Curriculum Vitae

David Haussler

Investigator, Howard Hughes Medical Institute
Distinguished Professor, Biomolecular Engineering, University of California, Santa Cruz
Scientific Director, UC Santa Cruz Genomics Institute, University of California, Santa Cruz
Co-organizer, Global Alliance for Genomics and Health
Co-leader, Global Alliance for Genomics and Health, Data Working Group
Cofounder, Genome 10K Project
Affiliate, Crown College

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EMPLOYMENT HISTORY

2005-	Distinguished Professor, Biomolecular Engineering, University of California, Santa Cruz
2000-	Adjunct Professor, Department of Bioengineering and Therapeutic Sciences, University of California, San Francisco
2000-	Consulting Professor, Stanford University School of Medicine (Medical Informatics)
2000-	Investigator, Howard Hughes Medical Institute
8/1997-12/1997	Visiting Scientist and Co-Director of special scientific program, Isaac Newton Institute for Mathematical Sciences and Sanger Centre, Cambridge, England
1993-2004	Professor, Computer Science, University of California, Santa Cruz
9/1991-10/1991	Visiting Scientist, Mathematical Sciences Research Institute, Berkeley, CA
1989-1993	Associate Professor, Computer Science, University of California, Santa Cruz
1986-1989	Assistant Professor, Computer Science, University of California, Santa Cruz
4/1986-5/1986	Visiting Scientist, Université de Haute Normandie, Rouen, France
1982-1986	Assistant Professor, Mathematics and Computer Science, University of Denver, CO

CONSULTING AND COMMITTEES

09/2016-	Consultant and external advisory committee member, ChanZuckerburg Initiative
02/2016	External Advisor, Caltech, CA.
01/2016-	Member, Secretary of Energy (SEAB) Task Force on Biomedical Sciences
09/2015-	Vice Chair of Steering Committee, Global Alliance for Genomics and Heath
11/2014-	Consultant and external advisory committee member, Genomic Data Commons (GDC), Bethesda, MA
09/2014-	Consultant and external advisory committee member, Simons Center for Quantitative Biology, Cold Spring Harbor, NY

09/2014-	Consultant and scientific advisory board member, Canadian Bioinformatics Node, Toronto, Canada
08/2013-	Chief scientific advisor, Dovetail Genomics, Santa Cruz, CA
03/2013-	Consultant and scientific advisory board member, New York Genome Center, New York, NY
06/2013-	Founder and co-chair of Data Working Group, Global Alliance for Genomics and Heath
08/2012-	Consultant and scientific advisory board member, Two Pore Guys, Santa Cruz, CA
03/2011-	Consultant and scientific advisory board member, Five3 genomics, Santa Cruz, CA
11/2010-	Consultant and scientific advisory board member, PharmGKB, Stanford, CA
05/2010-	Advisor, Xconomy San Francisco, San Francisco, CA
1/10-07/12	Scientific advisory board member, International Barcode of Life, Toronto, Ontario, Canada
01/07-09/13	Consultant and scientific advisory board member, Pacific Biosciences, Menlo Park, CA
2009-	External Advisor, Beckman Institute at Caltech, CA.
2008-2010	Member, The Cancer Genome Atlas Steering Committee, National Cancer Institute.
01/2006-	Scientific advisory board member, Eli & Edythe L. Broad Institute Board of Scientific Counselors, Boston, MA
1/01-12/07	Consultant and member of scientific advisory board, Affymetrix, Inc., Santa Clara, CA
1/97-6/99	Consultant and founding member, scientific advisory board, Neomorphic, Inc., Berkeley, CA
1/87-1/89	Consultant, Xerox, Inc., Xerox Park, Palo Alto, CA
4/84-10/84	Consultant, Seville Technology, Boulder, CO
6/81-10/81	Consultant, Interactive Systems Corp., Santa Monica, CA

EDUCATION

Ph.D. 1982	University of Colorado at Boulder, Computer Science, Received Graduate Student Research Award
M.S. 1979	California Polytechnic State University at San Luis Obispo, Applied Mathematics, Received Mathematics Award
B.A. 1975	Connecticut College, New London, CT, Mathematics Magna Cum Laude, Phi Beta Kappa, received Julia Bower Mathematics Award

