

# Zichen Wang, Ph.D.

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<https://wangz10.github.io>

## 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

- 04/2021 - present      **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

### Computational Drug Discovery

1. 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
2. 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
3. **Wang Z**, Lachmann A, Ma'ayan A: Mining data and metadata from the gene expression omnibus. *Biophysical Reviews* 2019, 11(1):103-110

4. **Wang Z**, He E, Sani K, Jagodnik KM, Silverstein M, Ma'ayan A: Drug Gene Budger (DGB): An application for ranking drugs to modulate a specific gene based on transcriptomic signatures. **Bioinformatics** 2018, bty763
5. **Wang Z**, Lachmann A, Keenan AB, Ma'ayan A: L1000FWD: Large-scale visualization of drug-induced transcriptomic signatures. **Bioinformatics** 2018, bty060
6. 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
7. 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
8. 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
9. **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.
10. 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.
11. **Wang Z**, Clark NR, Ma'ayan A: Drug-induced adverse events prediction with the LINCS L1000 data. **Bioinformatics** 2016, 32(15):2338-2345.
12. 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.
13. 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
14. 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.
15. 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

16. 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
17. Li S, Jun T, **Wang Z**, Kao YH, Schadt E, Konig MF, Bettegowda C, Vogelstein JT, Papadopoulos N, Parsons R, Chen R, Schadt EE, Li L, Oh WK: COVID-19 outcomes among hospitalized men with or without exposure to alpha-1-adrenergic receptor blocking agents. **medRxiv** 2021, 2021.04.08.21255148
18. 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. **medRxiv** 2021, 2021.03.23.21254178

19. 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. *medRxiv* 2021, 2021.03.16.21253746
20. 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. *medRxiv* 2021, 2021.03.01.21252691
21. **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
22. Ellis RJ, **Wang Z**, Genes N, Ma'ayan A: Predicting opioid dependence from electronic health records with machine learning. *BioData Mining* 2019, 12(3)
23. **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

24. 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
25. 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
26. Heitman N, Sennett R, Mok KW, Saxena N, Srivastava D, Martino P, Grisanti L, **Wang Z**, Ma'ayan A, Rempel P, Rendl M: Dermal sheath contraction powers stem cell niche relocation during hair cycle regression. *Science* 2020, 367(6474):161-166
27. 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, Björkegren JLM, Kim-Schulze S, Gnjatich 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
28. Nakahara F, Borger DK, Wei Q, Pinho S, Maryanovich M, Zahalka A, Suzuki M, Greally 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
29. 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
30. 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

31. 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
32. 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
33. 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
34. 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)
35. 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
36. 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
37. 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
38. 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
39. 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
40. 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
41. 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.
42. von Schimmelmamm M, Feinberg PA, Sullivan JM, Ku SM, Badimon A, Duff MK, **Wang Z**, Lachmann A, Dewell S, Ma'ayan A, Han M-H, Tarakhovsky A, Schaefer A: Polycomb repressive complex 2 (PRC2) silences genes responsible for neurodegeneration. **Nature Neuroscience** 2016, 19, 1321-1330
43. 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.
44. 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.

45. **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).
46. Rouillard AD, Gunderson 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.
47. 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.
48. 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
49. 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.
50. 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.
51. **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.
52. 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.
53. 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.
54. 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.
55. 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.

## Softwares

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|--|---|
| L1000FWD ( <a href="https://maayanlab.cloud/L1000FWD/">https://maayanlab.cloud/L1000FWD/</a> ) | L1000 fireworks display: large-scale visualization of drug-induced transcriptomic signatures                                      |
| msea ( <a href="https://pypi.org/project/msea/">https://pypi.org/project/msea/</a> )           | A Python package implementing Microbe-Set Enrichment Analysis (MSEA) for functional interpretation of sets of microbial organisms |
| PAEA ( <a href="http://amp.pharm.mssm.edu/PAEA/">http://amp.pharm.mssm.edu/PAEA/</a> )         | Principal Angle Enrichment Analysis: dimensionally reduced multivariate gene set enrichment analysis tool                         |
| LJP-BCNB ( <a href="https://amp.pharm.mssm.edu/LJP/">https://amp.pharm.mssm.edu/LJP/</a> )     | LINCS Joint Project - Breast Cancer Network Browser   |

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| DGB ( <a href="https://maayanlab.cloud/DGB/">https://maayanlab.cloud/DGB/</a> )  | Drug Gene Budger: identify drugs and small molecules to regulate expression of target genes                                  |
| CREEDS ( <a href="https://amp.pharm.mssm.edu/CREEDS/">https://amp.pharm.mssm.edu/CREEDS/</a> )   | A search engine for collections of processed gene, drug and disease signatures from GEO                                      |
| SEP-L1000 ( <a href="https://maayanlab.net/SEP-L1000/">https://maayanlab.net/SEP-L1000/</a> )  | Side effect prediction for drugs based on L1000 data   |
| react-scatter-board ( <a href="https://github.com/MaayanLab/react-scatter-board">https://github.com/MaayanLab/react-scatter-board</a> )    | A React package implementing the THREE.js 2d/3d scatter plots  |
| GeoDEpy ( <a href="https://github.com/MaayanLab/geode">https://github.com/MaayanLab/geode</a> )  | A Python package for the Characteristic Direction: a geometrical approach to differential expression and gene-set enrichment |
| Zika-RNAseq-Pipeline ( <a href="https://github.com/MaayanLab/Zika-RNAseq-Pipeline">https://github.com/MaayanLab/Zika-RNAseq-Pipeline</a> ) | An open RNA-Seq data analysis pipeline build in Docker and Jupyter Notebook  |
| Hair-GEL ( <a href="http://hair-gel.net/">http://hair-gel.net/</a> )   | A searchable gene expression library for hair follicles  |

## Invited Presentations

- 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

Bioinformatics, PLoS Computational Biology, Statistical Methods in Medical Research, Nature Communications, Oncogene, Scientific Reports, IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 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

## Teaching Experience

|           |   |
|-----------|---|
| 2014-2015 | Network Analysis in Systems Biology<br>(Coursera), TA                                       |
| 2017-2018 | Data Analysis and Software Development in Big Data Biomedicine<br>(ISMMS BSR6806), Lecturer |

## 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,<br>2019 |
| Charlotte Zuber | Visiting undergraduate       | Rutgers University, New Brunswick, NJ                    | 2017          |
| Randall Ellis   | Rotation PhD student         | Icahn School of Medicine at Mount Sinai,<br>New York, NY | 2017-2018     |
| Katherine Chew  | Visiting undergraduate       | Massachusetts Institute of Technology,<br>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     |