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## EDUCATION

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- 1996-2002    **Ph.D.** in Mathematics, University of California, San Diego.  
Thesis Title: *A Computational Investigation of Spectral Sets and Rational Dilations over Multiply-Connected Domains*. Advisor: Professor Jim Agler.
- 1992-1996    **S.B.** in Mathematics, **S.B. Minor** in Biology, Massachusetts Institute of Technology.

## EXPERIENCE

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- 2016-        **Professor**, Department of Computer Science, Princeton University
- 2013-2016   **Director**, Center for Computational Molecular Biology, Brown University
- 2011-2016   **Associate Professor**, Department of Computer Science & Center for Computational Molecular Biology, Brown University
- 2006-2011   **Assistant Professor**, Department of Computer Science & Center for Computational Molecular Biology, Brown University
- 2005-2006   **Burroughs Wellcome Postdoctoral Fellowship** in Computer Science (Bioinformatics), University of California, San Diego. Sponsor: Professor Pavel Pevzner.
- 2002-2004   **Alfred P. Sloan Postdoctoral Fellowship** in Computer Science (Bioinformatics), University of California, San Diego. Sponsor: Professor Pavel Pevzner.

## PUBLICATIONS

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Author order generally follows convention in biology, with senior/corresponding author listed last. Underlined authors are trainees. † indicates undergraduates. \* indicates joint first or last author.

### Refereed Journal and Conference Research Papers

P. Sashittal, H. Zhang, C.A. Iacobuzio-Donahue, **B.J. Raphael**. [ConDoR: Tumor phylogeny inference with a copy-number constrained mutation loss model](#). (2023) *Genome Biology* 24 (1), 272

\*P. Sashittal, \*H. Schmidt, M.M. Chan, **B.J. Raphael**. [Startle: a star homoplasmy approach for CRISPR-Cas9 lineage tracing](#) (2023). *Cell Systems* 14 (12), 1113-1121. e9. [Also: *International Conference on Research in Computational Molecular Biology (RECOMB) 2023*.]

X Liu, **B.J. Raphael**. [Representation Learning for Spatial Multimodal Data Integration with Optimal Transport](#). (2023) NeurIPS 2023 AI for Science Workshop.

X. Liu, R. Zeira, **B.J. Raphael**. (2023) [PASTE2: Partial Alignment of Multi-slice Spatially Resolved Transcriptomics Data](#). *Genome Research* 33 (7), 1124-1132. [Also: *International Conference on Research in Computational Molecular Biology (RECOMB) 2023*.]

H. Schmidt, P. Sashittal, **B.J Raphael**. (2023) [A zero-agnostic model for copy number evolution in cancer](#). *PLOS Computational Biology* [Also: RECOMB Workshop on Computational Cancer Biology, 2023]

N. Terekhanova\* , A. Karpova\* , W. Liang\* , A. Strzalkowski, [...36 co-authors including Cong Ma, Hirak Sarkar ...], **B.J. Raphael\***, L.Ding\* (2023). [Epigenetic Regulation During Cancer Transitions Across 11 Tumor Types](#). *Nature* 623, pages 432–441.

D.Zhang, Y.Deng, P.Kukanja, E.Agirre, M.Bartosovic, M.Dong, C.Ma, S.Ma, G.Su, S.Bao, Y.Liu, Y. Xiao, G. B. Rosoklija, A.J. Dwork, J.J Mann, K.W. Leong, M. Boldrini, L.Wang, M. Haeussler, **B.J Raphael**, Y. Kluger, G. Castelo-Branco, R.Fan. (2023) [Spatial epigenome–transcriptome co-profiling of mammalian tissues](#). *Nature* 616 (7955), 113-122.

A.Zivanovic, J.T. Miller, S.A. Munro, T.P. Knutson, Y. Li, C.N. Passow, P. Simonaitis, M. Lynch, L. Oseth, S.G. Zhao, F.Y. Feng, P. Wikström, E. Corey, C. Morrissey, C. Henzler, **B.J. Raphael**, S.M. Dehm. (2023) [Co-evolution of AR gene copy number and structural complexity in endocrine therapy resistant prostate cancer](#). *NAR Cancer*, 5 (3).

S. Rajan, S. Zaccaria, M.V. Cannon, M. Cam, A.C Gross, **B.J Raphael**, R.D Roberts. (2023) [Structurally complex osteosarcoma genomes exhibit limited heterogeneity within individual tumors and across evolutionary time](#). *Cancer Research Communications* 3 (4), 564-575.

R. Zeira, M. Land<sup>†</sup> and **B.J. Raphael**. (2022) [Alignment and Integration of Spatial Transcriptomics Data](#). *Nature Methods* 19 (5), 567-575. [Also: *International Conference on Research in Computational Molecular Biology (RECOMB) 2021*.]

U.Chitra\*, T.Y. Park, **B.J. Raphael**. (2022) NetMix2: Unifying network propagation and altered subnetworks. *Journal of Computational Biology* 29 (12), 1305-1323. [Also: *International Conference on Research in Computational Molecular Biology (RECOMB) 2022*.]

C. Ma\*, U.Chitra\*, S. Zhang<sup>†</sup> **B.J. Raphael**. (2022) Belayer: Modeling distinct cell type clusters and continuous variation of expression in spatial transcriptomics from layered tissues. *Cell Systems* 13 (10), 786-797. e13. [Also: *International Conference on Research in Computational Molecular Biology (RECOMB) 2022*.]

T.Y. Park, M.D.M Leiserson, G.W. Klau, **B.J Raphael**. (2022) Integrating genetic dependencies and genomic alterations across pathways and cancer types. *Cell Genomics*. Feb 9;2(2):1000992.

S. Arunachalam, K. Szlachta, S.W. Brady, X. Ma, B. Ju, B. Shaner, H.L. Mulder, J. Easton, **B.J. Raphael**, M. Myers, C. Tinkle, S.J. Allen, B.A. Orr, C.J. Wetmore, S.J. Baker, J. Zhang. (2022) Convergent

evolution and multi-wave clonal invasion in H3 K27-altered diffuse midline gliomas treated with a PDGFR inhibitor. *Acta neuropathologica Communications* 10 (1), 80.

P. Simonaitis, **B.J. Raphael**. A Maximum Parsimony Principle for Multichromosomal Complex Genome Rearrangements. (2022) 22nd *International Workshop on Algorithms in Bioinformatics* (WABI 2022).

S. Zaccaria and **B.J. Raphael**. (2021) Characterizing the allele- and haplotype-specific copy number landscape of cancer genomes at single-cell resolution with CHISEL. *Nature Biotechnology*. Feb;39(2):207-214.

