others have now taught to >300 learners from >15 departments at MSU.

## MENTORING AND PROFESSIONAL DEVELOPMENT

### Team Members / Mentees

Postdoctoral Researchers (03)		Graduate Students (09)		Undergraduate Students (22)	
Current	Sarah Percival	Current	Kayla Johnson	Current	Filip Jevtic
Past	S. Hickey C. Mancuso		Renming Liu Alex McKim Hao Yuan Kewalin Samart	Past	A. Agarwal, A. Almounajed, M. Artuso, N. Davis, L. Guare, A. Hashsham, E. Hunter, J. Lee, R. Liu, M. Maldaver, A. Metto, G. Murali, C. Nnawulezi, K. Samart, D. Singla, J. Santaniello, S. Sundar, P. Tuyishime, J. Vasquez, S. Vatti, K. Warfle
		Past	N. Hawkins A. Yannakopoulos		
		Rotation	F. Mir, R. Fidis, M. Eithun		
Research Scientists (03)		Post-bac Researchers (02)		High School Students (07)	
Current	Christopher Mancuso Stephanie Hickey Mansooreh Ahmadian	Current	Jacob Krol	Past	R. Banerjee, E. Bruce, D. Gomez, N. Kanneganti, A. Ge, T. Kiker, J. Shah
		Past	J. Canfield		



## Honors and Awards to Mentees

Christopher Mancuso	NIGMS NIH Kirschstein-NRSA Postdoctoral Fellowship (F32)
Stephanie Hickey	Brain & Behavior Research Foundation's Young Investigator Grant
Anna Yannakopoulos	MSU Engineering Distinguished Graduate Fellowship
Kayla Johnson	Honorable Mention, NSF Graduate Research Fellowship Program (GRFP) Outstanding Graduate Student Award, Biochemistry and Molecular Biology
Alex McKim	MSU Engineering Distinguished Graduate Fellowship
Renming Liu	Outstanding Graduate Student Award, Computational Math, Science & Engineering
Nathaniel Hawkins	Rasmussen Doctoral Recruitment Award MSU Engineering Distinguished Graduate Fellowship
Jake Canfield	MSU Undergraduate Physiology Research Award and Service Award
Kewalin Samart	McCartney Endowed Educational Enrichment Fund (Math) Engineering Distinguished Graduate Fellowship Rasmussen Doctoral Recruitment Award
Matthew Artuso	Rasmussen Doctoral Recruitment Award

## Student Graduate Committees

### MSU Graduate Students (22)

Current		Mehrsa Mardikoraem	Chemical Engineering
Muneeza Azmat	Biomedical Engineering	Ana-Maria Raicu	Biochemistry & Molecular Biology
Al Masraf Basma	Cell & Molecular Biology	Warren Sink	Env & Integrative Toxicological Sci
Danielle Barnes	Computational Math, Science & Egr	Ethan Tu	Biomedical Engineering
Emily Bolger	Computational Math, Science & Egr		
Evan Brenner	Comparative Med & Integrative Bio	Past	
David Filipovic	Biomedical Engineering	Reid Blanchett	Neuroscience
Fabio Gomez	Biochemistry & Molecular Biology	Christine Ponnampalam	Genetics & Genome Sciences
MacKenzie Jacobs	Molecular Plant Sciences	Justin Lee	Microbiology & Molecular Genetics
Thilani Jayakody	Plant Breeding, Genetics & Biotech	Samuel Lotz	Molecular Biophysics
Omar Kana	Biomedical Engineering	Serena Lotreck	Plant Biology; CMSE
Nick Moreno	Biochem & Molc. Plant Science	Brian Nohomovich	Microbiology & Molecular Genetics
		Wei Wang	Computer Science & Engineering

External thesis examiner: Amrita School of Engineering, India

## Professional Development

- 2022–: Mentor, CU Anschutz Women in STEM
- 2022: CU Anschutz NRSA Mock Study Section
- 2020–2022: Advisory Board, *Plant Postdocs*
- 2018–2020: *Surviving, Enjoying, and Excelling in your PhD*  
Conducted at MSU and Rutgers University
- 2018–: *Planning and Executing an Effective Postdoc Training*  
Conducted at MSU, Rutgers University, and Plant Postdoc Online Community.
- 2017, 2018: Session on *Faculty Job Search* | Conducted at MSU.

## CONTRIBUTIONS TO DIVERSITY, EQUITY, AND INCLUSION

### Research Mentoring Trainees from Underrepresented Groups

#### High-school students (03)

- Female: R Banerjee, N. Kanneganti
- African American: E. Bruce

#### Undergraduate students (11)

- African American + Female: E. Hunter, A. Metto, C. Nnawulezi, P. Tuyishime
- Latinx: J. Vasquez
- Female: L. Guare, K. Samart, J. Santaniello, S. Sundar, S. Vatti, K. Warfle

**Graduate students (05)**

- Female: K. Johnson, K. Smart, A. Yannakopoulos, F. Mir [rotation]
- African American: R. Fidis [rotation]

**Postdocs, Research Scientists (03)**

- Female: M. Ahmadian, S. Hickey, S. Percival

**Leadership of Programs for Research & Training for URM Students and Community Members**

- **PI: MSU Explore Computational Research Experience (Google exploreCSR)**  
Computing research experience for undergrads in Michigan community colleges from extremely underrepresented backgrounds.
- **Senior Personnel: Increasing Accessibility through Building Alternative Data Science Pathways (NSF HDR-DSC)**  
A BS/MS program between Spelman College (Atlanta), a historically black liberal arts college for women, and MSU.
- **Faculty Advisor: *R-Ladies East Lansing*, >500-member local chapter of R-Ladies Global**  
Provides a safe space for women and gender minorities to learn, present, and discuss R and data science.

