

Lior Pachter

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Positions Held

California Institute of Technology (1/17–present)

- Bren Professor of Computational Biology
Departments of Biology and Computing & Mathematical Sciences

University of California, Berkeley (8/99–present)

- Raymond and Beverly Sackler Chair in Computational Biology (7/12–present)
- Director, Center for Computational Biology (1/10–6/13)
- Professor of Mathematics, Molecular & Cell Biology and Computer Science (7/09–present)
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

- Keynote Speaker: ISBCB (2014), ISMB (2013), FPSAC (2011)
- Bren Chair in Computational Biology (2017)
- 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, Board of Directors, Black Pine Circle School, 1/15–present.
- Member, Scientific Advisory Board, Maverix Biomics, 3/12–present.
- Member, Scientific Advisory Board, Mathematical Biosciences Institute, 11/08–12/11.
- Testimony as an expert witness (biotechnology and bioinformatics).

Grants

- 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).

Fundraising

- Tata Consulting Services
Research agreement with the Center for Computational Biology.
6/11–6/15 (\$900,000 with additional \$3 million in-kind contribution).
- David des Jardins (private donor)
Funding for construction and support of the Laboratory for Mathematics and Computational Biology.
3/08–6/13 (\$500,000)

Publications

Books

1. L. Pachter and B. Sturmfels: [Algebraic Statistics for Computational Biology](#), Cambridge University Press, October 2005.

Journal Publications

108. N. Bray, H. Pimentel, P. Melsted and L. Pachter, [Near-optimal probabilistic RNA-Seq quantification](#), *Nature Biotechnology*, 34 (2016), p 525–527.
107. A. Mittal, L. Pachter, J.L. Nelson, H. Kjaergaard, M.K. Smed, V.L. Gildengorin, V. Zoffmann, M.L. Hetland, N.P. Jewell, J. Olsen and D. Jawaheer, [Pregnancy-Induced Changes in Systemic Gene Expression among Healthy Women and Women with Rheumatoid Arthritis](#), *PLoS One*, (2015).
106. N.K. Hanchate, K. Kondoh, Z. Lu, D. Kuang, X. Ye, X. Qiu, L. Pachter, C. Trapnell and L.B. Buck, [Single-cell transcriptomics reveals receptor transformations during olfactory neurogenesis](#), *Science*, 350 (2015), p 1251–1255.
105. H. Pimentel, M. Parra, S. Gee, N. Mohandas, L. Pachter and J. Conboy, [A dynamic intron retention program enriched in RNA processing genes regulates gene expression during terminal erythropoiesis](#), *Nucleic Acids Research*, 44 (2015), p 838–851.
104. D.J. Brat *et al.*, [Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas](#), *New England Journal of Medicine*, 372 (2015), p 2481–2498.
103. M. Singer and L. Pachter, [Controlling for conservation in genome-wide DNA methylation studies](#), *BMC Genomics*, 16 (2015), 420.
102. M. Singer, I. Kosti, L. Pachter and Y. Mandel-Gutfreund, [Diverse epigenetic landscape at human exons with implication for expression](#), *Nucleic Acids Research*, 43 (2015), p 3498–3508. .
101. S. Aviran and L. Pachter, [Rational experimental design for sequencing-based RNA structure mapping](#), *RNA*, 20 (2014), p 1864–1877.
100. R. Forster, K. Chiba, L. Schaeffer, S.G. Regaldo, C.S. Lai, Q. Gao, S. Kiani, H.F. Farin, H. Clevers, G.J. Cost, A. Chan, E.J. Rebar, F.D. Urnov, P.D. Gregory, L. Pachter, R. Jaenisch and D. Hockemeyer, [Human Intestinal Tissue with Adult Stem Cell Properties Derived from Pluripotent Stem Cells](#), *Stem Cell Reports*, 2 (2014), p 838–852.
99. V.L. Wong, C.E. Ellison, M.B. Eisen, L. Pachter and R. Brem, [Structural variation among wild and industrial strains of *Penicillium chrysogenum*](#), *PLoS One*, 9 (2014), e96784.

98. S. Takayama, J. Dhahbi, A. Roberts, G. Mao, S.-J. Heo, L. Pachter, D.I.K. Martin and D. Boffelli, [Genome methylation in *D. melanogaster* is found at specific short motifs and is independent of DNMT2 activity](#), *Genome Research*, 24 (2014), p 821–830.
97. H. Pimentel, M. Parra, S. Gee, D. Ghanem, X. An, J. Li, N. Mohandas, L. Pachter and J. Conboy, [A dynamic alternative splicing program regulates gene expression during terminal erythropoiesis](#), *Nucleic Acids Research*, 42 (2014), p 4031–4042.
96. A. Roberts, H. Feng and L. Pachter, [Fragment assignment in the cloud with eXpress-D](#), *BMC Bioinformatics*, 14 (2013), p 358.
95. A. Roberts, L. Schaeffer and L. Pachter, [Updating RNA-Seq analyses after re-annotation](#), *Bioinformatics*, 29 (2013), p 1631–1637.
94. A. Rahman and L. Pachter, [CGAL: computing genome assembly likelihoods](#), *Genome Biology*, 14 (2013), R8.
93. C. Trapnell, D.G. Hendrickson, M. Sauvageau, L. Goff, J.L. Rinn and L. Pachter, [Differential analysis of gene regulation at transcript resolution with RNA-seq](#), *Nature Biotechnology*, 31 (2013), p 46–53.
92. A. Roberts and L. Pachter, [Streaming fragment assignment for real-time analysis of sequencing experiments](#), *Nature Methods*, 10 (2013), p 71–73.
91. S.A. Mortimer, C. Trapnell, S. Aviran, L. Pachter and J.B. Lucks, [SHAPE-Seq: High throughput RNA structure analysis](#), *Current Protocols in Chemical Biology*, 4 (2012), p 275–297.
90. A. Kleinman, M. Harel and L. Pachter, [Affine and projective tree metric theorems](#), *Annals of Combinatorics*, 17 (2012), p 205–228.
89. V. Hower, R. Starfield, A. Roberts, and L. Pachter, [Quantifying uniformity in mapped reads](#), *Bioinformatics*, 28 (2012), 2680–2682.
88. L. Pachter, [A closer look at RNA editing](#), *Nature Biotechnology*, 30 (2012), p 246–247.
87. C. Trapnell, A. Roberts, L. Goff, G. Pertea, D. Kim, D.R. Kelley, H. Pimentel, S.L. Salzberg, J.L. Rinn and L. Pachter, [Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks](#), *Nature Protocols*, 7 (2012), p 562–578.
86. A. Roberts and L. Pachter, [RNA-Seq and find: entering the RNA deep field](#), *Genome Medicine*, 3 (2011), p 74.
85. F. Meacham, D. Boffelli, J. Dhahbi, D.I.K. Martin, M. Singer and L. Pachter, [Identification and correction of systematic error in high-throughput sequence data](#), *BMC Bioinformatics*, 12 (2011), 451.