G. Satas, S. Zaccaria, M. El-Kebir and **B.J. Raphael**. (2021) DeCiFering the Elusive Cancer Cell Fraction in Tumor Heterogeneity and Evolution. *Cell Systems* Oct 20;12(10):1004-1018.e10. Also: *International Conference on Research in Computational Molecular Biology (RECOMB) 2021*. **[Best Paper Runner-up Award, RECOMB 2021]**

R. Zeira, M. Land<sup>†</sup> and **B.J. Raphael**. (2021) Alignment and Integration of Spatial Transcriptomics Data. *International Conference on Research in Computational Molecular Biology (RECOMB) 2021*.

U.Chitra, K.Ding<sup>†</sup>, J.C.H. Lee, **B.J. Raphael**. (2021) Quantifying and Reducing Bias in Maximum Likelihood Estimation of Structured Anomalies. *International Conference on Machine Learning (ICML)*, 1908-1919.

R.Zeira, G.Mon<sup>†</sup>, **B.J Raphael**. (2021) Genome Halving and Aliquoting Under the Copy Number Distance. *21st International Workshop on Algorithms in Bioinformatics* (WABI 2021)

H.Sun\*, S.Cao\*, R. Jay Mashl\*, C-K Mo\*, S. Zaccaria\*, ... [42 additional co-authors] ..., **B.J. Raphael**, L.Ding. (2021) Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. *Nature Communications* Aug 24;12(1):5086.

M.A. Reyna, U.Chitra, R.Elyanow, **B.J Raphael** (2021) NetMix: A Network-Structured Mixture Model for Reduced-Bias Estimation of Altered Subnetworks. *Journal of Computational Biology* 28 (5), 469-484.

K. Huang, A.D. Scott, D. Cui Zhou, L. Wang, A. Weerasinghe, A. Elmas, R. Liu, Y.Wu, M.C. Wendl, M.A. Wyczalkowski, J. Baral, S. Sengupta, C. Lai, K. Ruggles, S.H. Payne, **B.J.Raphael**, D. Fenyö, K. Chen, G.Mills, L.Ding. (2021) Spatially interacting phosphorylation sites and mutations in cancer. *Nature Communications* Apr 19;12(1):2313.

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S. Aganezov and **B.J Raphael**. (2020) Reconstruction of clone-and haplotype-specific cancer genome karyotypes from bulk tumor samples. *Genome Research*. Sep;30(9):1274-1290. doi: 10.1101/gr.256701.119

M.A. Myers\*, S. Zaccaria\*, **B.J. Raphael**. (2020) Identifying tumor clones in sparse single-cell mutation data. *Bioinformatics* 36 S1 [Proceedings of ISMB 2020], i186-i193.

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M.A. Reyna, [multiple co-authors...] ICGC Pan-Cancer Analysis of Whole Genomes, J. Reimand, J.M. Stuart, **B.J. Raphael**. (2020) Pathway and network analysis of more than 2,500 whole cancer genomes. *Nature Communications*. 11 (1), 1-17. *Awarded: Top 50 Life and Biological Sciences Articles in Nature Communications for 2020*.

E. Rheinbay, [...92 co-authors including **B.J Raphael** ...], , G. Getz (2020) Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*. 578 (7793), 102-111.

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M.R. Reyna, M.D.M. Leiserson, **B.J. Raphael**. (2018) Hierarchical HotNet: identifying hierarchies of altered subnetworks. *Bioinformatics* [ECCB 2018 Proceedings] 34(17): i972–i980.

M.M. Parks, **B.J. Raphael**, C.E. Lawrence. (2018) Using controls to limit false discovery in the era of big data. *BMC Bioinformatics* 19 (1), 323.

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S. Zaccaria\*, M. El-Kebir\*, G.W. Klau, **B.J Raphael**. (2018) Phylogenetic Copy-Number Factorization of Multiple Tumor Samples. *Journal of Computational Biology*

L. Oesper, S. Dantas, **B.J Raphael**. (2017) Identifying Simultaneous Rearrangements in Cancer Genomes. *RECOMB Computational Cancer Biology 2017 and Bioinformatics*, (2), 346-352.

R. Elyanow, H.T. Wu, **B.J Raphael**. (2017) Identifying structural variants using linked-read sequencing data. *RECOMB Computational Cancer Biology 2017 and Bioinformatics*, 34 (2), 353-360.

J. Kuipers, K. Jahn, **B.J. Raphael**, N. Beerewinkel. (2017) Single-cell sequencing data reveal widespread recurrence and loss of mutational hits in the life histories of tumors. *Genome Research*, 27 (11), 1885-1894.

G. Satas, **B.J. Raphael**. (2017) Tumor Phylogeny Inference Using Tree-Constrained Importance Sampling. *ISMB 2017, Bioinformatics*. 33(14), i152-i160.

**BJ Raphael\***, RH Hruban\*, AJ Aguirre\*, TCGA Research Network (2017). Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. *Cancer Cell*, 32 (2), 185-203. e13.

R.J. Mashl, A.D. Scott, K. Huang, M.A. Wyczalkowski, C.J. Yoon, B. Niu, E. DeNardo, V.D. Yellapantula, R.E. Handsaker, K. Chen, D.C. Koboldt, K. Ye, D. Fenyö, **B.J. Raphael**, M.C. Wendl, L. Ding. (2017) GenomeVIP: a cloud platform for genomic variant discovery and interpretation. *Genome Research*, (8):1450-1459.

M. El-Kebir, **B.J. Raphael**, R. Shamir, R. Sharan, S. Zaccaria, M. Zehavi, R. Zeira. (2017) Complexity and algorithms for copy-number evolution problems. *Algorithms for Molecular Biology*, 12 (1), 13.

P. Nakka, N.P. Archer, H. Xu, P.J. Lupo, **B.J. Raphael**, J.J. Yang, S. Ramachandran. (2017) Novel gene and network associations found for lymphoblastic leukemia using case-control and family-based studies in multi-ethnic populations. *Cancer Epidemiology and Prevention Biomarkers* (10):1531-1539.

S. Zaccaria\*, M. El-Kebir\*, G.W. Klau, **B.J. Raphael**. (2017) The Copy-Number Tree Mixture Deconvolution Problem and Applications to Multi-Sample Bulk Sequencing Tumor Data. *International Conference on Research in Computational Molecular Biology (RECOMB)* 2017.

The Cancer Genome Atlas Research Network. (2017) Integrated genomic characterization of oesophageal carcinoma. *Nature* 541(7636):169-175.

M.D.M. Leiserson, M.A. Reyna, **B.J. Raphael**. (2016). A Weighted Exact Test for Mutually Exclusive Mutations in Cancer. *ECCB 2016/Bioinformatics*, 32(17):i736-i745.

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M. El-Kebir\*, G. Satas\*, L. Oesper, **B.J. Raphael** (2016). Inferring the Mutational History of a Tumor using Multi-State Perfect Phylogeny Mixtures. *Cell Systems*, 3(1):43-53.

