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EDUCATION

- 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

- 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

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. Schmidt, M.M. Chan, **B.J. Raphael**. Startle: a star homoplasy approach for CRISPR-Cas9 lineage tracing (2023). *Cell Systems* (in review). [Also: *International Conference on Research in Computational Molecular Biology (RECOMB) 2023*.]

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

N. Terekhanova* , A. Karpova* , W. Liang* , [...39 co-authors...], **B.J. Raphael***, L.Ding* (2023). Epigenetic Regulation During Cancer Transitions Across 11 Tumor Types. *Nature* (accepted, in press)

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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[†] 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[†] **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]

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U.Chitra, K.Ding[†], 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[†], **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.

S.C. Dentro, ... [46 co-authors],..., P. Van Loo, PCAWG Evolution and Heterogeneity Working Group, PCAWG Consortium. Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes (2021) *Cell* 184 (8), 2239-2254. e39.

R. Elyanow, R. Zeira, M. Land[†], **B.J. Raphael**. (2021) STARCH: Copy number and clone inference from spatial transcriptomics data. *Physical Biology*. 18 (3), 035001.

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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

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R. Zeira and **B.J. Raphael**. (2020). Copy Number Evolution with Weighted Aberrations in Cancer. *Bioinformatics*. *Bioinformatics* 36 S1 [Proceedings of ISMB 2020], i344-i352.

G. Satas, S. Zaccaria, G. Mon[†], and **B.J. Raphael**. (2020) SCARLET: Single-Cell Tumor Phylogeny Inference with Copy-Number Constrained Mutation Losses. *Cell Systems*. 10 (4), 323-332. e8. [Also: *International Conference on Research in Computational Molecular Biology (RECOMB) 2020*.]

M.A. Reyna*, U. Chitra*, R. Elyanow, **B.J. Raphael**. (2020) NetMix: A network-structured mixture model for less biased identification of altered subnetworks. *International Conference on Research in Computational Molecular Biology (RECOMB) 2020*. pp. 169-185.

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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G. Satas, **B.J. Raphael**. (2018) Haplotype phasing in single-cell DNA-sequencing data. *Bioinformatics [Proceedings of ISMB 2018]* 34 (13), i211-i217.

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

B.J 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.

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P.Nakka, **B.J. Raphael***, S Ramachandran* (2016) Gene and Network Analysis of Common Variants Reveals Novel Associations in Multiple Complex Diseases. *Genetics*, 204(2):783-798.

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*.

M. El-Kebir, G. Satas, L. Oesper, **B.J. Raphael** (2016). Multi-State Perfect Phylogeny Mixture Deconvolution and Applications to Cancer Sequencing. *RECOMB 2016*

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

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M.A. Myers, B.J. Arnold, V. Bansal, K.M. Mullen, S. Zaccaria, B.J. Raphael. (2023). HATCHet2: clone-and haplotype-specific copy number inference from bulk tumor sequencing data. *Genome Biology* (In Review)

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

- 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
- 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
3rd 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 75th 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
 5th Seoul National University Bioinformatics Workshop
 UCLA Computational Genomics Summer Institute
 1st 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, Switzerland 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 Bimolecular 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

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

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 1/1/2022 – 12/31/2023
Spatiotemporal analyses of tumor heterogeneity and metabolism
Role: PI
Total Amount: \$100,000

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 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

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

12/1/2023-11/30/2025

Measuring Metabolism Across Scales:

Role: Co-PI (PI: Joshua Rabinowitz)

Total Amount of Subaward: \$172,500

Completed (Previous 6 years only)

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

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

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), 2011-2022. 2018 (**Chair**).
Intelligent Systems in Molecular Biology (ISMB): 2010-2022.
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.
9th 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

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

Enrollments indicated in []

Princeton University

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

Brown University

2012-2015	Instructor , “ <i>CSCI1810: Computational Molecular Biology.</i> ” Fall 2015 [34], Fall 2014 [14], Fall 2013 [27]; Fall 2012 [42]; Spring 2012 [23]
2007-2015	Instructor (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	Instructor for “ <i>CSCI0220: Introduction to Discrete Mathematics,</i> ” a core course for CS concentrators. Spring 2011 [86]; Spring 2008 [67].
2009-2011	Guest lectures 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	Teaching Assistant , 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	Lecturer , 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. Maya Gupta (Computer Science), 2022-present
8. Madelyne Xiao (Computer Science), 2021-2022
9. Xinhao Liu (Computer Science), 2021-present
10. Ahmed Shuabi (Quantitative and Computational Biology), 2021-present
11. Alexander Strzalkowski (Computer Science), 2020-present.
12. Matthew Myers (Computer Science, Ph.D.), 2017-2022.
13. Tyler Park (Quantitative and Computational Biology, Ph.D.), 2018-2022
14. Uthsav Chitra (Computer Science), 2018-present
15. 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

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]

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.

University of California, San Diego

Undergraduate Research Mentoring

Sarah Aerni (2005-2006). [Finalist for Computing Research Association's Outstanding Undergraduate Award Program, 2006]