HONORS & AWARDS

2015	Dan David Prize, Tel Aviv University, 2015 Future - Bioinformatics
2013	Innovations in Networking Award, Corporation for Education Network Initiatives in California (Cenic)
2011	Weldon Memorial Prize, University of Oxford
2009	Curt Stern Award, American Society of Human Genetics

2009-	Fellow, International Society for Computational Biology
2008	Senior Scientist Accomplishment Award, International Society for Computational Biology
2006-	Member, National Academy of Sciences
2006-	Fellow, American Academy of Arts and Sciences
2006	Dickson Prize in Science, Carnegie Mellon University
2005	World Technology Network Award, IT Software Category
2005	Classic Paper Award, American Association of Artificial Intelligence, for “Quantifying the inductive bias in concept learning,” 1986
2005	Distinguished Engineering Alumni Award, University of Colorado, Boulder
2004	Allen Newell Award, Association for Computing Machinery and the American Association for Artificial Intelligence
2003	Distinguished Scientist of the Year Award Clinical Ligand Assay Society
2003	Tech Award Laureate, San Jose Tech Museum of Innovation
2002-	Fellow, American Association for the Advancement of Science
2001-2002	UCSC Faculty Research Lecturer
2001	Scientist of the Year Award, Research & Development Magazine
2001	Featured Scientist, Incyte Genomics
2001-	Fellow, California Academy of Sciences
2000-2003	Awarded UC Presidential Chair of Computer Science
1992-	Fellow, American Association of Artificial Intelligence

PROFESSIONAL SERVICE

Memberships

2015-	Member, IEEE
2015-	Member, Association for Computing Machinery
2015-	Member, Society of Immunotherapy of Cancer
2009-	Fellow, International Society for Computational Biology
2009-	Member, American Genetic Association
2008-	Member, American Association for Cancer Research
2006-	Member, National Academy of Sciences
2006-	Member, American Academy of Arts & Science
2006-	Member, International Society for Stem Cell Research

2003- Member, American Society of Human Genetics

2000- Member, Institute of Mathematical Statistics

2002- Fellow, American Association for the Advancement of Science

2001- Fellow, California Academy of Sciences

1992- Fellow, American Association of Artificial Intelligence

1979- Member, Association for Computing Machinery

Professional Associations

01/2013- Co-organizer, Global Alliance for Genomics and Health, New York.

04/2009- Co-founder, Genome 10K Project.

2009- Member, Extracellular Action Potential (EAP) Beckman Institute.

2009-2012 Member, Breast Cancer Dream Team, Stand up to Cancer (SU2C).

2008- Member, The Cancer Genome Atlas Steering Committee, National Cancer Institute.

PUBLICATIONS AND SCHOLARLY WORK

Contribution to Science

Citations to scientific papers: >129,000 citations, h-index 137, i10-index 260, May 1, 2017

Books and Book Chapters

Harte R A, Diekhans M, Kent WJ, Haussler D. Guide to the UCSC Genome Browser. Cambridge, MA: NPG Education, 2010. http://www.nature.com/scitable/ebooks/guide-to-the-ucsc-genome-browser-16569863.

Harte RA, Karolchik D, Kuhn RM, Kent WJ, Haussler D. Databases and Genome Browsers. In Speicher M, Antonarakis S, Motulsky AG. (eds): Vogel and Motulsky's Human Genetics, Principles and Approaches, 4th Edition, Springer, New York, 2009

Siepel A, Haussler D. Phylogenetic hidden Markov models. In Nielsen R (ed): Statistical Methods in Molecular Evolution, Springer, 2004.

Haussler D, Opper M. Metric entropy and minimax risk in classification. In Mycielski J, Rozenberg G, Salomaa A (eds): Lecture Notes in Computer Science: Studies in Logic and Computer Science, 1997:1261:212-35.

Haussler D, Barron A. How well do Bayes methods work for on-line prediction of +1,-1 values? In Proceedings of the Third NEC Symposium on Computation and Cognition, SIAM, Princeton, NJ, 1992:74-100.

Haussler D, Warmuth M. The probably approximately correct (PAC) and other learning models. In Workshop on Supervised Learning, Santa Fe Institute Press, 1995.

Haussler D, Warmuth M. The probably approximately correct (PAC) and other learning models. In Meyrowitz A, Chipman S (eds): Machine Learning: Induction, Analogy and Discovery.

Haussler D. Generalizing the PAC model. In Mehra P, Wah BW (eds): Artificial Neural Networks: Concepts and Theory, IEEE Society Press, 1992.