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M. El-Kebir, **B.J. Raphael**, R. Shamir, R. Sharan, S. Zaccaria, M. Zehavi, R. Zeira. (2016) Copy-Number Evolution Problems: Complexity and Algorithms. *Workshop on Algorithms for Bioinformatics (WABI)* 2016.

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S. Zheng, A.D. Cherniack, N. Dewal, R.A. Moffitt, L. Danilova, B.A. Murray, A.M. Lerario, T. Else, T.A. Knijnenburg, G. Ciriello, S. Kim, G. Assie, O. Morozova, R. Akbani, J. Shih, K.A. Hoadley, T.K. Choueiri, J. Waldmann, O. Mete, A.G. Robertson, **B.J. Raphael**, M. Meyerson, M.J. Demeure, F. Beuschlein, A.J. Gill, A.C. Latronico, M.C. Fragoso, L.M. Cope, E. Kebebew, M.A. Habra, T.G. Whitsett, K.J. Bussey, W.E. Rainey, S.L. Asa, J. Bertherat, M. Fassnacht, D.A. Wheeler, The Cancer Genome Atlas Research Network, G.D. Hammer\*, T.J. Giordano\*, R.G.W. Verhaak\*. (2015) Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. *Cancer Cell*. (2016) 29(5):723-36.

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C.Lu\*, M. Xie\*, M.C. Wendl\*, J. Wang\*, M.D. McLellan\*, M.D.M. Leiserson\*, M.A. Wyczalkowski, R. Jayasinghe, K. Huang, T. Banerjee, J. Ning, P. Tripathi, Q. Zhang, B. Niu, K. Ye, H.K. Schmidt, R.S. Fulton, J.F. McMichael, P. Batra, C. Kandoth, M. Bharadwaj, D.C. Koboldt, C.A. Miller, K.L. Kanchi, J.M. Eldred, D.E. Larson, J.S. Welch, M. You, B.A. Ozenberger, R. Govindan, M.J. Walter, M.J. Ellis, E.R. Mardis, T.A. Graubert, J.F. Dpersio, T.J. Ley, R.K. Wilson, P.J. Goodfellow, **B.J. Raphael**, F. Chen, K.J. Johnson, J.D. Parvin, L. Ding. (2015) Patterns and Functional Implications of Rare Germline Variants across 12 Cancer Types. *Nature Communications*. 6:10086.

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M.M. Parks, C.E. Lawrence, **B.J. Raphael**. (2015) Detecting non-allelic homologous recombination from high-throughput sequencing data. *Genome Biology* 16 (1), 72.

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### **Work in Review**

U. Chitra, B.J. Arnold, H. Sarkar, C.Ma, S. Lopez-Darwin, K. Sanno, **B.J. Raphael** (2024) [Mapping the topography of spatial gene expression with interpretable deep learning](#). *Nature Methods* (in review) [Also: *Proceedings of the International Conference on Research in Computational Molecular Biology (RECOMB 2024)*, In press]

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U. Mai\*, G. Chu\*, **B.J. Raphael** (2024) Maximum Likelihood Inference of Time-scaled Cell Lineage Trees with Mixed-type Missing Data. *Proceedings of the International Conference on Research in Computational Molecular Biology (RECOMB 2024)*, (In press)

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## **Patent Applications**

**B.J. Raphael**, M.D.M. Leiserson, F.Vandin, H.Wu (2015). Heat Diffusion Based Genetic Network Analysis. U.S. Patent Application No.: 62/057,479.

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## **Invited Talks**

2024 Duke University, Department of Cell Biology, Distinguished Lecture

2023 Oncosphere 2023, University of Bordeaux  
University of California Riverside, Department of Statistics  
National Cancer Institute Spring School on Algorithmic Cancer Biology  
Banff, Mathematical Methods in Cancer Biology, Evolution and Therapy  
Princeton Catalysis Symposium  
Computational Genomics Summer Institute, University of California, Los Angeles  
Environmental Mutagenesis & Genomics Society 54th Annual Meeting  
Institute of Medical Informatics of the University of Münster, Digital Health Symposium  
MD Anderson Cancer Center, Leading Edge Symposium  
Institute for Computational and Experimental Research in Mathematics (ICERM), Brown University

2022 Yale Center for Biomedical Data Science, Distinguished Speaker Seminar Series  
National Cancer Institute, CBIIT Data Science Seminar Series  
American Association for Cancer Research Annual Meeting  
Computational Genomics Summer Institute, University of California, Los Angeles  
3D Models of Cancer Conference, Jackson Laboratory  
BMFZ Meeting in Düsseldorf on Genomic Structural Variants  
European Society for Molecular Oncology (ESMO)  
Bertinoro Computational Biology (BCB) Meeting  
Digital Futures Workshop on Machine learning in Biology and Medicine, KTH Royal Institute of Technology  
New York Genome Center

2021 New York Genome Center  
University of Virginia, Public Health Genomics Seminar  
Columbia University, Department of Systems Biology, Distinguished Lecture  
University of Pittsburg, Department of Biomedical Informatics Seminar  
3<sup>rd</sup> Belgrade Bioinformatics Conference  
Intelligent Systems for Molecular Biology, Keynote  
International Conference on Intelligent Biology and Medicine, Philadelphia  
Institute for Mathematical and Statistical Innovation (IMSI), University of Chicago  
“Challenges of tumor profiling in translational research” Workshop, Budapest  
NCI Information Technologies for Cancer Research  
MIT Bioinformatics seminar  
Columbia University, Irving Institute for Cancer Dynamics



