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Education

- 12/2016 **Ph.D. Biomedical Science (Computational Biology)**
Icahn School of Medicine at Mount Sinai, New York, NY
- 06/2012 **B.S. Biochemistry and Molecular Biology**
China Agricultural University, Beijing, China

Work Experience

- 09/2022 - present **Sr. Applied Scientist**
Amazon Web Services
Amazon.com Services LLC, New York, NY
- 04/2021 - 09/2022 **Applied Scientist**
Amazon Web Services
Amazon.com Services LLC, New York, NY
- 09/2019 - 04/2021 **Principal Scientist**
Clinical Informatics
Sema4, Stamford, CT
- 06/2017 - 09/2019 **Assistant Professor (research track)**
Department of Pharmacological Sciences
Icahn School of Medicine at Mount Sinai, New York, NY
- 01/2017 - 06/2017 **Postdoctoral Fellow**
Department of Pharmacological Sciences
Icahn School of Medicine at Mount Sinai, New York, NY
- 05/2013 - 12/2016 **Doctoral Student**
Department of Genetics and Genomic Sciences
Icahn School of Medicine at Mount Sinai, New York, NY
- 11/2011 - 05/2012 **Research Assistant**
Institute of Biophysics
Chinese Academy of Sciences, Beijing, China

Publications

Machine Learning in Healthcare

1. Wu Y, Barton RA, **Wang Z**, Ioannidis VN, De Donno C, Price LC, Voloch LF, Karypis G: Predicting Cellular Responses with Variational Causal Inference and Refined Relational Information. *arXiv preprint* 2022, arXiv:2210.00116
2. Wu Y, Price LC, **Wang Z**, Ioannidis VN, Karypis G: Variational causal inference. *arXiv preprint* 2022, arXiv:2209.05935