Haussler D. Probably approximately correct (PAC) learning and decision-theoretic generalizations. In Smolensky P, Mozer MC, Rumelhart DE (eds): Mathematical Perspectives on Neural Networks, Lawrence Erlbaum Associates, Mahwah, NJ, 1996:651-706.

Haussler, D. Occam's razor; Quantifying inductive bias: AI learning algorithms and Valiant's learning framework; and what size net gives valid generalization. Reprinted in Shavlik J, Dietterich T (eds): Readings in Machine Learning, Morgan Kaufmann, Los Altos, CA, 1990.

Haussler D. Applying Valiant's learning framework to AI concept learning problems. In Michalski R, Kodratoff Y. (eds): Machine Learning: An Artificial Intelligence Approach, Vol. III, Morgan Kaufmann, Los Altos, 1990:641-69.

Edited Books

Proceedings of the Fifth ACM Workshop on Computational Learning Theory, ACM, 1992.

Proceedings of the Second Workshop on Computational Learning Theory, Morgan Kaufmann, Los Altos, CA, 1989. (with R. Rivest and M. Warmuth).

Proceedings of the First Workshop on Computational Learning Theory, Morgan Kaufmann, Los Altos, CA, 1988 (with L. Pitt).

Peer-Reviewed Journal Publications

Vivian J, Rao AA, Nothaft FA, Ketchum C, Armstrong J, Novak A, Pfeil J, Narkizian J, Deran AD, Musselman-Brown A, Schmidt H, Amstutz P, Craft B, Goldman M, Rosenbloom K, Cline M, O'Connor B, Hanna M, Birger C, Kent WJ, Patterson DA, Joseph AD, Zhu J, Zaranek S, Getz G, Haussler D, Paten B. Toil enables reproducible, open source, big biomedical data analyses. Nat Biotechnol. 2017 Apr 11;35(4):314-316. doi: 10.1038/nbt.3772. No abstract available. PMID: 28398314

Cherniack AD, Shen H, Walter V, Stewart C, Murray BA, Bowlby R, Hu X, Ling S, Soslow RA, Broaddus RR, Zuna RE, Robertson G, Laird PW, Kucherlapati R, Mills GB; Cancer Genome Atlas Research Network., Weinstein JN, Zhang J, Akbani R, Levine DA. Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell. 2017 Mar 13;31(3):411-423. doi: 10.1016/j.ccell.2017.02.010. PMID: 28292439

Fishbein L, Leshchiner I, Walter V, Danilova L, Robertson AG, Johnson AR, Lichtenberg TM, Murray BA, Ghayee HK, Else T, Ling S, Jefferys SR, de Cubas AA, Wenz B, Korpershoek E, Amelio AL, Makowski L, Rathmell WK, Gimenez-Roqueplo AP, Giordano TJ, Asa SL, Tischler AS; Cancer Genome Atlas Research Network., Pacak K, Nathanson KL, Wilkerson MD. Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell. 2017 Feb 2. pii: S1535-6108(17)30001-6. doi: 10.1016/j.ccell.2017.01.001. PMID: 28162975

Zerbino DR, Ballinger T, Paten B, Hickey G, Haussler D. Representing and decomposing genomic structural variants as balanced integer flows on sequence graphs. BMC Bioinformatics. 2016 Sep 29;17(1):400. PMID: 27687569Cancer Genome Atlas Research Network. Integrated genomic and molecular characterization of cervical cancer. Nature. 2017 Jan 23. doi: 10.1038/nature21386. PMID: 28112728

Putnam NH, O'Connell BL, Stites JC, Rice BJ, Blanchette M, Calef R, Troll CJ, Fields A, Hartley PD, Sugnet CW, Haussler D, Rokhsar DS, Green RE. Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. Genome Res. 2016 Mar;26(3):342-50. doi: 10.1101/gr.193474.115. PMID: 26848124

The UCSC Genome Browser database: 2017 update. Tyner C, Barber GP, Casper J, Clawson H, Diekhans M, Eisenhart C, Fischer CM, Gibson D, Gonzalez JN, Guruvadoo L, Haeussler M, Heitner S, Hinrichs AS, Karolchik D, Lee BT, Lee CM, Nejad P, Raney BJ, Rosenbloom KR, Speir ML, Villarreal C, Vivian J, Zweig AS, Haussler D, Kuhn RM, Kent WJ. Nucleic Acids Res. 2016 Nov 29. pii: gkw1134. PMID: 27899642