- 2020 Princeton Bioengineering Symposium  
 Princeton Innovation ENGAGE 2020: Data Science in Oncology and Immunology Symposium  
 Duke University Cancer Institute, Cancer Genetics and Genomics Seminar  
 Single-cell Cancer Genomics Workshop (SCANGEN), ISMB 2020  
 UCLA Computational Genomics Summer Institute at RECOMB 2020  
 Princeton Catalysis Initiative
- 2019 Memorial Sloan Kettering Cancer Center  
 UCLA Computational Medicine Department  
 Advances in Genome Biology and Technology (AGBT) 2019  
 M.D. Anderson Cancer Center, Computational Biology Department  
 Seoul National University Bioinformatics Workshop  
 UCLA Computational Genomics Summer Institute  
 CNIO – "la Caixa" Frontiers Meeting: Heterogeneity and Evolution in Cancer  
 Bertinoro Computational Biology Meeting  
 International Symposium on Mathematical and Computational Oncology (ISMCO)  
 Mathematical Biology Institute, Ohio State University
- 2018 Harvard Biostatistics - Biomedical Informatics - Big Data (B3D) Seminar  
 St. Jude's Children's Research Hospital  
 New York Genome Center  
 American Association for Cancer Research (AACR) Annual Meeting, Methods Workshop  
 Lewis Sigler Institute Cancer Symposium, Princeton University  
 Lorentz Institute, Leiden, Netherlands  
 Gordon Research Conference on Human Genetic Variation and Disease, Biddeford, ME  
 Computational ONcology TRaining Alliance (CONTRA) Workshop, Bertinoro, Italy  
 Computational Genomics Summer Institute (CGSI), University of California, Los Angeles  
 Cell Mapping Symposium, University of California San Diego  
 Future Forum, Beijing China  
 Symposium on Advances in Cancer Genomics, Cancer Institute of New Jersey, Rutgers  
 University  
 Princess Margaret Cancer Centre, Toronto, ON
- 2017 NIPS Workshop on Machine Learning in Computational Biology  
 Biomedical Data Science Industry Day, Princeton University  
 CPTAC 3.0 PI Meeting, National Institutes of Health  
 Bertinoro Computational Biology  
 Distinguished Lecture: Department of Computer Science, University of Illinois,  
 Urbana Champaign,  
 Francis Crick Institute, Systems Genetics of Cancer Workshop  
 Cell Mapping Symposium, University of California, San Francisco  
 Simons Institute for the Theory of Computing, Genomics Reunion  
 UCLA Computational Genomics Summer Institute  
 Lake Como Workshop and School on Cancer Development and Complexity  
 Keynote: RECOMB 2017  
 Boston University Bioinformatics Student Symposium  
 Mathematical Methods in Cancer Evolution and Heterogeneity Workshop, Institute  
 for Advanced Study, Princeton  
 Keynote: Informatics Technology for Cancer Research (ITCR) Annual Meeting,  
 University of California, Santa Cruz

- New York Genome Center, Five Points Lecture  
 Data Science Seminar, Brown University  
 MIT Mathematics and CSAIL Bioinformatics Seminar  
 Statistical and Computational Challenges in Large Scale Molecular Biology, Banff  
 Princeton-Rutgers Cancer Genomics Retreat  
 Rutgers Cancer Institute of New Jersey  
 Mount Sinai, Department of Genetics  
 University of California, San Diego Bioinformatics Program, Student invited speaker
- 2016 Simons Institute for the Theory of Computing, Genomics Bootcamp  
 Simons Institute for the Theory of Computing, Networks Biology Workshop  
 Michael Waterman 75<sup>th</sup> Birthday Symposium  
 Systems Approaches to Cancer Biology Conference.  
 Weill Cornell, Institute for Computational Biomedicine (ICB) Seminar  
 University of Pennsylvania, Penn Bioinformatics Forum  
 International Symposium on Pancreatic Cancer  
 5<sup>th</sup> Seoul National University Bioinformatics Workshop  
 UCLA Computational Genomics Summer Institute  
 1<sup>st</sup> Annual Cancer Cell Map Initiative Symposium  
 Simons Foundation, New York. Invited Lecture  
 Microsoft Research New England. Computational Aspects of Biological Information (CABI)  
 Conference  
 University of Toronto, Molecular Genetics Seminar.
- 2015 Princeton, Department of Computer Science, Seminar  
 Rhode Island Hospital, Department of Pathology Seminar  
 McGill Barbados Computational Biology Workshop  
 ETH, Zurich: Department of Biosystems Science and Engineering  
 Novartis, Basel, Switzerland  
 AstraZenca, Waltham, MA  
 MIT, Mathematics and CSAIL Bioinformatics Seminar  
 Pompeu Fabra University, Barcelona.  
 COST Action for Pancreas Cancer Workshop, Barcelona.  
 Foundation Medicine, Cambridge, MA.  
 The Cancer Genome Atlas (TCGA), Steering Committee Meeting.  
 Stanford University, Cancer Systems Biology Symposium  
 Carnegie Mellon University, Computational Biology Seminar  
 European Laboratory for Molecular Biology (EMBL), Cancer Genetics Meeting  
 RECOMB Workshop on Bioinformatics Education (RECOMB-BE)  
 CAS-MPG Partner Institute for Computational Biology, Shanghai  
 CSHA/AACR Joint Meeting: Big Data, Computation and Systems Biology in Cancer  
 Indiana University, Department of Computer Science Seminar  
 Jackson Laboratory for Genomic Medicine, Seminar
- 2014 Vanderbilt University: Department of Seminar  
 U. Illinois Urbana Champaign: Institute for Genomic Biology Seminar  
 Cambridge Healthtech: Molecular Medicine Tri-Conference  
 Keynote: RECOMB Workshop on Massively Parallel Sequencing.  
 Invited Talk: American Association of Cancer Research (AACR) Annual Meeting  
 Tufts University: Department of Computer Science Seminar

- Seminar: Novartis, Cambridge  
 Invited Talk: Institute for Pure and Applied Mathematics (IPAM)  
 Invited Talk: GE Research  
 Keynote: VarI-SIG at Intelligent Systems for Molecular Biology (ISMB) conference  
 BioConductor Annual Meeting  
 European Conference on Computational Biology (ECCB) Workshop  
 Kavli Institute for Theoretical Physics: Evolution of Drug Resistance Program  
 Brown University MPPB Department  
 Beyond the Genome Conference  
 UNC Charlotte: Department of Bioinformatics Seminar  
 Broad Institute  
 EMBL: Causal Inference Workshop  
 Keynote: UW Department of Genome Sciences Symposium  
 Boston University: Systems Biology Seminar
- 2013 Cold Spring Harbor Systems Biology: Networks Meeting  
 American Association of Cancer Research (AACR) Annual Meeting  
 TCGA Pan-Cancer Symposium  
 Illumina Sequencing Expert Panel  
 Institute for Pure and Applied Mathematics, UCLA, Program Reunion  
 Bertinoro Computational Biology Conference  
 Rhode Island College Biology Symposium  
 Genentech  
 International Cancer Genome Consortium (ICGC) Annual Meeting  
 American Society Human Genetics (ASHG) Annual Meeting  
 Microsoft Research, New England
- 2012 International Cancer Genome Consortium (ICGC) Annual Meeting  
 Cold Spring Harbor Quantitative Biology Seminar  
 The Cancer Genome Atlas (TCGA) Second Scientific Symposium  
 Vancouver Bioinformatics Group (VanBUG)  
 TCGA Pan-Cancer Workshop  
*Beyond the Genome* Conference, Boston, MA  
 Joint Statistical Meetings Session on “Design and Analysis Issues with Next-Generation Sequencing Data on Complex Traits”, San, Diego, CA.  
 Pacific Symposium on Biocomputing, Genomic Medicine Session.  
 Canadian Institute for Advanced Research, Genetic Networks Meeting.
- 2011 Program Final Retreat, Institute for Pure and Applied Mathematics, UCLA  
 Bioinformatics Rendezvous, Genome Quebec, Montreal, Canada  
 The Cancer Genome Atlas' 1st Annual Scientific Symposium  
 Cancer Genomics Workshop, Institute for Pure and Applied Mathematics, UCLA  
 Workshop, Statistical Analysis for Next Generation Sequencing, Birmingham, AL  
 Knight Cancer Center, Oregon Health Sciences University, Seminar  
 Third RECOMB Satellite Conference on Bioinformatics Education  
 Ascona, Swizerland Workshop: “Statistical Challenges and Biomedical Applications of Deep Sequencing Data”.  
 Cambridge Healthtech Institute, “X-Gen Congress and Exposition”  
 University of California, San Diego. Bioinformatics Seminar.  
 University of California, Los Angeles. Computer Science Seminar.