3. **Wang Z**, Combs SA, Brand R. *et al.*: LM-GVP: an extensible sequence and structure informed deep learning framework for protein property prediction. **Scientific Reports** 2022, 12:6832
4. Zhang L, **Wang Z**, Liu R, Li Z, Lin J, Wojciechowicz ML, Huang J, Lee K, Ma'ayan A, He JC: Connectivity Mapping Identifies BI-2536 as a Potential Drug to Treat Diabetic Kidney Disease. **Diabetes** 2021, 70(2):589-602
5. Keenan AB, Wojciechowicz ML, **Wang Z**, Jagodnik KM, Jenkins SL, Lachmann A, Ma'ayan A: Connectivity Mapping: Methods and Applications. **Annual Review of Biomedical Data Science** 2019, 2: 69-92
6. **Wang Z**, Lachmann A, Ma'ayan A: Mining data and metadata from the gene expression omnibus. **Biophysical Reviews** 2019, 11(1):103-110
7. **Wang Z**, He E, Sani K, Jagodnik KM, Silverstein M, Ma'ayan A: Drug Gene Budget (DGB): An application for ranking drugs to modulate a specific gene based on transcriptomic signatures. **Bioinformatics** 2018, bty763
8. **Wang Z**, Lachmann A, Keenan AB, Ma'ayan A: L1000FWD: Large-scale visualization of drug-induced transcriptomic signatures. **Bioinformatics** 2018, bty060
9. Fu J, **Wang Z**, Lee K, Wei G, Liu Z, Zhang M, Zhou M, Zhang W, Chuang P, Ma'ayan A, He JC, Liu Z: Transcriptomic analysis uncovers novel synergistic mechanisms in combination therapy for lupus nephritis. **Kidney International** 2018, 93(2):416-429
10. Hodos R, Zhang P, Duan Q, **Wang Z**, Clark NR, Ma'ayan A, Wang F, Lee HC, Kidd B, Sontag D, Hu J, Dudley JT: Prediction of drug-induced gene expression profiles using tensor completion. **Pacific Symposium on Biocomputing** 2018, 32-43
11. Niepel M, Hafner M, Duan Q, **Wang Z**, Paull EM, Chung M, Lu X, Stuart JM, Golub TR, Subramanian A, Ma'ayan A, Sorger PK: Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. **Nature Communications** 2017, 8(1):1186
12. **Wang Z**, Monteiro CD, Jagodnik KM, Fernandez NF, Gundersen GW, Rouillard AD, Jenkins SL, Feldmann AS, Hu KS, McDermott MG *et al.*: Extraction and analysis of signatures from the gene expression omnibus by the crowd. **Nature Communications** 2016, 7, 12846.
13. Duan Q, Reid SP, Clark NR, **Wang Z**, Fernandez NF, Rouillard AD, Readhead B, Tritsch SR, Hodos R, Hafner M, Niepel M, Sorger PK, Dudley JT, Bavari S, Panchal RG, Ma'ayan A: L1000CDS2: LINCS L1000 characteristic direction signatures search engine. **Npj Systems Biology And Applications** 2016, 2:16015.
14. **Wang Z**, Clark NR, Ma'ayan A: Drug-induced adverse events prediction with the LINCS L1000 data. **Bioinformatics** 2016, 32(15):2338-2345.
15. Duan Q, **Wang Z**, Fernandez NF, Rouillard AD, Tan CM, Benes CH, Ma'ayan A: Drug/Cell-line Browser: interactive canvas visualization of cancer drug/cell-line viability assay datasets. **Bioinformatics** 2014, 30(22):3289-3290.
16. Keenan AB, Jenkins SL, Jagodnik KM, Koplev S, He E, Torre D, **Wang Z**, *et al.*: The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. **Cell Systems** 2017, 6(1):13-24
17. **Wang Z**, Clark N, Ma'ayan A: Dynamics of the discovery process of protein-protein interactions from low content studies. **BMC Systems Biology** 2015, 9(1):26.
18. Rouillard AD, **Wang Z**, Ma'ayan A: Reprint of "Abstraction for data integration: Fusing mammalian molecular, cellular and phenotype big datasets for better knowledge extraction". **Computational Biology and Chemistry** 2015, 59, Part B:123-138.
19. Ma'ayan A, Rouillard AD, Clark NR, **Wang Z**, Duan Q, Kou Y: Lean Big Data integration in systems biology and systems pharmacology. **Trends in Pharmacological Sciences** 2014, 35(9): 450-460.