Global Alliance for Genomics and Health. GENOMICS. A federated ecosystem for sharing genomic, clinical data. Science. 2016 Jun 10;352(6291):1278-80. doi: 10.1126/science.aaf6162. No abstract available. PMID: 27284183

Siu LL, Lawler M, Haussler D, Knoppers BM, Lewin J, Vis DJ, Liao RG, Andre F, Banks I, Barrett JC, Caldas C, Camargo AA, Fitzgerald RC, Mao M, Mattison JE, Pao W, Sellers WR, Sullivan P, Teh BT, Ward RL, ZenKlusen JC, Sawyers CL, Voest EE. Facilitating a culture of responsible and effective sharing of cancer genome data. Nat Med. 2016 May 5;22(5):464-71. doi: 10.1038/nm.4089. PMID: 27149219

Gordon D, Huddleston J, Chaisson MJ, Hill CM, Kronenberg ZN, Munson KM, Malig M, Raja A, Fiddes I, Hillier LW, Dunn C, Baker C, Armstrong J, Diekhans M, Paten B, Shendure J, Wilson RK, Haussler D, Chin CS, Eichler EE. Long-read sequence assembly of the gorilla genome. Science. 2016 Apr 1;352(6281):aae0344. doi: 10.1126/science.aae0344. PMID: 27034376

Putnam NH, O'Connell BL, Stites JC, Rice BJ, Blanchette M, Calef R, Troll CJ, Fields A, Hartley PD, Sugnet CW, Haussler D, Rokhsar DS, Green RE. Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. Genome Res. 2016 Feb 4.PMID: 26848124

Ceccarelli M, Barthel FP, Malta TM, Sabedot TS, Salama SR, Murray BA, Morozova O, Newton Y, Radenbaugh A, Pagnotta SM, Anjum S, Wang J, Manyam G, Zoppoli P, Ling S, Rao AA, Grifford M, Cherniack AD, Zhang H, Poisson L, Carlotti CG Jr, Tirapelli DP, Rao A, Mikkelsen T, Lau CC, Yung WK, Rabadan R, Huse J, Brat DJ, Lehman NL, Barnholtz-Sloan JS, Zheng S, Hess K, Rao G, Meyerson M, Beroukhim R, Cooper L, Akbani R, Wrensch M, Haussler D, Aldape KD, Laird PW, Gutmann DH; TCGA Research Network, Noushmehr H, Iavarone A, Verhaak RG. Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell. 2016 Jan 28;164(3):550-63. doi: 10.1016/j.cell.2015.12.028. PMID: 26824661

Hinrichs AS, Raney BJ, Speir ML, Rhead B, Casper J, Karolchik D, Kuhn RM, Rosenbloom KR, Zweig AS, Haussler D, Kent WJ. UCSC Data Integrator and Variant Annotation Integrator. Bioinformatics. 2016 Jan 6. pii: btv766. PMID: 26740527

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Speir ML, Zweig AS, Rosenbloom KR, Raney BJ, Paten B, Nejad P, Lee BT, Learned K, Karolchik D, Hinrichs AS, Heitner S, Harte RA, Haeussler M, Guruvadoo L, Fujita PA, Eisenhart C, Diekhans M, Clawson H, Casper J, Barber GP, Haussler D, Kuhn RM, Kent WJ. The UCSC Genome Browser database: 2016 update. Nucleic Acids Res. 2015 Nov 20. pii: gkv1275. PMID: 26590259

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1000 Genomes Project Consortium, Auton A, Brooks LD, Durbin RM, Garrison EP, Kang HM, Korbel JO, Marchini JL, McCarthy S, McVean GA, Abecasis GR. A global reference for human genetic variation. Nature. 2015 Oct 1;526(7571):68-74. doi: 10.1038/nature15393. PMID: 26432245

Novak AM, Rosen Y, Haussler D, Paten B. Canonical, Stable, General Mapping using Context Schemes. Bioinformatics. 2015 Jul 27. pii: btv435. [Epub ahead of print] PMID: 26220960