IEEE Workshop on Computational Advances for Next Generation Sequencing (CANGS 2011).  
University of Chicago, Departments of Statistics and Cancer Biology Seminar.

- 2010 Mathematical Association of America, Northeast Section Regional Meeting.  
Washington University in St. Louis, Computer Science Seminar.  
University of Virginia, Biochemistry and Molecular Genetics Seminar.  
Memorial Sloan-Kettering Cancer Center, Computational Biology Seminar.  
Next Generation Sequencing Data Analysis Symposium, Brown University  
Washington University in St. Louis, Genetics Seminar.  
Cold Spring Harbor Laboratory, "Personal Genomes" Meeting  
Massachusetts Institute of Technology, Bioinformatics Seminar.  
University of Rhode Island  
Genome Informatics Alliance (Illumina)  
SIAM Conference on Discrete Mathematics
- 2009 University of California, Berkeley, Mathematics Colloquium  
Rhode Island Research Alliance Symposium.  
Cambridge Healthtech Institute, "Next-Generation Sequence Data Analysis" Meeting  
Cold Spring Harbor Laboratory, "Biology of Genomes" Meeting  
Helicos BioSciences, Cambridge, MA
- 2008 Washington University St. Louis Genome Sequencing Center  
SIAM Conference on Discrete Mathematics  
University of Connecticut, Department of Computer Science Colloquium  
University of California, Los Angeles, Bioinformatics Seminar  
Second Annual Bertinoro Systems Biology Meeting
- 2007 Mathematical Sciences Research Institute, "Mathematical Systems Biology of Cancer II"  
Harvard Medical School - Partners Healthcare Center for Genetics and Genomics  
GEM4 Conference on Cancer, Singapore  
Fifth Annual Bertinoro Computational Biology Meeting  
University of Virginia, Department of Mathematics  
Sixth Annual McGill Workshop on Bioinformatics in Barbados
- 2006 Tufts University, Department of Computer Science  
Brown University, Center for Statistical Sciences  
Mathematical Sciences Research Institute, "Mathematical Systems Biology of Cancer"  
University of California, San Diego, Department of Mathematics  
University of Southern California, Department of Computational and Molecular Biology  
University of Minnesota, Department of Computer Science  
Washington University St. Louis, Department of Genetics  
Boston University, Bioinformatics Program  
Brown University, Department of Computer Science  
University of California, Irvine, Department of Computer Science  
University of California, Santa Cruz, Department of Biomolecular Engineering  
Fred Hutchinson Cancer Research Center  
Purdue University, Department of Computer Science  
University of Wisconsin, Department of Biomedical Informatics  
Memorial Sloan-Kettering Cancer Center  
University of Maryland, Department of Computer Science

Georgia Tech, Department of Computer Science  
University of California, San Diego, Cancer Center

2004 RECOMB Satellite Meeting on Comparative Genomics, Bertinoro, Italy  
Duke University, Department of Computer Science  
North Carolina State University, Bioinformatics Seminar  
Intelligent Systems in Molecular Biology (ISMB), Glasgow, Scotland.

2003 European Conference on Computational Biology (ECCB), Paris, France.

## **RESEARCH GRANTS**

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### **Current**

NIH U24CA264027 9/22/2021 - 9/30/2026  
*Pathway, Network and Spatiotemporal Integration of Cancer Genomics Data*

Role: PI

Total Amount: \$1,567,260

Chan Zuckerberg Initiative 12/1/2023-11/30/2025  
*Measuring Metabolism Across Scales:*

Role: Co-PI (PI: Joshua Rabinowitz)

Total Amount of Subaward: \$172,500

Princeton Catalysis Initiative 7/1/2022 – 6/30/2024  
*Probing the cellular origins of development disorders with CRISPR-Cas9 lineage tracing*

Role: Multi-PI (with Michelle Chan, Department of Molecular Biology, Princeton University)

Total Amount: \$120,000

NIH U24CA264010 10/01/2021 - 9/30/2026  
*Deep exploration of drivers, evolution, and microenvironment toward discovering principal themes in cancer*

Role: Co-investigator. PI: L. Ding (University of Washington, St. Louis)

Total Amount of Subaward: \$202,492

Princeton Ludwig Institute 1/1/2021 – 12/31/2024  
*Spatiotemporal analyses of tumor heterogeneity and metabolism*

Role: PI

Total Amount: \$300,000

NIH U24CA248453 9/24/2020 – 8/31/2025  
*Comprehensive and Robust Tools for Analysis of Tumor Heterogeneity and Evolution*

Role: PI

Total Amount: \$4,036,410

Princeton Catalysis Initiative 7/1/2020 – 6/30/2022  
*Mapping Cell Receptor Interactomes in Cancer*

Role: Multi-PI (with David MacMillan, Department of Chemistry, Princeton University)

Total Amount: \$120,000

NIH R01CA218668-01A1 4/1/2018 – 3/31/2023  
*Computational methods for identifying non-coding cancer drivers*  
Role: Investigator (PI: Ekta Khurana)  
Total Amount of Subaward: \$91,491

**Pending**

Chan Zuckerberg Initiative 8/1/2024 – 1/31/2026  
*Modeling tissue organization and cell-cell interactions over space and time*  
Role: PI  
Total Amount: \$400,000

**Completed (Previous 6 years only)**

NIH R01DA042742-01A1 4/1/2018 – 3/31/2023  
*Integrative Prioritization of Alcohol and Drug-Addiction Related Genetic Loci*  
Role: Investigator (PI: Rohan Palmer)  
Total Amount of Subaward: \$32,486

National Cancer Institute (NCI) U24-CA211000 9/15/2016-8/31/2021  
*Pathway and Network Integration of Cancer Genomics and Clinical Data*  
Role: PI  
Total Amount: \$1,678,218

NIH DP1DA042103-01 9/15/2017 – 8/31/2022  
*The Kinship Risk Score: An Integrative Tool to Prioritize Alcohol and Drug-Addiction Related Genes for Enhanced Risk prediction*  
Role: Investigator (PI: Rohan Palmer)  
Total Amount of Subaward: \$135,000