Machine Learning and RWE Mining using EHR

20. Zheutlin AB, Vieira L, Li S, **Wang Z**, Schadt E, Gross S, Stone J, Schadt E, Li L: Improving postpartum hemorrhage risk prediction using longitudinal electronic medical records. *Journal of the American Medical Informatics Association* 2022, 29 (2), 296-305
21. Zheutlin AB, Vieira L, Li S, **Wang Z**, Schadt E, Gross S, Stone J, Schadt E, Li L: A comprehensive digital phenotype for postpartum hemorrhage. *Journal of the American Medical Informatics Association* 2022, 29 (2), 321-328
22. Li S*, **Wang Z***, Vieira LA, Zheutlin AB, Ru B, Schadt E, Wang P, Copperman AB, Stone J, Gross SJ, Schadt EE, Li L: Improving Pre-eclampsia Risk Prediction by Modeling Individualized Pregnancy Trajectories Derived from Routinely Collected Electronic Medical Record Data. *npj Digital Medicine* 2022, 5(1), 1-16
23. Li S, Jun T, Tyler J, Kao YH, Schadt E, **Wang Z**, Konig MF, Bettgowda C, Vogelstein JT, Papadopoulos N, Parsons R, Chen R, Schadt EE, Li L, Oh WK: Inpatient Administration of Alpha-1-Adrenergic Receptor Blocking Agents Reduces Mortality in Male COVID-19 Patients. *Frontiers in medicine* 2022, 9: 849222
24. Li S, Sarangarajan R, Jun T, Kao YH, **Wang Z**, Hao K, Schadt E, Kiebish MA, Granger E, Narain NR, Chen R, Schadt EE, Li L: In-hospital use of ACE inhibitors/angiotensin receptor blockers associates with COVID-19 outcomes in African American patients. *The Journal of clinical investigation*. 2021, 131(19)
25. Ho KS, Narasimhan B, Difabrizio L, Rogers L, Bose S, Li L, Chen R, Sheehan J, El-Halabi MA, Sarosky K, **Wang Z**, Eisenberg E, Powell C, Steiger D: Impact of corticosteroids in hospitalised COVID-19 patients. *BMJ Open Respiratory Research* 2021, 8(1): e000766
26. **Wang Z**, Zheutlin A, Kao Y-H, Ayers K, Gross S, Kovatch P, Nirenberg S, Charney A, Nadkarni G, De Freitas JK, O'Reilly P, Just A, Horowitz C, Martin G, Branch A, Glicksberg BS, Charney D, Reich D, Oh WK, Schadt E, Chen R, Li L: Hospitalised COVID-19 patients of the Mount Sinai Health System: a retrospective observational study using the electronic medical records. *BMJ Open* 2020, 10(10): e040441
27. Ellis RJ, **Wang Z**, Genes N, Ma'ayan A: Predicting opioid dependence from electronic health records with machine learning. *BioData Mining* 2019, 12(3)
28. **Wang Z**, Li L, Glicksberg BS, Israel A, Dudley JT, Ma'ayan A: Predicting Age by Mining Electronic Medical Records with Deep Learning Characterizes Differences between Chronological and Physiological Age. *Journal of Biomedical Informatics* 2017, 76:59-68

Bioinformatics Analyses and Applications in Biomedical Science

29. Sevilla A, Papatsenko D, Mazloom AR, Xu H, Vasileva A, Unwin RD, LeRoy G, Chen EY, Garrett-Bakelman FE, Lee DF, Trinite B, Webb RL, **Wang Z**, Su J, Gingold J, Melnick A, Garcia BA, Whetton AD, MacArthur BD, Ma'ayan A, Lemischka IR: An Esrrb and Nanog Cell Fate Regulatory Module Controlled by Feed Forward Loop Interactions. *Frontiers in Cell and Developmental Biology* 2021, 9:502
30. Edwards JJ, Rouillard AD, Fernandez NF, **Wang Z**, Lachmann A, Shankaran SS, Bisgrove BW, Demarest B, Turan N, Srivastava D, Bernstein D, Deanfield J, Giardini A, Porter G, Kim R, Roberts AE, Newburger JW, Goldmuntz E, Brueckner M, Lifton RP, Seidman CE, Chung WK, Tristani-Firouzi M, Yost HJ, Ma'ayan A, Gelb BD: Systems Analysis Implicates WAVE2 Complex in the Pathogenesis of Developmental Left-Sided Obstructive Heart Defects. *JACC: Basic to Translational Science* 2020, 5(4):376-386
31. Heitman N, Sennett R, Mok KW, Saxena N, Srivastava D, Martino P, Grisanti L, **Wang Z**, Ma'ayan A, Rompolas P, Rendl M: Dermal sheath contraction powers stem cell niche relocation during hair cycle regression. *Science* 2020, 367(6474):161-166