84. M. Singer, A. Engstrom, A. Schoenhuth and L. Pachter, [Determining coding CpG islands by identifying regions significant for pattern statistics on Markov chains](#), *Statistical Applications in Genetics and Molecular Biology*, 10 (2011), Article 43.
83. D. Martin, M. Singer, J. Dhahbi, G. Mao, L. Zhang, G. Schroth, L. Pachter and D. Boffelli, [Phyloepigenomic comparison of great apes reveals a correlation between somatic and germline methylation states](#), *Genome Research*, 21 (2011), p 2049–2057.
82. A. Roberts, H. Pimentel, C. Trapnell and L. Pachter, [Identification of novel transcripts in annotated genomes using RNA-Seq](#), *Bioinformatics*, 27 (2011), p 2325–2329.
81. S. Snir and L. Pachter, [Tracing the most parsimonious indel history](#), *Journal of Computational Biology*, 8 (2011), p 1–20.
80. S. Aviran, C. Trapnell, J.B. Lucks, S.A. Mortimer, S. Luo, G.P. Schroth, J.A. Doudna, A.P. Arkin and L. Pachter, [Modeling and automation of sequencing-based characterization of RNA structure](#), *Proceedings of the National Academy of Sciences*, 108 (2011), p 11069–11074.
79. J.B. Lucks, S.A. Mortimer, C. Trapnell, S. Luo, S. Aviran, G.P. Schroth, L. Pachter, J.A. Doudna and A.P. Arkin, [Multiplexed RNA Secondary and Tertiary Structure Characterization with SHAPE-Seq](#), *Proceedings of the National Academy of Sciences*, 108 (2011), p 11063–11068.
78. A. Roberts, C. Trapnell, J. Donaghey, J.L. Rinn and L. Pachter, [Improving RNA-Seq expression estimates by correcting for fragment bias](#), *Genome Biology*, 12 (2011), R22.
77. V. Hower, S.N. Evans and L. Pachter, [Shape-based peak identification for ChIP-Seq](#), *BMC Bioinformatics*, 12 (2011), 15.
76. D. Levy and L. Pachter, [The neighbor-net algorithm](#), *Advances in Applied Mathematics*, 47 (2011), p 240–258.
75. S.M. Willerth, H.A. Pedro, L. Pachter, L.M. Humeau, A.P. Arkin and D.V. Shaffer, [Development of a Low Bias Method for Characterizing Viral Populations Using Next Generation Sequencing Technology](#), *PLoS One*, 5 (2010), e13564.
74. M. Singer, D. Boffelli, J. Dhahbi, A. Schoenhuth, G.P. Schroth, D.I.K. Martin and L. Pachter, [MetMap Enables Genome-Scale Methyltyping for Determining Methylation States in Populations](#), *PLoS Computational Biology*, 6 (2010), e1000888.
73. S.N. Evans, V. Hower and L. Pachter, [Coverage statistics for sequences census methods](#), *BMC Bioinformatics*, 11 (2010), 430.
72. T.C. Levin, A.M. Glazer, L. Pachter, R.B. Brem and M.B. Eisen, [Exploring the Genetic Basis of Variation in Gene Predictions with a Synthetic Association Study](#), *PLoS One*, 5 (2010), e11645.

71. A. Lapuk, H. Marr, L. Jakkula, H. Pedro, S. Bhattacharya, E. Purdom, Z. Hu, K. Simpson, L. Pachter, S. Durinck et al., [Micorarrays and next generation sequencing identifies alternatively spliced markers and therapeutic targets in breast cancer](#), *Molecular Cancer Research*, 8 (2010), 961.
70. C. Trapnell, B.A. Williams, G. Pertea, A. Mortazavi, M.J. van Baren, S.L. Salzberg, B.J.Wold and L. Pachter, [Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation](#), *Nature Biotechnology*, 28 (2010), p 511–515.
69. R. Bradley, X-Y. Li, C. Trapnell, S Davidson, L. Pachter, H-C. Chu, L. Tonkin, M. Biggin and M.B. Eisen, [Binding site turnover produces pervasive quantitative changes in transcription factor binding between closely related Drosophila species](#), *PloS Biology*, 8 (2010), e1000343.
68. M. Hilty, C. Burke, H. Pedro, A. Ervine, L. Poulter, L. Pachter, M.F. Moffatt and W.O.C. Cookson, [Molecular detection of differences in airway microbial communities in normal adults and subjects with asthma and chronic obstructive pulmonary disease](#), *PLoS One*, 5 (2010), e8578.
67. C. Trapnell, L. Pachter and S.L. Salzberg, [TopHat: discovering splice junctions with RNA-Seq](#), *Bioinformatics*, 25 (2009), p 1105–1111.
66. J. Morton, L. Pachter, A. Shiu, B. Sturmfels and O. Wienand, [Convex rank tests and semigraphoids](#), *SIAM Journal on Discrete Mathematics* 23 (2009), p 1117–1134.
65. D. Levy, R. Mihaescu and L. Pachter, [Why neighbor joining works](#), *Algorithmica*, volume 54 (2009), p 1–24.
64. R. Bradley, A. Roberts, M. Smoot, S. Juvekar, J. Do, C. Dewey, I. Holmes and L. Pachter, [Fast statistical alignment](#), *PLoS Computational Biology*, 5 (2009), e1000392.
63. R. Bradley, L. Pachter and I. Holmes, [Specific alignment of structured RNA: stochastic grammars and sequence annealing](#), *Bioinformatics*, 24 (2008), p 2677–2683.
62. R. Mihaescu and L. Pachter, [Combinatorics of least squares trees](#), *Proceedings of the National Academy of Sciences*, 105 (2008), p 13206–13211.
61. M-L. Dequéant et al., [Comparing pattern detection methods in microarray time series of the segmentation clock](#), *PLoS One*, 3 (2008), e2856.
60. K. Eickmeyer, P. Huggins, L. Pachter and R. Yoshida, [On the optimality of neighbor-joining](#), *Algorithms for Molecular Biology*, 3 (2008), 5.
59. N. Eriksson, L. Pachter, S.Y. Rhee, Y. Mitsuya, R.W. Shafer and N. Beerenwinkel, [Viral population estimation using pyrosequencing](#), *PLoS Computational Biology*, Volume 4 (2008), e1000074.

