

Lior Pachter

Bren Professor of Computational Biology
Division of Biology and Bioengineering and
Department of Computing & Mathematical Sciences
California Institute of Technology
Pasadena, CA 91125, USA

Phone: (626) 395-4059
lpachter@caltech.edu
<http://pachterlab.github.io/>

Positions Held

California Institute of Technology (1/17–present)

- Bren Professor of Computational Biology

University of California, Berkeley (8/99–6/18)

- Raymond and Beverly Sackler Chair in Computational Biology (7/12–6/18)
- Director, Center for Computational Biology (1/10–6/13)
- Professor of Mathematics, Molecular & Cell Biology and Computer Science (7/09–6/18)
 - Member, Graduate Groups in Computational Biology, Biostatistics, Computational Science and Engineering and the Joint UCSF/Berkeley Program in Bioengineering
 - Member, QB3 California Institute for Quantitative Biomedical Research
 - Member, Synthetic Biology Institute
 - Affiliate, Simons Institute for Theory of Computing
- Associate Professor of Mathematics, Molecular & Cell Biology and Computer Science (7/08–7/09)
- Associate Professor of Mathematics & Computer Science (7/06–7/08)
- Associate Professor of Mathematics (7/05–7/06)
- Assistant Professor of Mathematics (8/01–6/05)
- Visiting Assistant Professor of Mathematics (8/99–8/01)

University of Oxford (9/06–07/07)

- Visiting Professor (while on sabbatical)
 - Visitor, Mathematical Institute, hosted by Professor Philip K. Maini
 - Visitor, Department of Statistics, hosted by Professor Jotun Hein

Education

Massachusetts Institute of Technology (9/94–6/99)

- PhD in Mathematics. Advisor: Professor Bonnie A. Berger
Co-advisors Professor Eric S. Lander and Professor Daniel J. Kleitman.

California Institute of Technology (9/90–6/94)

- B.S. in Mathematics.
Caltech merit award for academic achievement.

Honors, Awards and Fellowships

- Fellow of the International Society of Computational Biology (2017)
- Bren Chair in Computational Biology (2017)
- Keynote Speaker: ISBCB (2014), ISMB (2013), FPSAC (2011)
- Glenn Award (2013)
- Raymond and Beverly Sackler Chair in Computational Biology (2012)
- Cufflinks paper highlighted as a breakthrough of the year by Nat. Biotech. (2010).
- Miller Research Professorship (2009)
- Winner of best paper award for “multiple alignment by sequence annealing”,
(joint with Ariel Schwartz).
2006 European Conference on Computational Biology.
- NSF Faculty Early Career Development (CAREER) Award (2004).
- Sloan Research Fellow (2003–2004)
computational and evolutionary molecular biology.
- Federal Laboratory Consortium for Technology Transfer Award (2003).

Professional Activities

- Member, Data and Analytics Scientific Advisory Board, Amgen, 12/21–present.
- Member, Board of Trustees, Crestview Preparatory School, 6/19–6/23.
- Member, Board of Directors, Black Pine Circle School, 1/15–1/18.
- Member, Scientific Advisory Board, Maverix Biomics, 3/12–6/17.
- Member, Scientific Advisory Board, Mathematical Biosciences Institute, 11/08–12/11.
- Testimony as an expert witness on matters related to genomics and biotechnology.

Grants

- Mathematical models for studying stochastic systems biology of the cell with single-cell genomics data
8/25 – 8/27 (\$150,000)
- Center for Mouse Genomic Variation at Single Cell Resolution, PI
co-PI (with Ali Mortazavi, Barbara Wold, Kim Green and Grant MacGregor)
8/21 – 5/26 (\$2,534,261)
- SUGAR-seq: A New Technology for Single-Cell Glycan and Gene Expression Profiling in Alzheimer's disease
co-PI (with Linda-Hsieh Wilson)
9/18 – 9/23 (\$3,278,468)
- A Comprehensive Whole-Brain Atlas of Cell Types in the Mouse,
co-PI (with Honkgui Zeng, David J Anderson, Andreas Tolias and Xiaowei Zhuang)
9/17 – 9/22 (\$1,194,784)
- Algorithms and Software for Provably Accurate De Novo RNA-Seq Assembly
co-PI (with David Tse and Sreeram Kannan)
9/15–9/18 (\$476,329), NIH (R01).
- Streaming algorithms for whole genome assembly,
co-PI (with Páll Melsted)
1/15–12/15 (9,950,000 ISK = \$83,000), Icelandic Research Fund.
- UCSC Center of Excellence for Big Data Computing in the Biomedical Sciences
co-PI (Center PIs: David Haussler and David Patterson)
9/14–9/18 (\$100,000), NIH (U54).
- Center for RNA Systems Biology
co-PI computational core (Center PI: Jaimie Cate)
9/12–9/15 (\$465,000 computational core), NIH (P50).
- Metagenome quantification using high-throughput sequencing,
co-PI (with Kevin McLoughlin)
7/12–7/13 (\$296,498), UC Lab Fees Research Program Award.
- Association mapping without genotyping, co-PI (with Michael Eisen)
4/12–4/15 (\$406,120), NIH (R21).
- Agilent Research grant (funded through the Synthetic Biology Institute), PI
3/12–3/13 (\$60,000).
- Erythroid stage-specific transcriptome expression, dynamics, and regulation,
co-PI (with John Conboy)
9/11–5/16 (\$2,380,104), NIH (R01).
- Methods for the analysis of RNA-Seq and related sequence census based experiments, PI
8/11–5/16 (\$1,114,512), NIH (R01).
- Fundamental laws of biology, co-PI (with Bernd Sturmfels)
9/05–3/09 (\$750,000), DARPA.
- CAREER: Comparison and Annotation of Multiple Whole Genomes, PI
6/04–6/09 (\$400,000), NSF.