**Mentorship on Research, Career Path, and Professional Development**

- 2022–: Mentor for junior researchers — Women in STEM (WiSTEM), CU Anschutz
- 2022: St. Mary's Academy High School (for girls) via the WiSTEM High School Mentorship Program, CU Anschutz
- 2021: Onsite Undergraduate Research+Mentorship, Anna Louise James Minority Pre-Pharmacy Organization, MSU
- 2021: Mentor – Machine Learning for Health (ML4H) Conference Submission Mentorship Program
- 2020: Charles Drew Science Scholars program, MSU; Emphasis on historically underrepresented groups in STEM
- 2019: Females in STEM student group at East Lansing High School, MI
- 2017: Latinos-2-College Program for high school students (8<sup>th</sup>-10<sup>th</sup> grade) from the Lansing School District

**Membership in Departmental DEI Committees, Interest Groups**

- MSU: Dept. of Computational Math, Science & Engineering and Dept. of Biochemistry and Molecular Biology
- CU Anschutz: Dept. of Biomedical Informatics

**OUTREACH**

- 2020: Open bioinformatics primers and co-work sessions
- 2019: “Biology on Tap” public talk on “Data & algorithms for better health & medicine”.
- 2018: “Skype a Scientist” – 1 hour Q and A sessions with classrooms across the world.
- 2009, 2010: “Mutant plants!” – education booths at Virginia Tech and at the USA Science & Engineering Festival.

**SERVICES AND PROFESSIONAL MEMBERSHIPS****University and Departmental Services**

- Faculty search committee membership:
  - Chair: Fixed-Term Assistant Professor, Dept. Computational Math, Sci. and Engr. (CMSE) 2020–2021
  - Member: TT Assistant Professor, Precision Pediatrics and Human Genomics 2018–2019
  - Member: TT Assistant Professor, CMSE & Biomedical Engineering 2018–2019
- Departmental committee membership:
  - Postdoc mentoring, Dept. Computational Math, Sci. and Engr. (CMSE) 2021–2022
  - Diversity, equity, and inclusion, Dept. Biochemistry and Molecular Biology 2020–2022
  - Diversity, equity, and inclusion, CMSE 2020–2021
  - Graduate studies, CMSE 2018–2019
  - Data science curriculum, CMSE 2019–2020
  - Advisory committee, CMSE 2018–2020
  - Long-term planning, CMSE 2019–2020
- University-level committee membership:
  - Biomedical Sciences Program Admissions 2022–Present
  - Research Implementation Team, MSU 2022
  - Executive Committee, Cell and Molecular Biology graduate program, MSU 2021–2022

- Center for Research in Autism, Intellectual & other Neurodevelopmental Disabilities, MSU 2019–2022
- Trifecta Initiative for Interdisciplinary Health Research, MSU 2020–2022

### Membership and Services in Professional Communities

- Guest Editor, *PLoS Computational Biology* 2021–Present
- Session Chair, Organization for the Study of Sex Differences 2022
- Posters Co-chair/Chair, Intelligent Systems for Molecular Biology (ISMB) 2017–2019
- Program committee:
  - Great Lakes Bioinformatics Conference 2019, 2021
  - Intelligent Systems for Molecular Biology 2021–2022
- Faculty Fellow (Teaching & Technology) at the Hub@MSU 2019–2020
- Science Ambassador – Science Gateways Community Institute 2019–2020

### Peer Review

- Academic Journals (25):  
*BioData Mining* | *Bioinformatics* | *BMC Bioinformatics* | *Briefings in Bioinformatics* | *Circulation: Cardiovascular Genetics* | *F1000 Research* | *G3: Genes, Genomes, Genetics* | *Genome Biology* | *IEEE/ACM Transactions on Computational Biology and Bioinformatics* | *Journal of Theoretical Biology* | *Journal of Transactions on Computational Biology and Bioinformatics* | *Journal of Machine Learning* | *Molecular Autism* | *Molecular Breeding* | *mSystems* | *Nature Communications* | *Nature Neuroscience* | *npj Systems Biology and Applications* | *Nucleic Acids Research* | *Plant Physiology* | *Plant Molecular Biology* | *PLoS Computational Biology* | *PLoS ONE* | *Proceedings of the National Academy of Sciences* | *Reviewer Commons* | *Scientific Reports*
- Academic Conferences (05):
  - Intelligent Systems for Molecular Biology
  - Great Lakes Bioinformatics Conference
  - Pacific Symposium of Biocomputing
  - ACM Conference on Bioinformatics and Computational Biology
  - Annual Biomedical Research Conference for Minority Students
- Post-publication review: F1000 Biology 2008–2011
- Funding Agencies (02)
  - National Science Foundation
    - Ad-hoc reviewer of proposals/applications 2017, 2019–2022
  - National Institutes of Health
    - Biodata Management and Analysis Study Section 2019, 2021
    - Ad-hoc reviewer 2020, 2022