32. Fernandez DM, Rahman AH, Fernandez NF, Chudnovskiy A, Amir ED, Amadori L, Khan NS, Wong CK, Shamailova R, Hill CA, **Wang Z**, Remark R, Li JR, Pina C, Faries C, Awad AJ, Moss N, Bjorkegren JLM, Kim-Schulze S, Gnjatic S, Ma'ayan A, Mocco J, Faries P, Merad M, Giannarelli: Single-cell immune landscape of human atherosclerotic plaques. *Nature Medicine* 2019, 25(10): 1576-1588
33. Nakahara F, Borger DK, Wei Q, Pinho S, Maryanovich M, Zahalka A, Suzuki M, Grealley J, Cruz C, **Wang Z**, Ma'ayan A, Xu C, Boulais P, Frenette PS: Engineering a haematopoietic stem cell niche by revitalizing mesenchymal stromal cells. *Nature Cell Biology* 2019, 21: 560-567
34. Ochsner SA, Abraham D, Martin K, Ding W, McOwiti A, Kankanamge W, **Wang Z**, Andreano K, Hamilton RA, Chen Y, Hamilton A, Gantner ML, Dehart M, Qu S, Hilsenbeck SG, Becnel, Dave Bridges LB, Ma'ayan A, Huss JM, Stossi F, Foulds CE, Kralli A, McDonnell DP, McKenna NJ: The Signaling Pathways Project, an integrated 'omics knowledgebase for mammalian cellular signaling pathways. *Scientific Data* 2019, 6(1):1-21
35. Duncan A, Heyer MP, Ishikawa M, Caligiuri SPB, Liu X, Chen Z, Di Bonaventura MVM, Elayouby KS, Ables JL, Howe WM, Bali P, Fillinger C, Williams M, O'Connor RM, **Wang Z**, Lu Q, Kamenecka TM, Ma'ayan A, O'Neill HC, Ibanez-Tallon I, Geurts AM, Kenny PJ: Habenular TCF7L2 links nicotine addiction to diabetes. *Nature* 2019 574(7778):372-377
36. Keenan AB, Torre D, Lachmann A, Leong AK, Wojciechowicz ML, Utti V, Jagodnik KM, Kropiwnicki E, **Wang Z**, Ma'ayan A: ChEA3: transcription factor enrichment analysis by orthogonal omics integration. *Nucleic Acids Research* 2019, 47(W1):W212-W224
37. Mok KW, Saxena N, Heitman N, Grisanti L, Srivastava D, Muraro M, Jacob T, Sennett R, **Wang Z**, Su Y, Yang LM, Ma'ayan A, Ornitz DM, Kasper M, Rendl M: Dermal Condensate Niche Fate Specification Occurs Prior to Formation and Is Placode Progenitor Dependent. *Developmental Cell* 2019, 48(1):32-48.e5
38. Gomes AM, Kurochkin I, Chang B, Daniel M, Law K, Satija N, Lachmann A, **Wang Z**, Ferreira L, Ma'ayan A, Chen BK, Papatsenko D, Lemischka IR, Moore KA, Pereira CF: Cooperative Transcription Factor Induction Mediates Hemogenic Reprogramming. *Cell Reports* 2018, 25(10) 2821-2835.e7
39. Strub T, Ghiraldini FG, Carcamo S, Li M, Wroblewska A, Singh R, Goldberg MS, Hasson D, **Wang Z**, Gallagher SJ, Hersey P, Ma'ayan A, Long GV, Scolyer RA, Brown B, Zheng B, Bernstein E: SIRT6 haploinsufficiency induces BRAF V600E melanoma cell resistance to MAPK inhibitors via IGF signalling. *Nature Communications* 2018, 9(3440)
40. Breen MS, Ozcan S, Ramsey JM, **Wang Z**, Ma'ayan A, Rustogi N, Gottschalk MG, Webster MJ, Weickert CS, Buxbaum JD, Bahn S: Temporal proteomic profiling of postnatal human cortical development. *Translational Psychiatry* 2018, 8(1) 267
41. Guo Y, Pace J, Li Z, Ma'ayan A, **Wang Z**, Revelo MP, Chen E, Gu X, Attalah A, Yang Y, Estrada C, Yang VW, John C. He JC, Mallipattu SK: Podocyte-Specific Induction of Krüppel-Like Factor 15 Restores Differentiation Markers and Attenuates Kidney Injury in Proteinuric Kidney Disease. *Journal of the American Society of Nephrology* 2018, ASN.2018030324
42. Clarke DJB, Kuleshov MV, Schilder BM, Torre D, Duffy ME, Keenan AB, Lachmann A, Feldmann AS, Gundersen GW, Silverstein MC, **Wang Z**, Ma'ayan A: eXpression2Kinases (X2K) Web: linking expression signatures to upstream cell signaling networks. *Nucleic Acids Research* 2018, gky450
43. Harel A, Sperling D, Petracca M, Ntranos A, Kats-Sand I, Krieger S, Lublin F, **Wang Z**, Liu Y, Inglese M: Brain microstructural injury occurs in patients with RRMS despite 'no evidence of disease activity'. *Journal of Neurology, Neurosurgery & Psychiatry* 2018
44. Torre D, Krawczuk P, Jagdonik KM, Lachmann A, Kuleshov MV, **Wang Z**, Wang L, Kuleshov MV, Ma'ayan A: Datasets2Tools, repository and search engine for bioinformatics datasets, tools and canned analyses. *Scientific Data* 2018, 5:180023