- GENCODE: The Encyclopedia of Genes and Gene Variants (main PI: Roderic Guigó)
10/03–10/06 (\$72,000), NIH.
- Cross-species gene finding and annotation, PI
6/02–6/05 (\$928,728), NIH (R01).

Publications

- [286] Meichen Fang, Gennady Gorin, and Lior Pachter. “Trajectory inference from single-cell genomics data with a process time model”. In: *PLoS computational biology* 21.1 (2025), e1012752.
- [285] Meichen Fang and Lior Pachter. “Extrinsic biological stochasticity and technical noise normalization of single-cell RNA sequencing data”. In: *bioRxiv* (2025), pp. 2025–05.
- [284] Yeokyoung Kil and Lior Pachter. “Differential Analysis Reveals Isoform Switching Following Pneumococcal Vaccination”. In: *bioRxiv* (2025), pp. 2025–03.
- [283] Rebekah K Loving et al. “Long-read sequencing transcriptome quantification with lr-kallisto”. In: *bioRxiv* (2025), pp. 2024–07.
- [282] Laura Luebbert and Lior Pachter. “Agnostic viral detection at single-cell resolution reveals novel viruses”. In: *Nature Biotechnology* (2025).
- [281] Laura Luebbert et al. “Detection of viral sequences at single-cell resolution identifies novel viruses associated with host gene expression changes”. In: *Nature Biotechnology* (2025), pp. 1–10.
- [280] Lambda Moses et al. “Geospatially informed representation of spatial genomics data with SpatialFeatureExperiment”. In: *bioRxiv* (2025).
- [279] Conrad G Oakes and Lior Pachter. “Transcriptomic responses to endurance exercise training in rats”. In: *bioRxiv* (2025), pp. 2025–07.
- [278] Elisabeth Rebboah et al. “Systematic cell-type resolved transcriptomes of 8 tissues in 8 lab and wild-derived mouse strains captures global and local expression variation”. In: *bioRxiv* (2025), pp. 2025–04.
- [277] Delaney K Sullivan, Mayuko Boffelli, and Lior Pachter. “Pseudoassembly of k-mers”. In: *bioRxiv* (2025), pp. 2025–05.
- [276] Delaney K Sullivan et al. “Accurate quantification of nascent and mature RNAs from single-cell and single-nucleus RNA-seq”. In: *Nucleic acids research* 53.1 (2025), gkae1137.
- [275] Delaney K Sullivan et al. “kallisto, bustools and kb-python for quantifying bulk, single-cell and single-nucleus RNA-seq”. In: *Nature Protocols* 20.3 (2025), pp. 587–607.
- [274] Eduardo da Veiga Beltrame et al. *Efficient combinatorial bead barcoding*. US Patent 12,286,621. Apr. 2025.
- [273] A Sina Boeshaghi, Ángel Gálvez-Merchán, and Lior Pachter. “Algorithms for a Commons Cell Atlas”. In: *bioRxiv* (2024), pp. 2024–03.
- [272] A Sina Boeshaghi et al. “Quantifying orthogonal barcodes for sequence census assays”. In: *Bioinformatics Advances* 4.1 (2024), vbad181.