National Cancer Institute (NCI) 9/15/2016-8/31/2021  
*Deep Discovery and Clinical Interpretation of the Germline and Somatic Cancer Drivers*  
Role: Co-investigator. PI: L. Ding (University of Washington, St. Louis)  
Total Amount of Subaward: \$125,000

Chan Zuckerberg Initiative 4/1/2018-3/30/2019  
*Analysis of molecular and cellular interactions by combining network algorithms and human insight*  
Role: PI  
Total Amount: \$218,807

National Science Foundation 1/1/2011-12/31/2019  
*CAREER: Algorithms for Next-Generation Genomics*  
Role: PI  
Total Amount: \$450,000

NIH/NHGRI 1R01HG007069 9/1/2013-8/31/2019  
*Computational Characterization of Genetic Heterogeneity*  
Role: PI  
Total Amount: \$1,119,000

NIH/NHGRI 1R01HG005690 1/01/2011-12/31/2016  
*Computational Approaches for Structural Variation Studies in Genomes*  
Role: PI  
Total Amount: \$2,616,370

Sloan Research Fellowship 9/1/2010-8/31/2016  
Role: PI  
Total Amount: \$50,000

Burroughs Wellcome Career Award at the Scientific Interface 1/1/2005-2/15/2017  
*High-resolution analysis of Tumor Genome Architectures*  
Role: PI  
Total Amount: \$500,000

NIH/National Institute of General Medical Sciences 12/1/2014 – 11/30/2019  
*COBRE Center for Computational Biology of Human Disease*  
Role: PI of Biomedical Big Data Core (PI: David Rand)  
Total Amount: \$3,556,896  
[PI of the Biomedical Big Data Core. Relinquished this role on move to Princeton.]

National Science Foundation 10/1/2012-9/30/2018  
*BIGDATA: Mid-Scale: DA: Analytical Approaches to Massive Data Computation with Applications to Genomics*  
Role: Co-PI (with PI: Eli Upfal). [Relinquished this role on move to Princeton.]  
Total Amount: \$1,566,685

NIH/NCI 1R01CA180776-01 6/18/2013-3/31/2017  
Role: PI (MPI: with Eli Upfal). [Relinquished this role on move to Princeton.]  
Additional funding for the NSF BIGDATA award listed above.  
Total Amount: \$285,316

National Science Foundation 8/15/2010-07/31/2015  
*III: Small: Algorithmic Approaches for Pathway and Gene Group Analysis in Genetic Studies*  
Role: PI  
Total Amount: \$500,000

NIH/NIAID R01 AI083636-01A1 6/15/10-5/31/15  
*Phosphoproteomic Analysis of T Cell Activation Pathways*  
Role: Co-Investigator (PI: Art Salomon, MCB Department, Brown University)  
Total Amount: \$1,936,800

National Institutes of Health 7/1/2012-6/30/2015  
*Genome-wide evaluation of therapeutic targets for axonopathies*  
Role: Co-Investigator (PI: A. DiAntonio, Washington University in St. Louis)  
Total Amount of Subcontract: \$480,743

## **EDUCATION GRANTS**

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National Science Foundation, Research Experiences for Undergraduates (REU)  
Supplemental Funding for Summer Undergraduate Research.

2013: \$24,000 (Four students)  
2012: \$15,627 (Two students)

## **SERVICE**

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### **Princeton University**

Chair, Faculty Search Committee, Department of Computer Science, 2022-2023  
Director of Graduate Studies, Department of Computer Science, 2019-2021  
Member, Graduate School Policy Subcommittee, 2020-2021  
Member, Dean for Research Limited Prize Submissions Committee, 2020-2021  
Chair, Faculty Search Committee, Department of Computer Science, 2017-2018  
Admissions Committee, Department of Computer Science, 2019-2020; 2018-2019; 2016-2017  
Freshman B.S.E. Advisor, 2017-2018.  
Sophomore, B.S.E. Department Advisor, 2018-2019.  
Department Undergraduate Advisor, 2019-2020.

### **Brown University**

Director, Center for Computational Molecular Biology, 2013-2016.  
Member, Biomedical Informatics Faculty Search Committee, 2015.  
Member, Bioinformatics Faculty Search Committee, 2014.  
Member, Pediatrics Department Chair Search Committee, 2013-2014.  
Director of Graduate Studies, Computational Biology Ph.D. Program, 2011-2013.  
Member, Computer Science Department Vision Committee, 2011-13.  
Member, Faculty Executive Committee, 2010-2011.  
Executive Committee, Center for Computational Molecular Biology, 2006-present.  
Member, Faculty Search Committee, Center for Computational Molecular Biology, 2006-09.  
Member, Graduate Student Admissions Committee, Dept. of Computer Science, 2006-12.  
Member, Research Computing and Support Working Group, 2008.  
Sheridan Center Liaison, Computer Science Department, 2008-2009.  
Library Liaison, Computer Science Department, 2008-2009.  
Member, Strategic Planning Committee on Centers, Programs & Institutes, 2009-10.

### **To the Profession**

#### ***Steering Committees:***

RECOMB Satellite Workshop on Computational Cancer Biology, 2007-present.  
RECOMB Satellite Workshop on Massively Parallel Sequencing, 2012-present.  
NCI Informatics Tools for Cancer Research (ITCR) program, 2022.  
UCLA Computational Genomics Summer Institute, 2016-present.

#### ***Program Committees:***

Research in Computational Molecular Biology (RECOMB), 2011-2024. 2018 (**Chair**).  
Intelligent Systems in Molecular Biology (ISMB): 2010-2024.  
Pacific Symposium on Biocomputing, 2013-2015.  
RECOMB Satellite Workshop on Massively Parallel Sequencing, 2014-2015.  
Workshop on Algorithms in Bioinformatics (WABI): 2008, 2009, 2012 (**Chair**), 2013, 2015.  
IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCBMS): 2011, 2012.  
ACM Conference on Bioinformatics, Computational Biology and Biomedicine: 2011.



European Conference on Computational Biology (ECCB): 2010, 2012.  
High-Throughput Sequencing (HiTSeq) SiG of ISMB, 2014, 2015  
First International Conference on Bioinformatics and Computational Biology (BICoB) 2009.  
International Symposium on Bioinformatics Research and Applications, 2008.  
RECOMB Satellite Workshop on Computational Cancer Biology. 2007(**Chair**), 2010, 2015  
(**Co-chair**).  
Sixth IEEE International Workshop on High Performance Computational Biology (HiCOMB)  
2007.  
VLDB Workshop on Data Mining in Bioinformatics, 2007.  
9<sup>th</sup> Annual Conference on Computational Genomics, 2006.  
RECOMB Satellite Workshop on Systems Biology, 2005-2007.  
RECOMB Satellite Workshop on and Regulatory Genomics, 2005.  
RECOMB Satellite Workshop on Comparative Genomics, 2005-2006.