Paten B, Diekhans M, Druker BJ, Friend S, Guinney J, Gassner N, Guttman M, James Kent W, Mantey P, Margolin AA, Massie M, Novak AM, Nothaft F, Pachter L, Patterson D, Smuga-Otto M, Stuart JM, Van't Veer L, Wold B, Haussler D. The NIH BD2K center for big data in translational genomics. J Am Med Inform Assoc. 2015 Jul 13. pii: ocv047. doi: 10.1093/jamia/ocv047. PMID: 26174866

Cancer Genome Atlas Research Network, Brat DJ, Verhaak RG, Aldape KD, Yung WK, Salama SR, Cooper LA, Rheinbay E, Miller CR, Vitucci M, Morozova O, Robertson AG, Noushmehr H, Laird PW, Cherniack AD, Akbani R, Huse JT, Ciriello G, Poisson LM, Barnholtz-Sloan JS, Berger MS, Brennan C, Colen RR, Colman H, Flanders AE, Giannini C, Grifford M, Iavarone A, Jain R, Joseph I, Kim J, Kasaian K, Mikkelsen T, Murray BA, O'Neill BP, Pachter L, Parsons DW, Sougnez C, Sulman EP, Vandenberg SR, Van Meir EG, von Deimling A, Zhang H, Crain D, Lau K, Mallery D, Morris S, Paulauskis J, Penny R, Shelton T, Sherman M, Yena P, Black A, Bowen J, Dicostanzo K, Gastier-Foster J, Leraas KM, Lichtenberg TM, Pierson CR, Ramirez NC, Taylor C, Weaver S, Wise L, Zmuda E, Davidsen T, Demchok JA, Eley G, Ferguson ML, Hutter CM, Mills Shaw KR, Ozenberger BA, Sheth M, Sofia HJ, Tarnuzzer R, Wang Z, Yang L, Zenklusen JC, Ayala B, Baboud J, Chudamani S, Jensen MA, Liu J, Pihl T, Raman R, Wan Y, Wu Y, Ally A, Auman JT, Balasundaram M, Balu S, Baylin SB, Beroukhim R, Bootwalla MS, Bowlby R, Bristow CA, Brooks D, Butterfield Y, Carlsen R, Carter S, Chin L, Chu A, Chuah E, Cibulskis K, Clarke A, Coetzee SG, Dhalla N, Fennell T, Fisher S, Gabriel S, Getz G, Gibbs R, Guin R, Hadjipanayis A, Hayes DN, Hinoue T, Hoadley K, Holt RA, Hoyle AP, Jefferys SR, Jones S, Jones CD, Kucherlapati R, Lai PH, Lander E, Lee S, Lichtenstein L, Ma Y, Maglinte DT, Mahadeshwar HS, Marra MA, Mayo M, Meng S, Meyerson ML, Mieczkowski PA, Moore RA, Mose LE, Mungall AJ, Pantazi A, Parfenov M, Park PJ, Parker JS, Perou CM, Protopopov A, Ren X, Roach J, Sabedot TS, Schein J, Schumacher SE, Seidman JG, Seth S, Shen H, Simons JV, Sipahimalani P, Soloway MG, Song X, Sun H, Tabak B, Tam A, Tan D, Tang J, Thiessen N, Triche T Jr, Van Den Berg DJ, Veluvolu U, Waring S, Weisenberger DJ, Wilkerson MD, Wong T, Wu J, Xi L, Xu AW, Yang L, Zack TI, Zhang J, Aksoy BA, Arachchi H, Benz C, Bernard B, Carlin D, Cho J, DiCara D, Frazer S, Fuller GN, Gao J, Gehlenborg N, Haussler D, Heiman DI, Iype L, Jacobsen A, Ju Z, Katzman S, Kim H, Knijnenburg T, Kreisberg RB, Lawrence MS, Lee W, Leinonen K, Lin P, Ling S, Liu W, Liu Y, Liu Y, Lu Y, Mills G, Ng S, Noble MS, Paull E, Rao A, Reynolds S, Saksena G, Sanborn Z, Sander C, Schultz N, Senbabaoglu Y, Shen R, Shmulevich I, Sinha R, Stuart J, Sumer SO, Sun Y, Tasman N, Taylor BS, Voet D, Weinhold N, Weinstein JN, Yang D, Yoshihara K, Zheng S, Zhang W, Zou L, Abel T, Sadeghi S, Cohen ML, Eschbacher J, Hattab EM, Raghunathan A, Schniederjan MJ, Aziz D, Barnett G, Barrett W, Bigner DD, Boice L, Brewer C, Calatozzolo C, Campos B, Carlotti CG Jr, Chan TA, Cuppini L, Curley E, Cuzzubbo S, Devine K, DiMeco F, Duell R, Elder JB, Fehrenbach A, Finocchiaro G, Friedman W, Fulop J, Gardner J, Hermes B, Herold-Mende C, Jungk C, Kendler A, Lehman NL, Lipp E, Liu O, Mandt R, McGraw M, Mclendon R, McPherson C, Neder L, Nguyen P, Noss A, Nunziata R, Ostrom QT, Palmer C, Perin A, Pollo B, Potapov A, Potapova O, Rathmell WK, Rotin D, Scarpace L, Schilero C, Senecal K, Shimmel K, Shurkhay V, Sifri S, Singh R, Sloan AE, Smolenski K, Staugaitis SM, Steele R, Thorne L, Tirapelli DP, Unterberg A, Vallurupalli M, Wang Y, Warnick R, Williams F, Wolinsky Y, Bell S, Rosenberg M, Stewart C, Huang F, Grimsby JL, Radenbaugh AJ, Zhang J. Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. N Engl J Med. 2015 Jun 25;372(26):2481-98. doi: 10.1056/NEJMoa1402121. 2015 Jun 10. PMID: 26061751