- [271] Ali Sina Booeshaghi, Xi Chen, and Lior Pachter. “A machine-readable specification for genomics assays”. In: *Bioinformatics* 40.4 (2024), btae168.
- [270] Maria Carilli and Lior Pachter. “Studying RNA dynamics from single-cell RNA sequencing snapshots”. In: *Nature Methods* 21.8 (2024), pp. 1418–1419.
- [269] Maria Carilli et al. “Biophysical modeling with variational autoencoders for bimodal, single-cell RNA sequencing data”. In: *Nature Methods* 21.8 (2024), pp. 1466–1469.
- [268] Tara Chari, Gennady Gorin, and Lior Pachter. “Biophysically interpretable inference of cell types from multimodal sequencing data”. In: *Nature Computational Science* 4.9 (2024), pp. 677–689.
- [267] Tara Chari, Gennady Gorin, and Lior Pachter. “Stochastic Modeling of Biophysical Responses to Perturbation”. In: *bioRxiv* (2024).
- [266] Tanya B Dorff et al. “PSCA-CAR T cell therapy in metastatic castration-resistant prostate cancer: a phase 1 trial”. In: *Nature medicine* 30.6 (2024), pp. 1636–1644.
- [265] Meichen Fang, Gennady Gorin, and Lior Pachter. “Trajectory inference from single-cell genomics data with a process time model”. In: *bioRxiv* (2024), pp. 2024–01.
- [264] Catherine Felce, Gennady Gorin, and Lior Pachter. “A Biophysical Model for ATAC-seq Data Analysis”. In: *bioRxiv* (2024), pp. 2024–01.
- [263] Ángel Gálvez-Merchán, A Sina Booeshaghi, and Lior Pachter. “A human commons cell atlas reveals cell type specificity for OAS1 isoforms”. In: *bioRxiv* (2024), pp. 2024–03.
- [262] Gennady Gorin and Lior Pachter. “New and notable: Revisiting the “two cultures” through extrinsic noise”. In: *Biophysical Journal* 123.1 (2024), pp. 1–3.
- [261] Gennady Gorin et al. “Spectral neural approximations for models of transcriptional dynamics”. In: *Biophysical Journal* 123.17 (2024), pp. 2892–2901.
- [260] Ingileif B Hallgrímsdóttir, Maria Carilli, and Lior Pachter. “Estimating cis and trans contributions to differences in gene regulation”. In: *bioRxiv* (2024), pp. 2024–07.
- [259] Kayla C Jackson et al. “Identification of spatial homogeneous regions in tissues with concordex”. In: *bioRxiv* (2024), pp. 2023–06.
- [258] Laura Luebbert and Lior Pachter. “The miscalibration of the honeybee odometer”. In: *arXiv preprint arXiv:2405.12998* (2024).
- [257] Laura Luebbert et al. “Fast and scalable querying of eukaryotic linear motifs with gget elm”. In: *Bioinformatics* 40.3 (2024), btae095.
- [256] Joseph M Rich et al. “The impact of package selection and versioning on single-cell RNA-seq analysis”. In: *bioRxiv* (2024), pp. 2024–04.
- [255] Noémie C Sierra et al. “A novel approach to comparative RNA-seq does not support a conserved set of orthologs underlying animal regeneration”. In: *Genome Biology and Evolution* 16.6 (2024), evae120.

- [254] Delaney K Sullivan and Lior Pachter. “Flexible parsing, interpretation, and editing of technical sequences with splitcode”. In: *Bioinformatics* 40.6 (2024), btae331.
- [253] Delaney K Sullivan et al. “De novo mutation discovery in a mouse model and a human patient sample of non-Hodgkin’s lymphoma”. In: *Cancer Research* 84.6_Supplement (2024), pp. 6246–6246.
- [252] Zsofia Torok et al. “Resilience of A Learned Motor Behavior After Chronic Disruption of Inhibitory Circuits”. In: *bioRxiv* (2024), pp. 2023–05.
- [251] A Sina Booeshaghi, Delaney K Sullivan, and Lior Pachter. “Universal preprocessing of single-cell genomics data”. In: *bioRxiv* (2023).
- [250] A Sina Booeshaghi et al. “Author Correction: Principles of open source bioinstrumentation applied to the poseidon syringe pump system”. In: *Scientific Reports* 13.1 (2023), p. 14834.
- [249] Maria Carilli et al. “Biophysical modeling with variational autoencoders for bimodal, single-cell RNA sequencing data”. In: *bioRxiv* (2023).
- [248] Tara Chari, Gennady Gorin, and Lior Pachter. “Biophysically informed modeling for mapping the effects of genetic and environmental perturbation on cell states”. In: *APS March Meeting Abstracts*. Vol. 2023. 2023, N00–303.
- [247] Tara Chari and Lior Pachter. “The specious art of single-cell genomics”. In: *PLOS Computational Biology* 19.8 (2023), e1011288.
- [246] IGVF Consortium. “The Impact of Genomic Variation on Function (IGVF) Consortium”. In: *arXiv preprint arXiv:2307.13708* (2023).
- [245] Meichen Fang, Gennady Gorin, and Lior Pachter. “Interpretable models for transcriptional dynamics during cell fate transitions”. In: *APS March Meeting Abstracts*. Vol. 2023. 2023, N00–308.
- [244] Kelli D Fenelon et al. “Cell-specific occupancy dynamics between the pioneer-like factor Opa/ZIC and Ocelliless/OTX regulate early head development in embryos”. In: *Frontiers in Cell and Developmental Biology* 11 (2023), p. 1126507.
- [243] Ángel Gálvez-Merchán et al. “Metadata retrieval from sequence databases with ffq”. In: *Bioinformatics* 39.1 (2023), btac667.
- [242] Gennady Gorin and Lior Pachter. “Length biases in single-cell RNA sequencing of pre-mRNA”. In: *Biophysical Reports* 3.1 (2023).
- [241] Gennady Gorin and Lior Pachter. “The telegraph process is not a subordinator”. In: *bioRxiv* (2023).
- [240] Gennady Gorin, John J Vastola, and Lior Pachter. “Studying stochastic systems biology of the cell with single-cell genomics data”. In: *Cell Systems* 14.10 (2023), pp. 822–843.