**Organizing Committees:**

Simons Institute for the Theory of Computing, Computational Cancer Biology, 2016.  
Mathematical Biosciences Institute, Models for Oncogenesis, Clonality and Tumor  
Progression, 2016.  
Keystone Symposia, The Cancer Genome, 2016.  
Institute for Pure and Applied Mathematics, Cancer Genomics Workshop, 2011.  
Bertinoro Computational Biology, 2008.  
RECOMB Satellite Workshop on Computational Cancer Biology, 2007, 2010,2015.  
Sixth Annual McGill Workshop on Bioinformatics in Barbados, 2007.  
RECOMB Satellite Workshops on Systems Biology and Regulatory Genomics, 2005.  
RECOMB Satellite Workshop on Regulatory Genomics, 2004.

**Journal Reviewing:**

*Nature, Science, Nature Genetics, Nature Biotechnology, Nature Methods, Cell Stem Cell,  
Proceedings of the National Academy of Sciences, Genome Research, Bioinformatics, Journal of  
Computational Biology (also guest editor), Journal of the Association for Computing  
Machinery (ACM), ACM Transactions on Algorithms, Genome Biology, Trends in Genetics, BMC  
Bioinformatics, BMC Genetics, PLOS One, Parallel Computing.*

**Grant Review Panels:**

National Cancer Institute, 2011, 2021.  
NIH Study Section Member (ad hoc). MABS (2016), BDMA (2012, 2013), GCAT (2012).  
National Human Genome Research Institute, 2012.  
National Institute of General Medical Science, 2008.  
National Science Foundation, 2008, 2010, 2012, 2017.  
Cancer Prevention and Research Institute of Texas, 2021-present  
National Cancer Institute of Canada, 2008, 2013.  
Ministry of Education, Singapore, 2009-2010.

**Scientific Advisory Boards:**

National Cancer Institute, Board of Scientific Counselors, 2023-present  
Cancer Cell Map Initiative, 2017-2022  
Reactome, 2018-2022  
NSF-EPSCoR Rhode Island Genomics and Sequencing Center, 2008-2016.

**Other:**

Co-leader, GDAN Diffuse Large B-Cell Lymphoma Analysis Working Group, 2021-present  
Co-leader, TCGA Pancreatic Cancer Analysis Working Group, 2014-2017.  
Co-leader, ICGC Pan-Cancer Analysis Working Group on Networks, 2014-2020.  
Leader, Structural Aberration Detection subgroup, International Cancer Genome Consortium (ICGC), 2010-2013.  
Member NIH Cancer Genome Atlas, Genome Data Analysis Group, 2008-present.  
Career Panel Member, Howard Hughes Medical Institute Interfaces Scholars Meeting, 2008.  
Founder/Member, Bioinformatics Consulting Group, UCSD Computer Science Department, 2004-2006.  
Founder/Member, Graduate Mathematics Consulting Group, UCSD Mathematics Department, 1999-2002.

### **Professional Memberships:**

International Society for Computational Biology, 2002-present.  
Association for Computing Machinery, 2016-present  
American Association of Cancer Research, 2013-present.  
American Statistical Society, 2012-2014.  
American Mathematical Society, 1996-2002.

### **HONORS/AWARDS**

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Association for Computing Machinery (ACM) Fellow, 2023  
Test of Time Award, RECOMB Conference, 2023  
Test of Time (Runner-up) Award, RECOMB Conference, 2022  
International Society for Computational Biology (ISCB) Innovator Award, 2021  
Best Paper (Runner-up) Award, RECOMB Conference, 2021  
American Association for Cancer Research Team Science Award, 2020  
Elected Fellow, International Society of Computational Biology (ISCB), 2020  
Best Paper Award, RECOMB Conference, 2013.  
National Science Foundation CAREER Award, 2011.  
Sloan Research Fellowship (\$50,000), 2010.  
Brown Center for Computational Molecular Biology, Research Seed Award (\$5000), 2009.  
Brown ADVANCE Program Faculty Early Career Development Award (\$11,500), 2008.  
Institutional Nominee for Packard Foundation Fellowship, 2007.  
Brown Center for Computational Molecular Biology, Scholarship Innovator Award (\$5000), 2007.  
Named one "Tomorrow's PI's" by *Genome Technology* magazine, 2006.  
Burroughs Wellcome Career Award at the Scientific Interface, 2005-2010.  
Intelligent Systems in Molecular Biology (ISMB), Best Poster Award, 2005.  
Alfred P. Sloan Foundation / DOE Fellowship in Computational Biology, 2002-04.  
U.S. Department of Education, GAANN Fellowship in Mathematics (declined), 1999.

### **TEACHING**

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Enrollments indicated in []

#### Princeton University

2023            **Instructor**, "COS Independent Work Seminar" Fall 2023 [4]

2022	<b>Instructor</b> , “COS343: Algorithms for Computational Biology”, Spring 2023 [83] <b>Instructor</b> , “COS597D: Computational Methods for Single-cell and Spatial Biology” , Fall 2022 [17] <b>Instructor</b> , “COS302: Mathematics for Numerical Computing and Machine Learning”, Spring 2022 [39]
2021	<b>Instructor</b> , “COS343: Algorithms for Computational Biology”, Spring 2021 [17]
2020	<b>Instructor</b> , “COS597F: Computational Biology of Single Cells”, Fall 2020 [11] <b>Instructor</b> , “COS343: Algorithms for Computational Biology”, Spring 2020 [19]
2019	<b>Instructor</b> , “ <i>COS Independent Work Seminar</i> ” Fall 2019 [14] <b>Instructor</b> , “COS 598E: Computational Biology of Single Cells”, Spring 2019 [8]
2018	<b>Instructor</b> , “COS343: Algorithms for Computational Biology”, Spring 2018 [37]
2017	<b>Instructor</b> , “ <i>COS Independent Work Seminar</i> ” Fall 2017 [9]
2017	<b>Instructor</b> , “ <i>COS598 : Advanced Topics in Computer Science: Algorithms in Computational Biology</i> ”. Spring 2017 [7]