58. R. Satija, L. Pachter and J. Hein, [Combining statistical alignment and phylogenetic footprinting to detect regulatory elements](#), *Bioinformatics*, 24 (2008), p 1236–1242.
57. A. Stark et al., [Discovery of functional elements in 12 Drosophila genomes using evolutionary signatures](#), *Nature*, 450 (2007), p 219–232.
56. Drosophila Comparative Genome Sequencing and Analysis Consortium, [Evolution of genes and genomes in the context of the Drosophila phylogeny](#), *Nature*, 45 (2007), p 203–218.
55. D.J. Begun et al., [Population genomics: whole-genome analysis of polymorphism and divergence in Drosophila simulans](#), *PLoS Biology*, 5 (2007), e310.
54. P. Huggins, L. Pachter and B. Sturmfels, [Towards the human genotype](#), *Bulletin of Mathematical Biology*, 69 (2007), p 2723–2725.
53. N. Beerenwinkel, L. Pachter and B. Sturmfels, [Epistasis and the shapes of fitness landscapes](#), *Statistica Sinica*, 17 (2007), p 1317–1342.
52. J. Morton, L. Pachter, A. Shiu and B. Sturmfels, [The cyclohedron test for finding periodic genes in time course expression studies](#), *Statistical Applications in Genetics and Molecular Biology*, 6 (2007), 1544–6115.
51. The ENCODE Project Consortium, [Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project](#), *Nature*, 447 (2007), p 799–816.
50. E.H. Margulies *et al.*, [Analysis of deep mammalian sequence alignments and constraint predictions for 1% of the human genome](#), *Genome Research*, 17 (2007), p 760–774.
49. S. Chatterji and L. Pachter, [Patterns of gene duplication in the ENCODE regions suggest a confounding factor](#), *Genomics*, 90 (2007), p 44–48.
48. L. Pachter, [Interpreting the unculturable majority](#) *Nature Methods*, 4 (2007), p 479–480.
47. N. Beerenwinkel, L. Pachter, B. Sturmfels, S. Elena and R. Lenski, [Analysis of epistatic interactions and fitness landscapes using a new geometric approach](#), *BMC Evolutionary Biology*, 7 (2007), 60.
46. L. Pachter and B. Sturmfels, [The mathematics of phylogenomics](#), *SIAM review*, 49 (2007), p 3–31.
45. C. Dewey, P. Huggins, K. Woods, B. Sturmfels and L. Pachter, [Parametric alignment of Drosophila genomes](#), *PLoS Computational Biology*, 2 (2006), e73.
44. C. Dewey and L. Pachter, [Evolution at the Nucleotide Level: The Problem of Multiple Whole Genome Alignment](#), *Human Molecular Genetics*, 15 (2006), R51 – R56.

43. S. Chatterji and L. Pachter, [Reference based annotation with Gene-Mapper](#), *Genome Biology*, 7 (2006), R29.
42. D. Levy, L. Pachter and R. Yoshida, [Beyond pairwise distances: neighbor joining with phylogenetic diversity estimates](#), *Molecular Biology and Evolution*, 23 (2006), p 491–498.
41. S. Lall, D. Grün, A. Krek, K. Chen, Y. Wang, C. Dewey, P. Sood, T. Colombo, N. Bray, P. MacMenamin, H. Kao, K.C. Gunsalus, L. Pachter, F. Piano and N. Rajewsky, [A genome-wide map of conserved microRNA targets in *C. elegans*](#), *Current Biology*, 16 (2006), p 460–471.
40. A. Caspi and L. Pachter, [Identification of transposable elements using multiple alignments of related genomes](#), *Genome Research*, 16 (2006), p 260–270.
39. K. Chen and L. Pachter, [Bioinformatics for whole-genome shotgun sequencing of microbial communities](#), *PloS Computational Biology*, 1 (2005), p e24.
38. S. Chatterji and L. Pachter, [Multiple organism gene finding by collapsed Gibbs sampling](#), *Journal of Computational Biology*, 12 (2005), p 599–608.
37. J. D. McAuliffe, M. I. Jordan and L. Pachter, [Subtree power analysis finds optimal species for comparative genomics](#), *Proceedings of the National Academy of Sciences*, 102 (2005), p 7900–7905.
36. International Chicken Genome Sequencing Consortium, [Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution](#), *Nature*, 432 (2004) p 695 – 716.
35. D. Boffelli, C. V. Weer, L. Weng, K.D. Lewis, M. I. Shoukry, L. Pachter, D. N. Keys and E. M. Rubin, [Intra-species sequence comparisons for annotating genomes](#), *Genome Research*, 14 (2004), p 695–716.
34. K. A. Frazer, L. Pachter, A. V. Poliakov, E. M. Rubin and I. Dubchak, [VISTA–computational tools for comparative genomics](#), *Nucleic Acids Research*, 32 (2004), p 273–279.
33. L. Pachter and B. Sturmfels, [Parametric Inference for Biological Sequence Analysis](#), *Proceedings of the National Academy of Sciences*, 101 (2004), p 16138–16143.
32. L. Pachter and B. Sturmfels, [Tropical Geometry of Statistical Models](#), *Proceedings of the National Academy of Sciences*, 101 (2004), p 16132–16137.
31. The ENCODE Project Consortium, [The ENCODE \(ENCyclopedia of DNA Elements\) project](#), *Science*, 306 (2004), p 636–640.