- [239] Gennady Gorin, Shawn Yoshida, and Lior Pachter. “Assessing markovian and delay models for single-nucleus RNA sequencing”. In: *Bulletin of Mathematical Biology* 85.11 (2023), p. 114.
- [238] Kayla C Jackson and Lior Pachter. “A standard for sharing spatial transcriptomics data”. In: *Cell Genomics* 3.8 (2023).
- [237] Kayla C Jackson et al. “Quantitative assessment of single-cell RNA-seq clustering with CONCORDEX”. In: *bioRxiv* (2023), pp. 2023–06.
- [236] Yeokyoung Kil, Ali Sina Booeshaghi, and Lior Pachter. “Comparative survey-based study of saliva collection devices”. In: (2023).
- [235] T Joseph W Lazio et al. “Data-Driven Approaches to Searches for the Technosignatures of Advanced Civilizations”. In: *arXiv preprint arXiv:2308.15518* (2023).
- [234] Steinunn Liorsdóttir and Lior Pachter. “The virial theorem and the Price equation”. In: *arXiv preprint arXiv:2312.06114* (2023).
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- [232] Lambda Moses et al. “Voyager: exploratory single-cell genomics data analysis with geospatial statistics”. In: *bioRxiv* (2023).
- [231] Fairlie Reese et al. “The ENCODE4 long-read RNA-seq collection reveals distinct classes of transcript structure diversity”. In: *bioRxiv* (2023).
- [230] Delaney K Sullivan and Lior Pachter. “Flexible parsing and preprocessing of technical sequences with splitcode”. In: *bioRxiv* (2023), pp. 2023–03.
- [229] Delaney K Sullivan et al. “kallisto, bustools, and kb-python for quantifying bulk, single-cell, and single-nucleus RNA-seq”. In: *bioRxiv* (2023).
- [228] Zsofia Torok et al. “Recovery of a learned behavior despite partial restoration of neuronal dynamics after chronic inactivation of inhibitory neurons”. In: *bioRxiv* (2023).
- [227] Lingyun Xiong et al. “Direct androgen receptor control of sexually dimorphic gene expression in the mammalian kidney”. In: *Developmental Cell* 58.21 (2023), pp. 2338–2358.
- [226] A Sina Booeshaghi and Lior Pachter. “Pseudoalignment facilitates assignment of error-prone Ultima Genomics reads”. In: *bioRxiv* (2022), pp. 2022–06.
- [225] A Sina Booeshaghi et al. “Depth normalization for single-cell genomics count data”. In: *BioRxiv* (2022), pp. 2022–05.
- [224] Kristján Eldjárn Hjörleifsson et al. “Accurate quantification of single-cell and single-nucleus RNA-seq transcripts using distinguishing flanking k-mers”. In: *bioRxiv* (2022), pp. 2022–12.
- [223] Adam Gayoso et al. “A Python library for probabilistic analysis of single-cell omics data”. In: *Nature biotechnology* 40.2 (2022), pp. 163–166.

- [222] Jase Gehring et al. *Sample multiplexing for single-cell RNA sequencing*. US Patent 11,492,610. Nov. 2022.
- [221] Gennady Gorin and Lior Pachter. “Distinguishing biophysical stochasticity from technical noise in single-cell RNA sequencing using Monod”. In: *bioRxiv* (2022), pp. 2022–06.
- [220] Gennady Gorin and Lior Pachter. “Modeling bursty transcription and splicing with the chemical master equation”. In: *Biophysical Journal* 121.6 (2022), pp. 1056–1069.
- [219] Gennady Gorin, Shawn Yoshida, and Lior Pachter. “Transient and delay chemical master equations”. In: *bioRxiv* (2022), pp. 2022–10.
- [218] Gennady Gorin et al. “Interpretable and tractable models of transcriptional noise for the rational design of single-molecule quantification experiments”. In: *Nature Communications* 13.1 (2022), p. 7620.
- [217] Gennady Gorin et al. “RNA velocity unraveled”. In: *PLOS Computational Biology* 18.9 (2022), e1010492.
- [216] Gennady Gorin et al. “Spectral neural approximations for models of transcriptional dynamics”. In: *Biophysical Journal* (2022).
- [215] Kristján Eldjárn Hjörleifsson, Lior Pachter, and Páll Melsted. “Annotation-agnostic discovery of associations between novel gene isoforms and phenotypes”. In: *bioRxiv* (2022), pp. 2022–12.
- [214] Lambda Moses and Lior Pachter. “Museum of spatial transcriptomics”. In: *Nature methods* 19.5 (2022), pp. 534–546.
- [213] Lior Pachter. “A decade of molecular cell atlases”. In: *arXiv e-prints* (2022), arXiv–2204.
- [212] Joshua S Bloom et al. “Massively scaled-up testing for SARS-CoV-2 RNA via next-generation sequencing of pooled and barcoded nasal and saliva samples”. In: *Nature Biomedical Engineering* 5.7 (2021), pp. 657–665.
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- [210] A Sina Booeshaghi, Fan Gao, and Lior Pachter. “Assessing the multimodal tradeoff”. In: *BioRxiv* (2021), pp. 2021–12.
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- [207] A Sina Booeshaghi* et al. “Low-cost, scalable, and automated fluid sampling for fluidics applications”. In: *HardwareX* (2021), e00201–co.
- [206] Tara Chari and Lior Pachter. “The Split Senate”. In: *APSA Preprints* (2021).