45. Asada N, Kunisaki Y, Pierce H, **Wang Z**, Fernandez N, Birbrair A, Ma'ayan A, Frenette P: Differential cytokine contributions of perivascular haematopoietic stem cell niches. **Nature Cell Biology** 2017, 19 (3), 214-223
46. Kong D-S, Kim J, Lee I-H, Kim ST, Seol HJ, Lee J-I, Park W-Y, Ryu G, **Wang Z**, Ma'ayan A, Nam D-H: Integrative radiogenomic analysis for multicentric radiophenotype in glioblastoma. **Oncotarget** 2016, 7(10), 11526.
47. von Schimmelmann M, Feinberg PA, Sullivan JM, Ku SM, Badimon A, Duff MK, **Wang Z**, Lachmann A, Dewell S, Ma'ayan A, Han M-H, Tarakhovskiy A, Schaefer A: Polycomb repressive complex 2 (PRC2) silences genes responsible for neurodegeneration. **Nature Neuroscience** 2016, 19, 1321–1330
48. Kuleshov MV, Jones MR, Rouillard AD, Fernandez NF, Duan Q, **Wang Z**, Koplev S, Jenkins SL, Jagodnik KM, Lachmann A *et al*: Enrichr: a comprehensive gene set enrichment analysis web server 2016 update. **Nucleic Acids Research** 2016, 44 (W1): W90-W97.
49. Rezza A, **Wang Z**, Sennett R, Qiao W, Wang D, Heitman N, Mok Ka W, Clavel C, Yi R, Zandstra P *et al*: Signaling Networks among Stem Cell Precursors, Transit-Amplifying Progenitors, and their Niche in Developing Hair Follicles. **Cell Reports** 2016, 14(12):3001-3018.
50. **Wang Z**, Ma'ayan A: An open RNA-Seq data analysis pipeline tutorial with an example of reprocessing data from a recent Zika virus study [version 1; referees: 3 approved]. **F1000Research** 2016, 5(1574).
51. Rouillard AD, Gundersen GW, Fernandez NF, **Wang Z**, Monteiro CD, McDermott MG, Ma'ayan A: The harmonizome: a collection of processed datasets gathered to serve and mine knowledge about genes and proteins. **Database** 2016, baw100.
52. Morgan DJ, Poolman TM, Williamson AJK, **Wang Z**, Clark NR, Ma'ayan A, Whetton AD, Brass A, Matthews LC, Ray DW: Glucocorticoid receptor isoforms direct distinct mitochondrial programs to regulate ATP production. **Scientific Reports** 2016, 6:26419.
53. Pfau ML, Purushothaman I, Feng J, Golden SA, Aleyasin H, Lorsch ZS, Cates HM, Flanigan ME, Menard C, Heshmati M, **Wang Z**, Ma'ayan A, Shen L, Hodes GE, and Russo SJ: Integrative analysis of sex-specific microRNA networks following stress in mouse nucleus accumbens. **Frontiers in Molecular Neuroscience** 2016, 9:144
54. Clark NR, Szymkiewicz M, **Wang Z**, Monteiro CD, Jones MR, Ma'ayan A: Principal Angle Enrichment Analysis (PAEA): Dimensionally Reduced Multivariate Gene Set Enrichment Analysis Tool. **Proceedings IEEE International Conference on Bioinformatics and Biomedicine** 2015, 2015:256-262.
55. Sennett R, **Wang Z**, Rezza A, Grisanti L, Roitershtein N, Sicchio C, Mok Ka W, Heitman Nicholas J, Clavel C, Ma'ayan A *et al*: An Integrated Transcriptome Atlas of Embryonic Hair Follicle Progenitors, Their Niche, and the Developing Skin. **Developmental Cell** 2015, 34(5):577-591.
56. Yu Z, Zhou X, Wang W, Deng W, Fang J, Hu H, **Wang Z**, Li S, Cui L, Shen J *et al*: Dynamic Phosphorylation of CENP-A at Ser68 Orchestrates Its Cell-Cycle-Dependent Deposition at Centromeres. **Developmental Cell** 2015, 32(1):68-81.
57. Duarte LF, Young ARJ, **Wang Z**, Wu H-A, Panda T, Kou Y, Kapoor A, Hasson D, Mills NR, Ma'ayan A, Narita M, Bernstein E: Histone H3.3 and its proteolytically processed form drive a cellular senescence programme. **Nature Communications** 2014, 5, 5210.
58. Chen E, Tan C, Kou Y, Duan Q, **Wang Z**, Meirelles G, Clark N, Ma'ayan A: Enrichr: interactive and collaborative HTML5 gene list enrichment analysis tool. **BMC Bioinformatics** 2013, 14(1):128.
59. Wang W, Wang L, Chen C, Xiong G, Tan X-Y, Yang K-Z, **Wang Z-C**, Zhou Y, Ye D, Chen L-Q: Arabidopsis CSLD1 and CSLD4 are required for cellulose deposition and normal growth of pollen tubes. **Journal of Experimental Botany** 2011, 62(14):5161-5177.