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29. J. D. McAuliffe, L. Pachter and M. I. Jordan, [Multiple-sequence functional annotation and the generalized hidden Markov phylogeny](#), *Bioinformatics*, 20 (2004), p 1850–1860.
28. Rat Genome Sequencing Consortium, [Evolution of the Mammalian Genome: Sequence of the Genome of the Brown Norway Rat](#), *Nature*, 428 (2004), p 493–521 .
27. N. Bray and L. Pachter, [MAVID, Constrained ancestral alignment of multiple sequences](#), *Genome Research*, 14 (2004), p 693–699.
26. K. Chakrabarti and L. Pachter, [Visualization of multiple genome annotations and alignments with the K-BROWSER](#) , *Genome Research*, 14 (2004), p 716–720.
25. C. Dewey, J.Q. Wu, S. Cawley, M. Alexandersson, R. Gibbs and L. Pachter, [Accurate identification of novel human genes through simultaneous gene prediction in human, mouse, and rat](#), *Genome Research*, 14 (2004), p 661–664.
24. V.B. Yap and L. Pachter, [Identification of evolutionary hotspots in the rodent genomes](#), *Genome Research*, 14 (2004), p 574–579.
23. S. Cawley and L. Pachter, [HMM sampling and applications to gene finding and alternative splicing](#), *Bioinformatics*, 19 Supplement 2 (2003), p 36–41.
22. F. Lam and L. Pachter, [Forcing Numbers for Stop Signs](#), *Theoretical Computer Science*, 303 (2003), p 409–416.
21. N. Bray and L. Pachter, [MAVID multiple alignment server](#), *Nucleic Acids Research*, 31 (2003), p 3525–3526.
20. S. Cawley, L. Pachter and M. Alexandersson, [SLAM web server for comparative gene finding and alignment](#), *Nucleic Acids Research*, 13 (2003), p 3507–3509.
19. F. Lam, M. Alexandersson, L. Pachter, [Picking Alignments from \(Steiner\) Trees](#), *Journal of Computational Biology*, 10 (2003), p 509–520.
18. M. Alexandersson, S. Cawley, L. Pachter, [SLAM- Cross-species gene finding and alignment with a generalized pair hidden Markov model](#), *Genome Research*, 13 (2003), p 496–502.
17. D. Boffelli, J. McAuliffe, D. Ovcharenko, K. D. Lewis, I. Ovcharenko, L. Pachter, E.M. Rubin, [Phylogenetic Shadowing of Primate Sequences to Find Functional Regions of the Human Genome](#), *Science*, Volume 299, Number 5611 (2003), p 1391–1394.
16. N. Bray, I. Dubchak and L. Pachter, [AVID: A Global Alignment Program](#), *Genome Research*, 13 (2003), p 97–102.

15. O. Couronne, A. Poliakov, N. Bray, I. Ovcharenko, T. Ishkhanov, D.V. Ryaboy, E. Rubin, L. Pachter and I. Dubchak, [Strategies and Tools for Whole Genome Alignments](#), *Genome Research*, 13 (2003), p 73–80.
14. Mouse Genome Sequencing Consortium, [Initial sequencing and comparative analysis of the mouse genome](#), *Nature*, 420 (2002), p 520–562.
13. L. Pachter, M. Alexandersson and S. Cawley, [Applications of Generalized Pair Hidden Markov Models to Alignment and Gene Finding Problems](#), *Journal of Computational Biology*, Volume 9, Number 2, 2002, p 389–400.
12. G. Loots, I. Ovcharenko, L. Pachter and I. Dubchak and E. M. Rubin, [Comparative sequence-based approach to high-throughput discovery of functional regulatory elements](#), *Genome Research*, 12 (2002), p 832–839.
11. I. Dubchak and L. Pachter, [The computational challenges of applying comparative-based computational methods to whole genomes](#), *Briefings in Bioinformatics*, 3 (2002), p 18–22.
10. A. Peter *et al.*, [Mapping and identification of essential gene functions on the X chromosome of Drosophila](#), *EMBO reports*, 3 (2001), p 34–38.
9. P. V. Benos *et al.*, [From First Base: The sequence of the tip of the X chromosome of *D. melanogaster*](#), *Genome Research*, 11 (2001), p 710–730.
8. C. Mayor, M. Brudno, J.R. Schwartz, A. Poliakov, E. M. Rubin, K. A. Frazer, L. Pachter and I. Dubchak, [VISTA: Visualizing global DNA sequence alignments of arbitrary length](#), *Bioinformatics*, 16 (2000), p 1046–1047.
7. I. Dubchak, C. Mayor, M. Brudno, L. Pachter, E. M. Rubin and K. A. Frazer, [Active conservation of noncoding sequences revealed by 3-way species comparisons](#), *Genome Research*, 10 (2000), p 1304–1306.
6. S. Batzoglou, L. Pachter, J. Mesirov, B. Berger and E. S. Lander, [Human and Mouse Gene Structure: Comparative Analysis and Application to Exon Prediction](#), *Genome Research*, 10 (2000), p 950–958.
5. L. Pachter, S. Batzoglou, V. I. Spitkovsky, E. Banks, E. S. Lander, B. Berger and D. J. Kleitman, [A dictionary based approach for gene annotation](#), *Journal of Computational Biology*, 6 (1999), p 419–430.
4. L. Pachter and P. Kim, [Forcing Matchings on Square Grids](#), *Discrete Mathematics*, 190 (1998), p 287–294.
3. D. J. Kleitman and L. Pachter, [Finding Convex Sets Among Points in the Plane](#), *Discrete and Computational Geometry*, 19 (3) (1998), p 405–410.

2. L. Pachter, [Constructing Status Injective Graphs](#), *Discrete Applied Mathematics*, 80 (1997), p 107–113.
1. L. Pachter, [Combinatorial Approaches and Conjectures for 2-Divisibility Problems Concerning Domino Tilings of Polyominoes](#), *Electronic Journal of Combinatorics*, 4 (1997), R29.

Refereed Conference Publications

14. N. Bray and L. Pachter, Rank regularized RNA-seq, *Proceedings of the Fourth Annual RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-Seq 2015)*, (2015), in press.
13. S. Aviran, J. Lucks and L. Pachter, [RNA structure characterization from chemical mapping experiments](#), *Proceedings of the Forty-Ninth Allerton Conference on Communication, Control and Computing*, (2011), p 1743–1750.
12. L. Pachter, [An introduction to reconstructing ancestral genomes](#), *Proceedings of Symposia in Applied Mathematics*, AMS Short Course Subseries, Volume 64 (2007), p 1–20.
11. A. Schwartz and L. Pachter, [Multiple alignment by sequence annealing](#), *Proceedings of the European Conference on Computational Biology, Bioinformatics 23* (2007), e24–e29.
10. J. Morton, L. Pachter, A. Shiu, B. Sturmfels and O. Wienand, [Geometry of Rank Tests](#), *Proceedings of the Third European Workshop on Probabilistic Graphical Models*, September 2006.
9. S. Snir and L. Pachter, [Phylogenetic Profiling of Insertions and Deletions in Vertebrate Genomes](#), *Proceedings of the Tenth Annual International Conference on Computational Molecular Biology (RECOMB 2006)*, p 265–280.
8. S. Chatterji and L. Pachter, [Multiple Organism Gene Finding by Collapsed Gibbs Sampling](#), *Proceedings of the Eighth Annual International Conference on Computational Molecular Biology (RECOMB 2004)*, p 187–193.
7. L. Pachter, F. Lam, M. Alexandersson, [Picking Alignments from \(Steiner\) Trees](#), *Proceedings of the Sixth Annual International Conference on Computational Molecular Biology (RECOMB 2002)*, p 246–253.
6. L. Pachter and M. Pachter, Avoiding points in the plane, *Proceedings of the 40th IEEE Conference on Decision and Control* (2001).
5. L. Pachter, M. Alexandersson, S. Cawley, [Applications of Generalized Pair Hidden Markov Models to Alignment and Gene Finding Problems](#), *Proceedings of the Fifth Annual International Conference on Computational Molecular Biology (RECOMB 2001)*, p 241–248.