- [205] Tara Chari* et al. “Whole-animal multiplexed single-cell RNA-seq reveals transcriptional shifts across *Clytia medusa* cell types”. In: *Science advances* 7.48 (2021), eabh1683–co.
- [204] Principal manuscript editors et al. “A multimodal cell census and atlas of the mammalian primary motor cortex”. In: *Nature* 598.7879 (2021), pp. 86–102.
- [203] Gennady Gorin and Lior Pachter. “Analysis of Length Biases in Single-Cell RNA Sequencing of Unspliced mRNA by Markov Modeling”. In: *Biophysical Journal* 120.3 (2021), 81a.
- [202] Gennady Gorin and Lior Pachter. “Analytical solutions of the chemical master equation with bursty production and isomerization reactions”. In: *bioRxiv* (2021), pp. 2021–03.
- [201] Johan Gustafsson et al. “BUTTERFLY: addressing the pooled amplification paradox with unique molecular identifiers in single-cell RNA-seq”. In: *Genome Biology* 22.1 (2021), p. 174.
- [200] Páll Melsted* et al. “Modular, efficient and constant-memory single-cell RNA-seq preprocessing”. In: *Nature biotechnology* (2021), pp. 1–6.
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- [195] Zizhen Yao et al. “A transcriptomic and epigenomic cell atlas of the mouse primary motor cortex”. In: *Nature* 598.7879 (2021), pp. 103–110.
- [194] A Sina Boeshaghi and Lior Pachter. “Decrease in ACE2 mRNA expression in aged mouse lung”. In: *bioRxiv* (2020), pp. 2020–04.
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Reviewing

- Previously on the editorial board of *Genome Biology*, and associate editor for *Bulletin of Mathematical Biology* and *Mathematical Medicine & Biology*.
- Referee for *Advances in Applied Mathematics*, *Bioinformatics*, *BMC Bioinformatics*, *Bulletin of Mathematical Biology*, *Discrete Mathematics*, *Electronic Journal of Combinatorics*, *Genome Biology*, *Genome Research*, *Journal of Computational Biology*, *Journal of Molecular Biology*, *Journal of Theoretical Biology*, *Journal of Symbolic Computation*, *Nature Biotechnology*, *Nature Genetics*, *Nature Methods*, *Nucleic Acids Research*, *PLoS Computational Biology*, *PLoS Genetics*, *Science*, *Statistica Sinica*, *Statistical Applications in Genetics and Molecular Biology*
- External reviewer for investigator proposals at the Wellcome Trust Sanger Institute.
- External reviewer for the Irish Science Foundation.
- External reviewer for the Icelandic Research Fund.
- Standing Panel Member, 2004–2006.
NIH Biological Data Management and Analysis grant review group.
- Reviewer for NIH GCAT and special genomics panels.
- Reviewer for NSF mathematical biology panels.

Committees

- Committee for the Protection of Human Subjects - Institutional Review Board, 2025 – present
- Librarian Hiring Committee, 2025
- Hiring Committee (CMS), 2024 – 2025
- Division Chair Selection Committee, 2024
- Faculty Board, 2023– present.
- Hiring Committee (BBE), 2022-2023.
- Miller 60th Anniversary Committee, 2014.
- Curriculum Committee, Department of Mathematics, 2014–2015.
- Education Committee, Department of Mathematics, 2013–2014.
- Ad Hoc Committee, 2014.
- Chair, Ad Hoc Committee, 2011.
- Chair, Joint MCB/CCB Search Committee, 2010–2011.
- Search Committee, School of Public Health, 2010–2011.
- Committee on Calculus and Courses, Department of Mathematics, 2010–2014.
- Graduate Council, 2008.
- Faculty Appointments Committee, Department of Mathematics, 2007–2008.
- Graduate Admissions Committee, Department of Computer Science, 2007–2008.
- Committee on the Profession of the American Mathematical Society, 2005–2008.
- Computational Biology Initiative Search Committee, 2004–2006.
- Executive committee

- Graduate group in computational and molecular biology, 2001–2017.
- Conference program committees
 - 11th International Conference on Research in Computational Molecular Biology, 2007.
 - First Argentine Conference on Mathematics and Biology, 2005.
 - First IEEE Computer Society Bioinformatics Conference, 2002.
 - Second Workshop on Algorithms in Bioinformatics, 2002.