Technical Blog Posts

1. **Wang Z**, Shi Y, Chen X: Euclidean geometry meets graph, a geometric deep learning perspective. *ICLR Blog Track* 2022
2. **Wang Z**, Senthivel S: Train graph neural nets for millions of proteins on Amazon SageMaker and Amazon DocumentDB (with MongoDB compatibility). *AWS Machine Learning Blog* 2022
3. **Wang Z**, Ioannidis VN: How AWS uses graph neural networks to meet customer needs. *Amazon Science* 2022

Softwares

L1000FWD (https://maayanlab.cloud/L1000FWD/)	L1000 fireworks display: large-scale visualization of drug-induced transcriptomic signatures
msea (https://pypi.org/project/msea/)	A Python package implementing Microbe-Set Enrichment Analysis (MSEA) for functional interpretation of sets of microbial organisms
PAEA (http://amp.pharm.mssm.edu/PAEA/)	Principal Angle Enrichment Analysis: dimensionally reduced multivariate gene set enrichment analysis tool
LJP-BCNB (https://amp.pharm.mssm.edu/LJP/)	LINCS Joint Project - Breast Cancer Network Browser
DGB (https://maayanlab.cloud/DGB/)	Drug Gene Budger: identify drugs and small molecules to regulate expression of target genes
CREEDS (https://amp.pharm.mssm.edu/CREEDS/)	A search engine for collections of processed gene, drug and disease signatures from GEO
SEP-L1000 (https://maayanlab.net/SEP-L1000/)	Side effect prediction for drugs based on L1000 data
react-scatter-board (https://github.com/MaayanLab/react-scatter-board)	A React package implementing the THREE.js 2d/3d scatter plots
GeoDEpy (https://github.com/MaayanLab/geode)	A Python package for the Characteristic Direction: a geometrical approach to differential expression and gene-set enrichment
Zika-RNAseq-Pipeline (https://github.com/MaayanLab/Zika-RNAseq-Pipeline)	An open RNA-Seq data analysis pipeline build in Docker and Jupyter Notebook
Hair-GEL (http://hair-gel.net/)	A searchable gene expression library for hair follicles

