

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

2017–Present	Assistant Professor Dept. of Computational Math, Science, and Engineering Dept. of Biochemistry and Molecular Biology	Michigan State University East Lansing, MI, USA
2013–2016 2011–2013	Associate Research Scholar Postdoctoral Research Associate Lewis-Sigler Institute for Integrative Genomics	Princeton University Princeton, NJ, USA
2010–2011 2006–2010	Postdoctoral Research Associate Graduate Research Assistant Virginia Bioinformatics Institute	Virginia Tech Blacksburg, VA, USA

PUBLICATIONS

[• Co-primary authors] [** Co-corresponding authors]

Preprints

1. Accurately modeling biased random walks on weighted graphs using *node2vec+*.
Liu R, Hirn M**, Krishnan A**
[arXiv \(2021\) 2109.08031](https://arxiv.org/abs/2021.08031). [Software: [PecanPy 2.0](#)]
2. Systematic tissue annotations of –omics samples by modeling unstructured metadata.
Hawkins NT, Maldaver M, Yannakopoulos A, Guare LA, Krishnan A
[bioRxiv \(2021\) 10.1101/2021.05.10.443525](https://arxiv.org/abs/2021.05.10.443525). [Software: [Txt2Onto](#)]
3. 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
[bioRxiv \(2021\) 10.1101/2021.03.06.434203](https://arxiv.org/abs/2021.03.06.434203).
4. Robust normalization & transformation techniques for constructing gene coexpression networks from RNA-seq data.
Johnson KA, Krishnan A
[bioRxiv \(2020\) 10.1101/2020.09.22.308577](https://arxiv.org/abs/2020.09.22.308577). [Code: [RNAseq_coexpression](#)]
5. 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://arxiv.org/abs/2020.05.19.104935).
6. 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://arxiv.org/abs/2017.10.1101/165894).

Peer-reviewed Journal Articles

1. 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](https://doi.org/10.1093/bib/bbab161). [Repo + [Live document](#)]
2. PecanPy: a fast, efficient, and parallelized Python implementation of *node2vec*.
Liu R, Krishnan A
[Bioinformatics \(2021\) doi.org/10.1093/bioinformatics/btab202](https://doi.org/10.1093/bioinformatics/btab202). [Software: [PecanPy](#)]

3. 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](#)]
4. 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](#)]
5. 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.
6. 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.
7. 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-interface: [URSAhd](#)]
8. 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.
9. 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-interface: [GIANT-v2](#)]
10. A loop-counting method for covariate-corrected low-rank biclustering of gene-expression and genome-wide association study data.
Rangan AV, McGruther 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.
11. 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-interface: [RECoN](#)]
12. Integrative networks illuminate biological factors underlying gene-disease associations.
Krishnan A**, Taroni JN, Greene CS**
Current Genetic Medicine Reports (2016) 4:155–162.
13. 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-interface: [ASD](#)]
14. 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.
15. 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.
16. 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.
17. 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-interface: [GIANT](#)]

18. 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-interface: [SEEK](#)]
19. 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-interface: [PathwayNet](#)]
20. 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](#).
21. 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](#).
22. 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](#).
23. 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](#).
24. 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-interface: [URSA](#)]
25. 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](#).
26. 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](#).
27. 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](#).
28. 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](#).
29. 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](#).
30. Diversity of En/Spm transposons in maize and rice.
Krishnan A, Greco R, Pereira A
[Maydica \(2009\) 53:181-187](#).
31. 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](#).
32. Integrative approaches for mining transcriptional regulatory programs in Arabidopsis.
Krishnan A, Pereira A
[Briefings in Functional Genomics and Proteomics \(2008\) 7:264-274](#).
33. 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. Mohapatra SK, **Krishnan A** (2009) Microarray data analysis. *Plant Rev. Genet.* Humana Press Inc., Totowa NJ, USA.
2. **Krishnan A**, Ambavaram MMR, Harb A, Batlang U, Wittich PE, Pereira A (2009) Genetic networks underlying plant abiotic stress responses. *Genes for Plant Abiotic Stress.* John Wiley & Sons, Inc., Ames IA, USA.

SOFTWARE AND WEB SERVERS

1. **Txt2Onto**: A Python tool for text-based 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. **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
3. **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.
4. **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.
5. **GenePlexus**: 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.
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 Research Awards | Extramural

NSF BIO DBI 2045651 Krishnan (PI) 05/21 – 04/26
 CAREER: 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 R35 GM128765 Maximizing Investigators' Research Award, NIGMS 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 R35 GM128765-04S1 Software Supplement, NIGMS 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] 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 Research Awards | Internal

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.