Conference organization

- Co-organizer of Chen Institute Data Science and AI for Neuroscience Summer School Caltech, 6/22.
- Co-organizer of Algorithms in Computational Genomics semester at the Simons Institute UC Berkeley, 1/16–6/16.
- Co-organizer of BAMBA 8 UC Berkeley, 9/12.
- Organizer of *Seq I Workshop UC Berkeley, 6/12.
- Session organizer (with Simon Myers) on “Computational Genomics” Cold Spring Harbor Laboratories meeting on “Biology of Genomes”, 2012.
- Organizer, IPAM program on mathematical and computational approaches to high throughput sequencing, 9/11.
- MSRI workshop organizer (with Serkan Hoşten and Bernd Sturmfels) on “Algebraic Statistics”, 2008.
- IMA workshop organizer (with Serkan Hoşten and Seth Sullivant) on “Applications of Algebraic Geometry to Biology, Dynamics and Statistics”, 2007.
- MSRI summer graduate workshop organizer (with Reinhard Laubenbacher) on “Mathematical aspects of computational biology”, 2006.
- Conference organizer (with Bernd Sturmfels and Seth Sullivant) on “Computational Biology and Algebraic Statistics”, Clay Institute, 2005.
- Session organizer (with Peer Bork) on “Computational Genomics” Cold Spring Harbor Laboratories meeting on “Biology of Genomes”, 2004.
- Session organizer (with Allan Bradley) on “Comparative Genomics” Cold Spring Harbor Laboratories meeting on “Genome Sequencing and Biology”, 2002.
- Session organizer (with Sean Eddy) on “Comparative Genomics” CSHL/Wellcome Trust joint meeting, 2002.
- Session organizer (with Serafim Batzoglou) on “Gene Regulation” Pacific Symposium on Biocomputing (PSB), 2003.
- Session organizer (with Inna Dubchak) on “Genome-wide Analysis and Comparative Genomics”, Pacific Symposium on Biocomputing (PSB), 2002.

Outreach

- Blog at [Bits of DNA](#) (8/13–present)
- Lecturer and invited speaker at Berkeley Math Circle– middle schoolers (10/14, 12/15)
- Guest lecturer, UCLA symposium on math education for biologists (5/14)
- VIGRE lecture, Department of Statistics, UC Berkeley (11/07)
- Palo Alto High School Mathematics Evening (5/05)
- Los Medanos College Computational Biology Lecture (2/05)

Recent Invited Talks

- Stanford University Information Theory Forum (12/22)
- RECOMB/ISCB Conference on Regulatory and Systems Genomics with DREAM Challenges (11/22)
- Vanderbilt University Quantitative Systems Biology Seminar (10/22)
- Cold Spring Harbor Laboratories Biology of Genomes (5/22)
- Conference on Quantitative Approaches in Biology (3/22)

Teaching

Classes developed

- Caltech course Bi1C
Introduction to Biology through the Lens of Computer Science, 2024–
- Caltech course BI/BE/CS 183
Computational Biology, 2017–
Introduction to Methods in computational biology with a focus on single-cell RNA-seq
- Berkeley graduate course MCB C243/MATH C243
**Seq methods and applications*, 2014–2018
Cross listed course between molecular biology and math on methods and applications of high-throughput sequencing.
- Berkeley undergraduate course Math 10
Methods in Mathematics:
Calculus, Probability & Statistics and Discrete Mathematics for the biological sciences
Developed over the course of three years, this new class replaces the existing freshman mathematics requirements for biology majors.
First taught as a pilot (Math 91) Fall 2011.
- Berkeley graduate course Math 239
Discrete Mathematics for the Life Sciences, 2007–2018
- Berkeley undergraduate course Math 127
Mathematical and Computational Methods in Molecular Biology, 1999–2018

Classes taught

- Introduction to Biology (Caltech Bi 1, 1/24, 1/25)
- Introduction to Probability and Statistics (Caltech Ma 3, 1/24, 1/25)
- Machine Learning and Data Mining (Caltech CS 155, 1/20)
- Computational Biology (Caltech BI/BE/CS 183, 1/18, 1/19, 1/21, 1/22, 1/23)
- Linear algebra and differential equations (UCB MATH 54, 1/15)
- *Seq methods and applications (UCB MCB C243/MATH C243)
Graduate course on methods and applications of high-throughput sequencing.
- Calculus, probability and statistics, and discrete mathematics for the biological sciences (UCB MATH 91/10, 9/11, 9/13, 1/16).
A new two semester freshman math course for biology majors.