4. S. Batzoglou, L. Pachter, J. Mesirov, B. Berger, E. S. Lander, [Comparative Analysis of Mouse and Human DNA and Applications to Exon Prediction](#), *Proceedings of the Fourth Annual International Conference on Computational Molecular Biology (RECOMB 2000)*, p 46–53.
3. L. Pachter, S. Batzoglou, V. I. Spitkovsky, W. Beebe, E. S. Lander, B. Berger and D. J. Kleitman, [A dictionary based approach for gene annotation](#), *Proceedings of the Third Annual International Conference on Computational Molecular Biology (RECOMB 1999)*, p 285–294.
2. S. Batzoglou, B. Berger, D. J. Kleitman, Eric S. Lander and L. Pachter, [Recent Developments in Computational Gene Recognition](#), *Documenta Mathematica, Extra Volume ICM 1998 I* (1998), p 649–658.
1. L. Pachter, H. Snevily and B. Voxman, [On Pebbling Graphs](#), *Proceedings of the Twenty-sixth Southeastern International Conference on Combinatorics, Graph Theory and Computing. Congressus Numerantium*, 107 (1995), p 65–80.

Book Chapters

2. M. Singer and L. Pachter, Bayesian networks in the study of genomewide DNA methylation, in [Probabilistic Graphical Models Dedicated to Applications in Genetics, Genomics, and Postgenomics](#) (Christine Sinoquet and Raphaël Mourad, editors), September 2014.
1. M. Alexandersson, N. Bray and L. Pachter, [Pair hidden Markov models](#), special review for the Encyclopedia of Genetics, Genomics, Proteomics and Bioinformatics (L. B. Jorde, P. Little, M. Dunn and S. Subramanian, editors), October 2005.

Other Manuscripts

11. A. Tambe, J. Doudna and L. Pachter, [Identifying RNA contacts from SHAPE-MaP by partial correlation analysis](#), 2015.
10. N. Bray and L. Pachter, [Comment on "Evidence of Abundant and Purifying Selection in Humans for Recently Acquired Regulatory Functions"](#), 2012.
9. L. Pachter, [Models for transcript quantification from RNA-Seq](#), 2011.
8. P. Huggins and L. Pachter, [Selecting universities: personal preference and rankings](#), 2008.
7. R. Mihaescu, D. Levy and L. Pachter, [Erratum to "On the edge \$l_\infty\$ radius of Saitou and Nei's method for phylogenetic reconstruction" \[Theoret. Comput. Sci. 369\(1-3\) \(2006\) 448-455\]](#), 2007.

6. A.S. Schwartz, E.W. Myers and L. Pachter, [Alignment metric accuracy](#), 2005.
5. L. Pachter, [A Nobel Prize in *Mathematical Biology*?](#) Mathematics Department Newsletter, UC Berkeley, 2006.
4. R. Guigó, E. Birney, M. Brent, E. Dermitzakis, L. Pachter, H.R. Crollius, V. Solovyev, M.Q. Zhang, [Needed for completion of the human genome: hypothesis driven experiments and biologically realistic mathematical models](#), 2004.
3. M. Alexandersson, S. Cawley and L. Pachter, HMMs for Gene Recognition, 2000.
2. N. Kitchloo and L. Pachter, [An interesting result about subset sums](#), 1993.
1. R. Dawson, B. McDonald, J. Mycielski and L. Pachter, [Light Traps](#), 1992.

Reviewing

- Member, editorial board of *Genome Biology*.
Previously 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.
- Frequent reviewer for NIH GCAT and special genomics panels.
- Frequent reviewer for NSF mathematical biology panels.

Committees

- 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–present.
- 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 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 Hosten and Bernd Sturmfels) on “Algebraic Statistics”, 2008.
- IMA workshop organizer (with Serkan Hosten 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 Medados College Computational Biology Lecture (2/05)

Invited Talks

Conferences and Workshops

- Allerton Conference on Communication, Control and Computing (tutorial) (9/14)
Sequencing based functional genomics (analysis)
- Biological Sequence Analysis and Probabilistic Models Workshop (7/14)
Probabilistic models for transcriptome analysis
- The 16th Annual Israeli Bioinformatics Symposium– keynote (6/14)
What gene expression reveals about a person (and their biology)
- UCSC RNA Summit (3/14)
Structure mapping by sequencing
- Simons Institute for the Theory of Computing– Population Genetics (2/14)
Quantifying the extent of geographic signature in the human genome
- Information Theory and Applications (ITA) (2/14)
Rank regularized analysis of high-throughput sequencing based experiments
- Prestige Lecture: New Directions in the Science of Information (11/13)
Sequencing based functional genomics
- Genome Informatics, CSHL– Keynote (11/13)
[Stories from the supplement](#)
- NGx, Providence RI (8/13)
RNA-Seq and find: entering the deep field
- ISMB, Berlin– Keynote (7/13)
Sequencing based functional genomics (analysis)
- UAI (tutorial) (7/13)
Statistical Methods in Genomics
- NIPS (12/12)
The streaming tree EM algorithm with applications to RNA-Seq
- MBI: Math Biology Looking at the Future (9/12)
The human genome: 10 years later
- Algebraic Statistics in the Alleghenies (6/12)
Latent allocation models and applications to high-throughput genomics
- Biology of Genomes, CSHL (5/12)
Editing editing estimates
- AGBT 2012 (2/12)
Streaming Algorithms for Analyzing and Maintaining RNA-Seq Data
- FPSAC 2011 (6/11)
Affine and projective tree metric theorems
- RECOMB Bioinformatics Education (5/10)
Proposal for a new math course for first year biology students at UC Berkeley
- Miller Institute lecture (2/10)
Sequencing: a new microscope for biology
- MBI workshop on mathematics inspired by biology (11/09)