MSU-DFI Discretionary Funding Initiative Zacharewski (PI) 01/21 – 01/22
 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.

[Awards to mentees] NRT IMPACTS T32 2019, 2020, 2021 Gomez-Cano, Chiu, Roberts (PI in each year) 01/19 – 12/22
Role: Co-advisor (with another MSU faculty member); Funding: 1 year of graduate fellowship (direct)

Christina Chiu: Transcriptomic and Metabolomic Network Analysis of Iron Deficiency- Induced Coumarin Secretion Pathways
 Miles Roberts: G basis of trade-offs in plants with a combination of genome- wide association and simulation
 Fabio Gomez-Cano: Characterizing gene regulatory networks in Maize

Active Education Awards | Extramural

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.

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 will provide undergraduate students in Michigan community colleges from extremely underrepresented backgrounds the opportunity to engage in a computing research experience at MSU.

Completed Awards

(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.

(Extramural) 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.

(Extramural) 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 | **External**

- 2021: Center for Health Artificial Intelligence, University of Colorado [Upcoming]
- 2021: Biochemistry/Chemistry Seminar, Purdue University Fort Wayne [Upcoming]
- 2021: NSF Data Science Working Group, Chicago [Upcoming]
- 2021: Biology Seminar, Hope College, Holland, Michigan [Upcoming]
- 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 | **Internal**

- 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 Talks

- 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] 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 methods in bioinformatics and computational biology: key analytical techniques, algorithms, and statistical/machine-learning approaches developed to address questions in biology and medicine. Students will 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 Statistical Data Analysis | BMB 961-301, CMSE 890-310

Fall 2018–Present | A short course discussing 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 various aspects of computational science, computational skills, and application-driven modeling of various systems, with applications to the physical, life, and social sciences, and also to engineering and mathematics. Each class involves students doing group-based hands-on problem solving building on pre-class learning materials.

University-wide Bioinformatics Workshops at MSU

Summer 2017 | 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 32 members of the MSU community including undergraduates, PhD students, and faculty members. These course materials form the basis of the 1-credit Bioinformatics modular courses, which I and others have now taught to >300 undergrads, grad students, and postdocs from >15 departments.

Past experiences (at Princeton University)

Spring 2015 | Co-taught ISC 233/234: An integrated, quantitative introduction to the natural sciences II
Spring 2014 | Co-taught COS557/MOL557: Analysis & visualization of large-scale genomic datasets

MENTORING AND PROFESSIONAL DEVELOPMENT

Mentees / Team Members

Postdoctoral Researchers (02)		Graduate Students (07)		Undergraduate Students (22)	
Current	Stephanie Hickey Christopher Mancuso Sarah Percival	Current	Nathaniel Hawkins Kayla Johnson Renming Liu Alex McKim	Current	Matthew Artuso, Emani Hunter, Filip Jevtic, Gokul Murali, Kewalin Samart, Sneha Sundar
		Past	Anna Yannakopoulos	Past	A. Agarwal A. Almounajed, N. Davis, L. Guare, A. Hashsham, J. Lee, R. Liu, M. Maldaver, A. Metto, C. Nnawulezi, D. Singla, J. Santaniello, P. Tuyishime, J. Vasquez, S. Vatti, K. Warfle
		Rotation	Faryal Mir Robert Fidis		
Post-bac Researchers (01)		Software Developers (03)		High School Students (05)	
Past	Jake Canfield	Current	Patrick Bills Douglas Krum Choonhan Yoon	Current	Neha Kanneganti
				Past	R. Banerjee, E. Bruce, D. Gomez, J. Shah

Honors and Awards to Mentees

Christopher Mancuso	NIGMS NIH Kirschstein-NRSA Postdoctoral Fellowship (F32)
Stephanie Hickey	Brain & Behavior Research Foundation's 2021 BBRF Young Investigator Grant
Anna Yannakopoulos	MSU Engineering Distinguished Graduate Fellowship
Kayla Johnson	Honorable Mention – NSF Graduate Research Fellowship Program (GRFP)
Alex McKim	MSU Engineering Distinguished Graduate Fellowship
Renming Liu	MSU CMSE Ginther Graduate Fellowship
Nathaniel Hawkins	Rasmussen Doctoral Recruitment Award; MSU Engineering Distinguished Graduate Fellowship
Jake Canfield	MSU Undergraduate Physiology Research Award and Service Award