- Genome Project Laboratory (UCB MCB 247, 1/09,1/10,1/11)
A hands-on graduate course on whole-genome sequencing, assembly and analysis co-taught with Rachel Brem and Michael Eisen.
- Discrete mathematics for the life sciences (UCB MATH 239, 1/08, 1/13)
An introductory graduate course at UC Berkeley on discrete mathematics and applications to current topics in biology.
- Mathematical and computational methods in molecular biology (UCB MATH 127, 9/00, 9/01, 9/02, 1/04, 9/07,9/10, 9/14). This is an undergraduate course at UC Berkeley for mathematicians interested in the applications of mathematics to molecular biology.
- Algebraic combinatorics (UCB MATH 249, 9/05, 1/09)
Taught from the notes *Combinatorial Theory*, by Gian-Carlo Rota.
- Graduate Research Seminar in Computational Biology (with Bernd Sturmfels, UCB MATH 290, 9/03, 1/05, 1/06).
- Graduate Research Seminar in Computational Biology (with Niko Beerenwinkel, UCB MATH 290, 9/05).
- Graduate Research Seminar in Computational Biology (with Richard Karp, UCB MATH 290, 1/00, 9/02).
- Topics in applied mathematics: algebraic statistics for computational biology (with Bernd Sturmfels UCB MATH 275, 9/04).
- Enumerative combinatorics (UCB MATH 199, 1/00).
An independent study course with two students. The study was based on Richard Stanley's Enumerative Combinatorics Vol. 1.
- Numerical analysis (UCB MATH 128a, 1/00, 1/01, 1/03).
- Linear algebra (UCB MATH 110, 9/99, 1/02).
- Multivariable calculus (UCB MATH 53, 1/04).
- Freshman calculus (MIT 18.01, 9/95, 9/96, UCB MATH 16B, 1/06).
Designed course and taught approximately 30 students as part of the MIT concourse program.

Short Courses

- Applications of algebraic statistics (5/07)
Course taught at the University of Barcelona, Spain.
- Algebraic statistics for computational biology (3/05)
Course taught at the National University of Córdoba, Argentina.
- Hidden Markov models for alignment, gene finding and protein motif detection
Harvard short course on "Statistics and Genomics", Boston (1/02)
- Multiple Sequence Alignment (11/06)
Lecture series at the Instituto Gulbenkian de Ciência, Oerias, Portugal.

Research Supervision

Current graduate students

- Maria Carilli (biochemistry and molecular biophysics)
- Vera Beilinson (biology)
- Catherine Felce (physics)
- Kayla Jackson (biology)
- Conrad Oakes (biology)
- Joseph Rich (biology)

Graduated students

39. Rebekah Loving (biology), Ph.D. thesis 5/25
Methods for Long Read RNA-seq Transcriptomics
38. Meichen Fang (bioengineering), Ph.D. thesis 5/25
A biophysical approach to normalization and trajectory inference in single-cell RNA sequencing data analysis
37. Delaney Sullivan (biology), Ph.D. thesis 5/25
Software, tools, and methods development for single-cell transcriptomics
co-advised by Mitchell Guttman
36. Anne Yeokyoung Kil (medical engineering), Ph.D. thesis 4/25
Engineering and Computational Tools for Salivary Biomedicine
35. Tara Chari (bioengineering), Ph.D. thesis 6/24
Perturbing the Genome: From Bench to Biophysics
34. Laura Luebbert (biology), Ph.D. thesis 3/24
Complexity of Transcriptomic Data Analysis and Implications for Biological Discovery
33. Taleen Dilanyan (chemistry), Ph.D. thesis 12/23
Open-Source Custom Beads for Single-Cell Transcriptomics
32. Gennady Gorin (chemical engineering), Ph.D. thesis 6/23
Stochastic Foundations for Single-Cell RNA Sequencing
31. Lambda Moses (biology), Ph.D. thesis 6/23
Computational Foundations for Spatial Transcriptomics
30. Ángel Gálvez-Merchán (biology), Ph.D. thesis 6/23
Studies of mRNA expression and degradation
29. Kristján Eldjárn Hjörleifsson (computer science), Ph.D. thesis 12/22
Graph modeling for genomics and epidemiology
28. Ali Sina Boeshaghi (mechanical engineering), Ph.D. thesis 6/22
Dissertation: Foundations and Applications of Single-Cell RNA-Sequencing
27. Lynn Yi (biology), Ph.D. thesis 6/19
Statistical Methods for Gene Differential Expression Analysis of RNA-Sequencing
26. Robert Tunney (computational biology), Ph.D. thesis 6/18
co-advised by Liana Laureau
Regression Modeling and Bias Correction of Ribosome Profiling Data