- Combinatorics of sequence alignment
- SIAM keynote lecture (7/09)
 - Combinatorics Inspired by Biology
- SIAM Minisymposium on computational biology (7/09)
 - Balanced minimum evolution
- Drosophila Development Workshop, MBI (6/09)
 - Studying Drosophila Genome Dynamics at the Nucleotide Level
- 9th Haifa Workshop on Interdisciplinary Applications of Graph Theory (5/09)
 - Affine and projective tree metric theorems
- 7th Australia–New Zealand Mathematics Convention (12/08)
 - Finding the trees in Darwin's forest
- SAMSI Opening Workshop on Algebraic Methods in Systems Biology and Statistics (9/08)
 - The algebra and statistics of biological sequence alignment
- High Dimensional Statistics in Biology, Newton Institute, Cambridge (4/08)
 - Functional genomics and the forest of life
- Banbury Meeting, Cold Spring Harbor (3/08)
 - Tutorial on Algebraic Statistics for Computational Biology
- Information Theory and Applications Workshop (12/07)
 - The neighbor-net algorithm and the traveling salesman problem
- Bay Area Mathematical Biology Day (11/06)
 - Towards the Human Genotype
- Summer school, Sophus Lie Conference Center, Nordfjordeid (6/06)
 - Algebraic statistics, tropical geometry and computational biology (6 lectures)
- Gordon Conference on Molecular Evolution (2/06)
 - Annotation and Alignment of the Drosophila Genomes
- AMS Special Session on Mathematical Biology, San Antonio (1/06)
 - Reconstructing Ancestral Genomes
- AMS Special Session on Algebraic Statistics, San Antonio (1/06)
 - The Posterior Map
- First Argentine Conference on Mathematics and Biology (12/05)
 - An Introduction to Algebraic Statistics for Computational Biology (3 lectures)
- Clay Workshop on Algebraic Statistics and Computational Biology (11/05)
 - Algebraic Statistics for Computational Biology
- Advanced Bioinformatics Course, Cold Spring Harbor (11/05)
 - Whole Genome Alignment
- Banff Research Station (8/04)
 - Parametric Sequence Alignment
- The Biology of the Genomes Meeting, Cold Spring Harbor (5/04)
 - Phylogenetic Methods in Genomics and Applications to Functional Element Identification
- Snowbird Learning Theory Workshop (4/04)
 - Parametric Inference for Biological Sequence Analysis
- Banbury Meeting, Cold Spring Harbor (3/04)

- Phylogenetic Methods in Genomics and Applications to Functional Element Identification
- Fundacion La Caixa, Barcelona (11/03)
 - Phylogenetic Shadowing
- Bertinoro Workshop on Computational Biology (6/03)
 - Mathematics of Phylogenetic Shadowing
- National Institute of Environmental and Health Safety, Toxigenomics meeting (5/03)
 - Comparative genomics by phylogenetic shadowing
- Frontiers of Grid Computing, Baton Rouge Louisiana (3/03)
 - Comparing the human and mouse genomes
- Mathematics Workshop, Taranaki New Zealand (1/03)
 - Mathematics of Gene Finding and Alignment
- Bay Area Discrete Math Day (10/02)
 - Picking alignments from (Steiner) Trees
- SIAM Conference on Discrete Mathematics (8/02)
 - Comparing the Human and Mouse Genomes
- Jackson Laboratories Workshop on Comparative Genomics (8/02)
 - Whole Genome Alignment and Gene Finding
- Human Genetics Meeting, Cold Spring Harbor (5/02)
 - Comparative Assembly
- Gordon Conference on Human Genetics (8/01)
 - Hidden Markov Models, Alignment, Gene Recognition and Mice
- PMMB workshop, Tucson (6/01)
 - Whole Genome Alignment and Gene Finding
- RECOMB satellite meeting on assembly, Los Angeles (5/01)
 - Comparative Assembly
- PMMB Workshop, Mathematical Sciences Research Institute (6/00).
 - Combinatorial and Computational Approaches to Gene Recognition

Biology/Genetics Departments and Institutes

- Stanford University: Frontiers in Biology (10/14)
 - Transcriptome Genetics
- Fred Hutchinson Cancer Research Center (5/14)
 - Making sense of RNA-Seq
- Genome Sciences, University of Washington (5/14)
 - Quantifying the extent of geographic signature in the human genome
- University of North Carolina, Chapel Hill– Jeffrey Hought Lecture (3/14)
 - Making sense of RNA-Seq
- Cold Spring Harbor Laboratories (2/14)
 - Recent developments in RNA-Seq technology and analysis
- Karolinska, Stockholm (7/13)
 - Analysis of gene expression at transcript resolution with RNA-Seq
- University of Virginia (5/13)

- Analysis of gene regulation at transcript resolution with RNA-Seq
- DECODE Genetics (7/12)
High-throughput sequence analysis for biological discovery
- UC Irvine (9/11)
RNA-Seq: experimental design, analysis and interpretation
- Tel Aviv University (5/09)
The neighbor joining algorithm
- University of California at Berkeley (5/08)
What is an alignment?
- University of Pennsylvania (3/08)
Functional Genomics and the Forest of Life
- The National Institutes of Health (5/07)
From Statistical Sampling to Collection and Interpretation of Metagenomics Data
- The Wellcome Trust Sanger Institute (11/06)
The Majority of Divergence between DNA Sequences is due to Indels
- Stowers Institute for Medical Research (3/06)
Geometry of Rank Tests and Applications to Microarray Time Series Analysis
- The Walter and Eliza Hall Institute of Medical Research, Melbourne, Australia (7/02)
Whole Genome Alignment and Gene Finding
- Whitehead Institute for Biomedical Research (5/02)
Whole Genome Alignment
- Johns Hopkins University (5/02)
Comparing the human and mouse genomes

Computational Biology Seminars

- Stanford University: Bio-X interdisciplinary frontiers (11/14)
Recent developments in RNA-Seq
- UCSF (10/14)
Transcriptome genetics
- IST Austria (6/14)
High-throughput analysis for sequencing based molecular biology
- Technion, Israel (6/14)
Differential analysis of DNA methylation
- KTH– Frontiers in Life Science Technology (12/13)
Sequence based functional genomics
- Université de Montréal (11/08)
Robert Cedergren Bioinformatics Colloquium
- Bioinformatics Research Seminar, University of California at Santa Cruz (5/08)
What is the neighbor-joining algorithm?
- Forefront of Genomics Colloquium, Genome Center, UC Davis (11/07)
High-throughput population genomics
- Center for Genomic Regulation, Barcelona (5/07)

- From Drosophila and Transposable Elements to the Neighbor-Net Algorithm
- University of East Anglia (4/07)
 - From Drosophila and Transposable Elements to the Neighbor-Net Algorithm
- North Carolina State University (3/07)
 - From Drosophila and Transposable Elements to Phylogenetic Networks
- University of Oxford (2/07)
 - Comparative Genomics of Drosophila
- Stockholm Bioinformatics Center (1/07)
 - Why Neighbor-Joining Works
- California Institute for Quantitative Biomedical Research Seminar (11/06)
 - The Majority of Divergence between DNA Sequences is due to Indels
- Center for Genome Sciences, Cuernavaca Mexico (5/06)
 - Annotation and Alignment of the Drosophila Genomes
- Ohio State University (4/06)
 - Annotation and Alignment of the Drosophila Genomes
- University of Pennsylvania – Penn Bioinformatics Forum (2/06)
 - Annotation and Alignment of the Drosophila Genomes
- Virginia Bioinformatics Institute (2/05)
 - Gene Finding
- Brown University (11/04)
 - Parametric Sequence Alignment
- University of California, San Francisco – Cancer Center (11/03)
 - Phylogenetic Shadowing
- Boston University (10/03)
 - Phylogenetic Shadowing
- Jackson Laboratories (8/02)
 - Finding genes in human using the mouse and finding genes in mouse using the human