### Brown University

2012-2015	<b>Instructor</b> , “ <i>CSCI1810: Computational Molecular Biology.</i> ” Fall 2015 [34], Fall 2014 [14], Fall 2013 [27]; Fall 2012 [42]; Spring 2012 [23]
2007-2015	<b>Instructor</b> (and course creator) “ <i>CSCI2950-C: Topics in Computational Biology: Genomes, Networks, and Cancer.</i> ” Spring 2015 [9]; Spring 2013 [6]; Fall 2011 [12]; Fall 2010 [7]; Fall 2009 [6]; Fall 2008, Fall 2007, Spring 2006.
2008, 2011	<b>Instructor</b> for “ <i>CSCI0220: Introduction to Discrete Mathematics,</i> ” a core course for CS concentrators. Spring 2011 [86]; Spring 2008 [67].
2009-2011	<b>Guest lectures</b> for “ <i>BIOL2010: Quantitative Approaches in Biology.</i> ”
2009	Designed and taught new course “ <i>CSCI1950-Z: Computational Methods for Biology.</i> ” Spring 2009 [14].
2006-2016	<i>Reading and Research (Graduate)</i> : Spring 2016 [ ]; Fall 2015 [ ]; Spring 2015 [5]; Fall 2014 [4]; Spring 2014 [3]; Fall 2013 [4]; Spring 2013 [5]; Fall 2012 [5]; Spring 2012 [6]; Fall 2011 [6]; Spring 2011 [2], Fall 2010 [3]; Spring 2010; Fall 2009; Spring 2009; Fall 2008; Spring 2008; Fall 2007; Spring 2007.
2007-2016	<i>Individual Independent Study (Undergraduate)</i> : Spring 2015 [1]; Fall 2014 [1]; Spring 2014 [6]; Fall 2013 [2]; Fall 2012 [2]; Spring 2012 [1], Fall 2011 [3], Spring 2011 [1], Fall 2010 [1]; Spring 2010; Fall 2009; Spring 2009; Fall 2008; Spring 2008; Fall 2007; Spring 2007; Fall 2006.
1996-2002	<b>Teaching Assistant</b> , Department of Mathematics, University of California, San Diego. Four years of experience leading weekly discussion sections in undergraduate courses including: Calculus, Differential Equations, Linear Algebra, and Introduction to Algorithms.
1996	<b>Lecturer</b> , Massachusetts Institute of Technology. Designed and taught intersession course <i>Introduction to Mathematical Proofs</i> with Henry Cohn.

### Advising

#### Princeton University, Princeton, NJ

Ph.D. Students Research Supervisor:

1. Gillian Chu (Computer Science), 2022-present
2. Peter Halmos (Computer Science), 2022-present
3. Gary Hu (Computer Science), 2022-present
4. Akhil Jakatdar (Computer Science), 2022-present
5. Clover Zheng (Computer Science), 2022-present

6. Henri Schmidt (Computer Science), 2022-present
7. Madelyne Xiao (Computer Science), 2021-2022
8. Xinhao Liu (Computer Science), 2021-present
9. Ahmed Shuabi (Quantitative and Computational Biology), 2021-present
10. Alexander Strzalkowski (Computer Science), 2020-present.
11. Matthew Myers (Computer Science, Ph.D.), 2017-2022.
12. Tyler Park (Quantitative and Computational Biology, Ph.D.), 2018-2022
13. Uthsav Chitra (Computer Science), 2018-present
14. Thomas Schaffner (Computer Science), 2016-2017

Postdoctoral Fellows:

1. Hongyu Zheng, 2023-present.
2. Uyen Mai, 2022-present. [Princeton Presidential Postdoctoral Research Fellow]
3. Metin Balaban, 2022-present
4. Palash Sashittal, 2021-present
5. Pijus Simonaitis, 2021-2022
6. Cong Ma, 2020-present
7. Ron Zeira, 2018-2022
8. Sergey Aganezov, 2017-2018
9. Simone Zaccaria, 2017-2021
10. Matthew Reyna, 2016-2018
11. Mohammed El-Kebir, 2016-2017

Master's students

Maya Gupta (Computer Science), 2022-2023

Ph.D. Thesis committees

1. Ariel Gerwitz, 2019-2022.
2. Chaitanya Aluru, 2020-2021.
3. Borislav Hristov, 2018-2019.
4. Pawel Przytycki, 2018.
5. Joshua Wetzl 2018-2019.
6. Shilpa Nadimpalli, 2016-2018.

Undergraduate Advising: [number of students]

1. Senior Thesis Advisor: 2017-2018 [2], 2018-2019 [1], 2019-2020 [1], 2020-2021 [3], 2021-2022 [2], 2022-2023 [1]

Brown University, Providence RI

Ph.D. Students Research Supervisor:

1. Rebecca Elyanow, 2015-2020.
2. Gryte Satas, 2014-2020. [Honorable Mention, NSF Graduate Research Fellowship (2015)]
3. Ashley Conard, 2015-2018. Completed Sc.M. [Recipient of NSF Graduate Research Fellowship (2015)]
4. Max Leiserson, 2011-2016. [Ph.D. completed, May 2016] [Recipient of NSF Graduate Research Fellowship (2012-2014)]
5. Hsin-Ta Wu, 2010-2016. [Ph.D. completed, May 2016]

6. Layla Oesper, 2010-2015. [Ph.D. completed, May 2015] [Recipient of NSF Graduate Research Fellowship (2011-2013). Recipient of Google Anita Borg Memorial Scholarship 2014].
7. Ahmad Mahmoody, 2011-2013. Completed Sc.M.
8. Matthew Parks [with Chip Lawrence], 2011-2014. [Ph.D. completed, May 2014]
9. Alexandra Papoutsaki, 2011-2013. Completed Sc.M.
10. Fabio Vandin, 2008-2010. [Visiting Ph.D. student from University of Padova]
11. Anna Ritz, 2006-2012. [Ph.D. completed, Oct. 2012] [Recipient of NSF Graduate Research Fellowship (2008-2011)]
12. Crystal Kahn, 2007-2010. [Ph.D. completed, Oct. 2010] [Recipient of NSF Graduate Research Fellowship (2005-2008)]

Postdoctoral Fellows:

1. Dora Erdos, 2015-2016.
2. Mohammed El-Kebir, 2014-2016.
3. Matthew Reyna, 2014-2016.
4. Iman Hajirasouliha, 2013-2014. [Recipient of NSERC Postdoctoral Fellowship, 2014]
5. Jason Dobson, 2013-2014.
6. Fabio Vandin, 2010-2013.
7. Suzanne Sindi, 2006-2012.

Master's Students Research Supervisor: [number of students]  
2007-2012 [5], 2013-2016 [3]

Ph.D. Thesis and Advising Committees: [number of students]  
2007-2012 [5], 2013-2016 [7]

Undergraduate Advising

- Honors Thesis Advising: 2009, 2012, 2014 [2], 2015
- Honors Thesis Reader: 2008, 2015 [2]
- Concentration Advisor for Computational Biology. (2008-2016)
- Concentration Advisor for Computer Science. (2007-2016)
- Sophomore Advising Program. (2009-2016).

External Ph.D. Thesis Committees

Harvard Biomedical Data Science, Joe Luquette, 2021. Joshua Cook, 2022.

Carnegie Mellon University, Department of Computational Biology, Cong Ma, 2018-2021

University of Toronto, Department of Computer Science, External Examiner, Amit Deshwar 2018

Worcester Polytechnic University, Nathan Johnson, 2016-2018.

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