25. Jase Gehring (molecular biology), Ph.D. thesis 6/18
Expanding Single-Cell RNA-Sequencing in Scale and Dimension
24. Askshay Tambe (molecular biology), Ph.D. thesis 6/16
co-advised by Jennifer Doudna
Developing experimental and computational tools for sequence-census assays
- 23 Lorian Schaeffer (molecular biology), Ph.D. thesis 6/16
Pseudoalignment for metagenomic and metatranscriptomic read assignment
22. Harold Pimentel (computer science), Ph.D. thesis 6/16
Fast and accurate quantification and differential analysis of transcriptomes
21. Isaac Joseph (computational biology), Ph.D. thesis 6/16
Sequencing-based computational methods for identifying impactful genomic alterations in cancers
20. Shannon Hateley (molecular biology), Ph.D. thesis 6/16
co-advised by Michael Eisen
Detection, Quantification, and Characterization of Diverse RNA Transcript Isoforms
19. Brielin Brown (computer science), Ph.D. thesis 6/16.
Computational approaches to understanding the genetic architecture of complex traits
18. Natth Bejraburnin (mathematics), Ph.D. thesis 12/15.
A Study on Correlations between Genes' Functions and Evolution
17. Emily Berger (mathematics), Ph.D. thesis 8/15.
Probabilistic Methods for Single Individual Haplotype Reconstruction: Haptree and Haptree-X
16. Aif Rahman (computer science), Ph.D. thesis 8/15.
Statistical Models for Genome Assembly and Analysis
15. Nicolas Bray (mathematics), Ph.D. thesis 12/14.
Methods for Measurement and Interpretation of Gene Expression
Postdoctoral Researcher at the Innovative Genomics Initiative with Jacob Corn and with Jennifer Doudna, UC Berkeley.
14. Adam Roberts (computer science), Ph.D. thesis 8/13.
Ambiguous fragment assignment for high-throughput sequencing experiments
Software Engineer, Google.
13. Meromit Singer (computer science), Ph.D. thesis 12/12.
Statistical algorithms in the study of DNA methylation
Postdoctoral Researcher, Broad Institute with Aviv Regev.
12. Aaron Kleinman (mathematics), Ph.D. thesis 5/12.
Combinatorial Phylogenetics of Reconstruction Algorithms
Research Scientist, 23andme.
11. Cole Trapnell (computer science) at the University of Maryland, co-advised by Steven Salzberg, Ph.D. thesis 5/10.
Transcript Assembly and Abundance Estimation with High-throughput RNA-sequencing.
Assistant Professor of Genome Sciences, University of Washington.
10. Anne Shiu (mathematics), co-advised by Bernd Sturmfels, Ph.D. thesis 5/10.

- Algebraic Methods for Biochemical Reaction Network Theory.*
Assistant Professor of Mathematics, Texas A & M University.
9. Peter Huggins (mathematics), co-advised by Bernd Sturmfels, Ph.D. thesis 5/08.
Polytopes in Computational Biology.
Senior Research Programmer, Carnegie Mellon University.
 8. Radu Mihaescu (mathematics), co-advised by Satish Rao, Ph.D. thesis 5/08.
Distance Methods for Phylogeny Reconstruction.
Winner of the Bernard Friedman Memorial Prize for an outstanding thesis in Applied Mathematics. Director, Knight Capital Group.
 7. Anat Caspi (bioengineering), Ph.D. thesis 5/07.
Comparative Genomics of Repeat Elements.
Director, Taskar Center for Accessible Technology, University of Washington.
 6. Ariel Schwartz (computer science), Ph.D. 12/06.
Posterior Decoding Methods for Optimization and Accuracy Control of Multiple Alignments.
Senior Scientist, Bioinformatics at Synthetic Genomics, San Diego.
 5. Colin Dewey (computer science), Ph.D. 5/06.
Whole-Genome Alignments and Polytopes for Comparative Genomics.
Associate Professor, Departments of Computer Science, Biostatistics & Medical Informatics, University of Wisconsin, Madison.
 4. Sourav Chatterji (computer science), Ph.D. 5/06.
Computational Analyses of Eukaryotic Gene Evolution.
Senior software engineer at Facebook.
 3. Kevin Chen (computer science), co-advised by Satish Rao, Ph.D. 12/05.
Three Variations on the Theme of Comparative Genomics: Metagenomics, Mitochondrial Gene Rearrangements and MicroRNAs.
Assistant Professor of Genetics, Rutgers.
 2. Dan Levy (mathematics), co-advised by Rainer Sachs, Ph.D. 12/05.
Applications of Graph Theory to Chromosome Rearrangements and Phylogenetics,
Assistant Professor, Cold Spring Harbor Laboratories.
 1. Eric H. Kuo (mathematics and computer science), Ph.D. 6/05.
Combinatorics of Viterbi Sequences.
Software Engineer, The MathWorks.

Former postdocs

21. Laura Luebbert (biology) –2024
20. Lambda Moses (biology) –2024
19. Ali Sina Boeshaghi (mechanical engineering) –2023
18. Jase Gehring (molecular biology) –2020
17. Valentine Svensson (computational biology) –2020
16. Vasilis Ntranos (information theory) –2019
15. Shannon McCurdy (physics) –2017

14. Bo Li (computer science) –2017
13. Sharon Aviran (information theory) –2014
12. Mathilde Paris (biology) –2013
11. Valerie Hower (mathematics) –2011
10. Megan Owen (mathematics) –2011
9. Alexander Schönhuth (computer science) –2010
8. Robert Bradley (biology) –2009
7. Niko Beerenwinkel (mathematics) –2009
6. Sagi Snir (mathematics and computer science) –2006
5. Mathias Drton (mathematics and statistics) –2005
4. Ruriko Yoshida (mathematics) –2004
3. Luis David Garcia-Puente (mathematics) –2004
2. Von Bing Yap (mathematics and statistics) –2004
1. Marina Alexandersson (mathematics and statistics) –2002