Invited Presentations

- 11/2022 Graph Neural Networks in Drug Discovery
R/Pharma Conference
Virtual location

- 10/2022 Graph Machine Learning for Healthcare and Life Sciences
DeepLearn 2022 Autumn, the 7th International School on Deep Learning
Luleå, Sweden
- 06/2022 Machine Learning Methods to Accelerate the Drug Discovery Cycle
Amazon re:MARS 2022
Las Vegas, NV
- 06/2022 Learning on Geometric Graphs
Machine Learning Research Seminar, Netflix Inc.
Virtual location
- 03/2019 Single-cell Approaches for the Dissection of Cell Lineage
Computational Genomics guest lecture, Weill Cornell Medicine
New York, NY
- 12/2018 L1000 Data Analysis and Visualization using Machine Learning
LINCS Connectivity Map Workshop Series, Broad Institute
Cambridge, MA
- 10/2018 Pharmacometrics in Big Data Era - Mission possible to find the needle in a haystack
American Conference on Pharmacometrics (ACoP9)
San Diego, CA
- 03/2018 Towards Large-scale Predictive Drug Safety: A Systems Pharmacology Perspective
American Medical Informatics Association (AMIA) Informatics Summit
San Francisco, CA

Ad-hoc Peer-Review Service

Journals: Bioinformatics (Oxford), PLoS Computational Biology, Statistical Methods in Medical Research, Nature Communications, Oncogene, Scientific Reports, Bulletin of Mathematical Biology, Gene, Meta Gene, Algorithms, EBioMedicine, BMC Medical Informatics and Decision Making, CPT: Pharmacometrics & Systems Pharmacology, Nucleic Acids Research, Royal Society Open Science, Frontiers in Genetics, F1000Research

Conferences: IEEE International Conference on Bioinformatics and Biomedicine (BIBM), International Conference on Learning Representations (ICLR), Learning on Graphs Conference (LoG)

Tutorials, Workshops, and Teaching Experience

- 2014-2015 Network Analysis in Systems Biology (Coursera)
- 2017-2018 Data Analysis and Software Development in Big Data Biomedicine (ISMMS BSR6806)
- 2022 Graph Neural Networks in Life Sciences: Opportunities and Solutions (the 28th ACM SIGKDD Conference on Knowledge Discovery and Data Mining)

Advising and Supervision

Kevin Sani	Visiting undergraduate	Harvard University, Cambridge, MA	2016
Daniel Clarke	Visiting undergraduate	Fairleigh Dickinson University, Teaneck, NJ	2016
Jennifer Lin	Visiting high school student	Oceanside High School, Oceanside, NY	2016
Damon Pham	Visiting undergraduate	Indiana University, Bloomington, IN	2017, 2019
Charlotte Zuber	Visiting undergraduate	Rutgers University, New Brunswick, NJ	2017
Randall Ellis	Rotation PhD student	Icahn School of Medicine at Mount Sinai, New York, NY	2017-2018
Katherine Chew	Visiting undergraduate	Massachusetts Institute of Technology, Cambridge, MA	2018
Vivek Sriram	Visiting undergraduate	Duke University, Durham, NC	2018
David Szanto	Visiting undergraduate	Harvard University, Cambridge, MA	2019
Yuhong Zhu	Data Scientist	Sema4, Stamford, CT	2020-2021
Yulun Wu	Applied Scientist Intern	Amazon, San Francisco, CA	2022
Ahsan Ali	Applied Scientist	Amazon, New York, NY	2022