Computer Science and Engineering Departments

- University of California, Berkeley (9/10)
 - Mathematical challenges in analyzing sequencing assays for functional genomics
- University of Pennsylvania (4/07)
 - From Drosophila and Transposable Elements to the Neighbor-Net Algorithm and Phylogenetic Networks
- University of California, Berkeley (10/05)
 - Robust Alignment for Drosophila Genomics.
- Iowa State University (8/04)
 - Whole Genome Alignment and Gene Finding
- University of California, Santa Cruz (1/04)
 - Parametric Inference for Biological Sequence Analysis
- University of California, Santa Cruz (1/02)
 - Hidden Markov Models, Alignment, Gene Recognition and Mice

- Johns Hopkins University (10/98)
Onion Peeling and Protein Folding

(Applied) Mathematics Departments

- Caltech (10/14)
Linear genetics
- KTH (12/13)
Challenges in combinatorial phylogenomics
- Duke University (11/13)
The mathematics of comparative transcriptomics
- University of California, Berkeley (11/10)
Mathematics for interpreting your genome
- University of Arizona (4/09)
Mathematical challenges of high-throughput genomics
- Fuzzy Vance Lecture at Oberlin College (2/09)
Finding the Trees in Darwin's Forest
- Freie Universität, Berlin (4/08)
Mathematics of Distance-Based Phylogenetics
- University of Pennsylvania (3/08)
Foundations of Distance-Based Phylogenetics
- University of California at Davis (11/07)
From Biology to Mathematics: The Neighbor-Joining Algorithm
- University of Minnesota (2/07)
From Drosophila and Transposable Elements to Phylogenetic Networks and Associahedra
- University of Utah (3/06)
Annotation and Alignment of the Drosophila Genomes
- Stanford University (5/04)
Parametric Inference for Biological Sequence Analysis
- University of California, Davis (2/01)
Hidden Markov Models, Alignment, Gene Recognition and Mice
- University of California, Berkeley (11/00)
Hidden Markov Models, Alignment, Gene Recognition and Mice
- University of Washington (5/00)
Counting Walks on Tilings
- University of California, San Diego (1/00)
The Erdős-Szekeres Theorem
- University of California, Berkeley (10/99)
The Erdős-Szekeres Theorem
- University of Southern California (10/99)
Comparative Genomics and Gene Recognition
- Iowa State University (3/99)
Dictionary Approaches for Gene Annotation

- Carnegie Mellon University (2/99)
Dictionary Approaches for Gene Annotation
- Johns Hopkins University (10/98)
The Erdős-Szekeres Theorem
- Oberlin College (2/98)
The Erdős-Szekeres Theorem
- University of Idaho (2/98)
The Erdős-Szekeres Theorem
- California Institute of Technology (2/98)
Combinatorial and Computational Approaches to Gene Recognition
- University of Washington (3/94)
Light Traps

Statistics and Biostatistics Departments

- Harvard School of Public Health (3/14)
Making sense of RNA-Seq
- University of California Berkeley (3/12)
Transcript level differential analysis of RNA-Seq experiments
- Biostatistics Seminar, UCSF (11/09)
Transcriptome assembly and expression analysis with RNA-Seq
- Statistics Seminar, University of Chicago (11/08)
Statistical foundations of distance-based phylogenetics
- University of California Berkeley – Neyman Seminar (11/08)
What is algebraic statistics and what is it good for?
- Biostatistics and Medical Informatics Seminar, University of Wisconsin (4/08)
Statistical foundations of distance-based phylogenetics
- University of Iceland (12/07)
Least squares tree metrics
- University of Washington (11/07)
Statistical foundations of distance-based phylogenetics methods
- University of Oxford (6/07)
What is Algebraic Statistics?
- University of Oxford (10/06)
Towards the Human Genome
- University of Oxford (11/05)
Alignment and Annotation of the *Drosophila* Genomes
- University of California Berkeley – Neyman Seminar (11/04)
Gene Finding
- Harvard University (1/02)
Hidden Markov Models, Alignment, Gene Recognition and Mice
- University of California Berkeley – Neyman Seminar (3/00)
Onion Peeling and Protein Folding

Teaching

Classes developed

- Berkeley graduate course MCB C243/MATH C243
**Seq methods and applications*, 2014–
 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–
- Berkeley undergraduate course Math 127
Mathematical and Computational Methods in Molecular Biology, 1999–

Classes taught

- 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 Cordoba, 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 Ciencia, Oerias, Portugal.

Research Supervision

Current graduate students

- Brielin Brown (computer science).
Ph.D. thesis 5/16.
- Isaac Joseph (bioengineering).
Ph.D. thesis 5/16.
- Shannon Hateley (molecular biology, joint with Michael Eisen).
Ph.D. thesis 5/16.
- Alex Padron (molecular biology)
Ph.D. thesis 5/17.
- Harold Pimentel (computer science)
Ph.D. thesis 5/16.
- Lorian Schaeffer (molecular biology)
Ph.D. thesis 5/17.
- Akshay Tambe (molecular biology, joint with Jennifer Doudna)
Ph.D. thesis 5/17.
- Faraz Tavakoli (computer science).
Ph.D. thesis 5/16.
- Robert Tunney (computational biology, joint with Liana Lareau).
Ph.D. thesis 5/18.

Graduated students

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.

Current postdocs

- Shannon McCurdy (Ph.D. physics)
Postdoctoral Researcher 2014–present.
- Bo Li (Ph.D. computer science)
Postdoctoral Researcher 2013–present.