Student Committees

MSU Graduate Students (17)

Al Masraf Basma	Danielle Barnes	Reid Blanchett	Norman Chamusah	David Filipovic	Fabio Gomez
MacKenzie Jacobs	Thilani Jayakody	Omar Kana	Justin Lee	Samuel Lotz	Brian Nohomovich
Christine Ponnampalam		Ana-Maria Raicu	Warren Sink	Ethan Tu	Wei Wang

External thesis examiner: Amrita School of Engineering, India

Professional Development

- 2020–: Advisory Board, *Plant Postdocs*
- 2018–2020: *Surviving, Enjoying, and Excelling in your PhD* | Conducted at MSU (Broadening Experiences in Scientific Training Program, DO-PhD Annual Student Retreat, BMB Exchange) and Rutgers University
- 2018–: *Planning and Executing an Effective Postdoc Training* | Conducted at MSU and Rutgers University.
- 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. Smart, J. Santaniello, S. Sundar, S. Vatti, K. Warfle

Graduate students (04)

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

Postdocs (02)

- Female: 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.

Discussion Forums and Ask-Me-Anything Sessions on Career Path and Research

- 2021: Onsite Undergraduate Research+Mentorship, Anna Louise James Minority Pre-Pharmacy Organization
- 2020: Charles Drew Science Scholars program
- 2019: Females in STEM student group at East Lansing High School
- 2017: Latinos-2-College Program for high school students (8th-10th grade) from the Lansing School District

Membership in Departmental DEI Committees

- Department of Computational Math, Science and Engineering
- Department of Biochemistry and Molecular Biology

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!” – hands-on education booths at Kid’s Tech University, Virginia Tech’s public outreach program; and at USA Science & Engineering Festival.

PROFESSIONAL MEMBERSHIPS AND SERVICES

University and Departmental Services

- Search committees at MSU
 - Chair: Fixed-Term Assistant Professor, Dept. Computational Math, Sci. and Engr. 2020–2021
 - Member: Precision Pediatrics and Human Genomics 2018–2019
 - Member: CMSE & Biomedical Engineering 2018–2019
- Other departmental committee membership:
 - Postdoc mentoring 2021–Present
 - Diversity, equity, and inclusion, Dept. Biochemistry and Molecular Biology 2020–Present
 - Diversity, equity, and inclusion, Dept. Computational Math, Sci. and Engr. 2020–2021
 - Graduate studies 2018–2019
 - Data science curriculum 2019–2020
 - Advisory committee 2018–2020
 - Long-term planning 2019–2020
- University-level advisory committee membership:
 - Center for Research in Autism, Intellectual & other Neurodevelopmental Disabilities 2019–Present
 - Trifecta Initiative for Interdisciplinary Health Research 2020–Present

Membership and Services in Professional Communities

- Guest Editor, PLoS Computational Biology
- Associate Editor, Frontiers in Bioinformatics (Section: Integrative Bioinformatics)
- Posters Co-chair (2017, 2018), Chair (2019) Intelligent Systems for Molecular Biology (ISMB).
- Program committee:
 - Great Lakes Bioinformatics Conference 2019, 2021
 - Intelligent Systems for Molecular Biology 2021
- 2019-2020 Faculty Fellow (Teaching & Technology) at the Hub@MSU.
- Science Ambassador – Science Gateways Community Institute
- Post-publication review: F1000 Biology.

Peer Review

- Academic Journals (21):
BioData Mining | Bioinformatics | BMC Bioinformatics | Circulation: Cardiovascular Genetics | F1000 Research | G3: Genes, Genomes, Genetics | Genome Biology | IEEE/ACM Transactions on Computational Biology and Bioinformatics | Journal of Theoretical Biology | Molecular Autism | Molecular Breeding | mSystems | Nature Communications | Nature Neuroscience | Nucleic Acids Research | Plant Physiology | Plant Molecular Biology | PLoS Computational Biology | PLoS ONE | Proceedings of the National Academy of Sciences | 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
- Funding Agencies (02)
 - National Science Foundation
 - Ad-hoc reviewer of proposals/applications 2017, 2019, 2020
 - National Institutes of Health
 - Biodata Management and Analysis Study Section temporary member 2019, 2021
 - Ad-hoc reviewer 2020