Former postdocs

13. Sharon Aviran (information theory).
Postdoctoral Researcher 2011–2014.
Assistant Professor, Department of Bioengineering, UC Davis.
12. Mathilde Paris (biology).
CNRS Researcher in evolutionary and developmental biology, IBDM, Marseille
Postdoctoral Researcher 2012–2013.
11. Valerie Hower (mathematics).
Postdoctoral Research Fellow, 2009–2011.
Assistant Professor, Department of Mathematics, University of Miami.
10. Megan Owen (mathematics).
Postdoctoral Research Fellow, 2010–2011.
Assistant Professor, Department of Computer Science, Lehman college CUNY.
9. Alexander Schönhuth (computer science).
Postdoctoral Research Fellow, 2009–2010.
Assistant Professor, Centrum Wiskunde & Informatica, Amsterdam.
8. Robert Bradley (biology).
Postdoctoral Research Fellow, 2008–2009.
Assistant Member, Fred Hutchinson Cancer Research Center.
7. Niko Beerenwinkel (mathematics).
Professor, Department of Biosystems Science and Engineering, ETH, Zurich.
6. Sagi Snir (mathematics and computer science).
Postdoctoral Research Fellow, 2004–2006.
Senior Lecturer, Department of Evolutionary and Environmental Biology,
University of Haifa, Israel.
5. Mathias Drton (mathematics and statistics).
Postdoctoral Research Fellow, 2004–2005.
Professor, Department of Statistics, University of Washington.
4. Ruriko Yoshida (mathematics).
Postdoctoral Research Fellow, Summer 2004.
Associate Professor, Departments of Mathematics and Statistics, University of Kentucky.
3. Luis David Garcia-Puente (mathematics).
Postdoctoral Research Fellow, Summer 2004.
Associate Professor of Mathematics, Sam Houston State University.
2. Von Bing Yap (mathematics and statistics).
Postdoctoral Research Fellow 2002–2004.

Associate Professor of Statistics and Applied Probability, National University Singapore.

1. Marina Alexandersson (mathematics and statistics).
Postdoctoral Research Fellow 2001-2002.
Docent, Chalmers University of Technology, Gotheburg, Sweden.

Former undergraduates

12. Harvey Feng (computer science)
Reserach on implementation of the EM algorithm in Spark, 2013.
11. Frazer Meacham (mathematics)
Research on systematic errors in Illumina sequence, 2011.
10. Matan Harel (mathematics)
Senior thesis: Split systems and phylogenies, 2008
9. Oscar Westesson (mathematics)
Senior thesis: phylogenetic hidden Markov models, 2007
8. Frances Hammock (mathematics).
Senior thesis: On minors of 4×4 matrices, 2005
7. Kushal Chakrabarti (computer science).
Senior thesis: Alignment visualization, 2004
6. Nicolas Bray (mathematics).
Senior thesis: Multiple alignment, 2003
5. Eli Rusman (mathematics).
Senior thesis: Genome compression, 2003
4. Fumei Lam (mathematics).
Senior thesis: Forcing numbers of graphs, 2000
3. Joshua Bao (computer science) and Romanos-Diogenes Malikiosis (mathematics).
Research Summer Institute 1997
2. Peter Kim (mathematics) and Patience Sethaba (mathematics).
Research Summer Institute 1996
1. Radoš Radoičić (mathematics).
Summer Program for Undergraduate Research 1997–1998

Doctoral Thesis Committees and Examinations

- Natth Bejraburnin (Mathematics) – Combinatorics.
- Nicolas Bray (Mathematics) – Mathematical biology.
- Robert Bradley (Bioengineering) – RNA folding.
- James Brown (Applied Sciences and Technology) – Algebraic statistics and genomics.
- Anat Caspi (Bioengineering) – Transposable elements.
- Andrew Chan (Computer Science) – Error correction of next-gen sequence.
- Kevin Chen (Computer Science) – Metagenomics.
- Mike Develin (Mathematics) – Topics in discrete geometry.
- Colin Dewey (Computer Science) – Multiple alignment.
- Jeffrey Doker (Mathematics) – Discrete geometry.
- Sourav Chatterji (Computer Science) – Gene finding.
- Peter Combs (Molecular and Cell Biology) – Drosophila patterning.
- Matt Davis (Molecular and Cell Biology) – *n*-butanol production.
- Isaac Elias (Computer Science) – Phylogenetics
Invited opponent for doctoral thesis defense at KTH, Stockholm.
- Nicholas Eriksson (Mathematics) – Algebraic combinatorics for computational biology.
- Hunter Fraser (Molecular and Cell Biology) – Molecular and genomic evolution.
- Tatiana Gurbich (Integrative Biology) – Sex determination in Drosophila.
- Aaron Hardin (Molecular and Cell Biology) – Drosophila population genomics.
- Emily Hare (Molecular and Cell Biology) – Gene regulation in Drosophila.
- Kelly Harris (Mathematics) – Population genetics.
- Ben Hsiung (Molecular and Cell Biology) – Regulation of NKG2D ligand expression.
- Peter Huggins (Mathematics) – Polyhedral geometry and computational biology.
- Venky Iyer (Molecular and Cell Biology) – Gene finding in Drosophila.
- Rob Johnson (Computer Science) – Network security.
- Wei-Chun Kao (Computer Science) – Base calling in next-gen sequence.
- Anna Kedzierksa (Mathematics) – Comparative genomics
Student at the Universitat Politècnica de Catalunya.
- Eric H. Kuo (Computer Science) – Combinatorics of hidden Markov models.
- Albert Lee (Engineering) – Numerical linear algebra.
- Dan Levy (Mathematics) – Graph theory and phylogenetics.
- Shaowei Lin (Mathematics) – Algebraic statistics.
- Jon McAuliffe (Statistics and Computer Science) – Graphical models.
- Kevin McLoughlin (Statistics) – Design of biodetection arrays.
- Adam Merberg (Mathematics) – Combinatorics.
- Radu Mihaescu (Mathematics) – Phylogenetics.
- Jason Morton (Mathematics) – Algebraic statistics and computational biology.
- Manikandan Narayanan (Computer Science) – Biological network comparison.
- Randilea Nicholas (Molecular and Cell Biology) – The adaptive immune system.
- Geoffrey Pike (Computer Science) – Storage optimizations for scientific programs.
- Celeste Riepe (Molecular and Cell Biology) – Ribosomal profiling

- Rahul Satija (Bioinformatics and Statistics) – Statistical alignment.
Student at the University of Oxford.
- Ariel Schwartz (Computer Science) – Multiple alignment.
- Anne Shiu (Mathematics) – Algebraic statistics and computational biology.
- Allan Sly (Statistics) – Glauber dynamics.
- Ngoc Mai Tran (Statistics) – Algebra and statistics of ranking.
- Caroline Uhler (Statistics) – Gaussian graphical models and semidefinite programming.
- Avinash Varadarajan (Bioengineering) – Statistical alignment.
- Na Xu (Statistics) - Comparative genomics.
- Josephine Yu (Mathematics) – Tropical geometry and combinatorics.
- Xiaoyue Zhao (Statistics) – Modeling of splice sites.

Personal Information

Born May 3, 1973, in Ramat Gan, Israel. Citizen of the United States.
Married to Ingileif Bryndís Hallgrímsdóttir. Three daughters.