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Krogh A, Mian IS, Haussler D. Parsing DNA with hidden Markov models. Alternative Readings of the Genetic Code, Parknasilla, County Kerry, Ireland, May 1993.

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Haussler D, Kearns M, Opper M, Schapire R. Estimating average-case learning curves using Bayesian, statistical physics and VC dimension methods. 5th Conference on Neural Information Processing Systems, Denver, CO, 1991.

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Haussler D, Kearns M, Schapire R. Bounds on the sample complexity of Bayesian learning using information theory and the VC dimension. 4th Workshop on Computational Learning Theory (COLT), Santa Cruz, CA, August 1991:61 74.

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Haussler D. Uniting the VC and TLS theories of generalization. Neural Networks for Computing, Snowbird, UT, April 1991.

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Haussler D. Probably approximately correct learning. AAAI, 1990:1101-8.

Haussler D. Sample size bounds for training multi-layer nets of quasi-linear, product and radial basis functions. Neural Networks for Computing, Snowbird, UT, April 1990.

Haussler D, Warmuth M. Analyzing the performance of learning algorithms. ONR Workshop on Knowledge Acquisition, Crystal City, VA, November 1989.

Milosavljevic A, Haussler D, and Jurka J. Parsimonious classification of aligned molecular sequences. Bio-Matrix, White Mountain Conference Center, Waterville Valley, NH, August 1989.

Haussler D. Generalizing the PAC Model: Sample size bounds from metric dimension-based uniform convergence results. 1989 IEEE Symp. on Foundations of Computer Science (FOCS), Research Triangle, NC, October 1989;40 5.

Milosavljevic A, Haussler D, Jurka J. Informed parsimonious inference of prototypical genetic sequences. 2nd Workshop on Computational Learning Theory, Santa Cruz, CA, August 1989.

Pagallo G, Haussler D. Two algorithms that learn DNF by discovering relevant features. 6th International Workshop on Machine Learning, Cornell University, Ithaca, NY, July 1989.

Baum E, Haussler D. What size net gives valid generalization. IEEE Conference on Neural Information Processing Systems, Denver, CO, November 1988.

Haussler D, Littlestone N, Warmuth M. Predicting 0,1-functions on randomly drawn points. 29th IEEE Symposium on Foundations of Computer Science, White Plains, NY, October 1988:100 9.

Haussler D, Kearns M, Littlestone N, Warmuth M. Equivalence for models of polynomial learnability. 1st Workshop on Computational Learning Theory, MIT, Cambridge, MA, August 1988.

Ehrenfeucht A, Haussler D. Learning decision trees from random examples. 1st Workshop on Computational Learning Theory, MIT, Cambridge, MA, August 1988.

Ehrenfeucht A, Haussler D, Kearns M, Valiant L. A general lower bound on the number of examples needed for learning. First Workshop on Computational Learning Theory, MIT, Cambridge, MA, August 1988.

Haussler D. Learning conjunctive concepts in structural domains. AAA, Seattle, WA, July 1987:466 70.

Haussler D. Bias, Version spaces and Valiant's learning framework. 4th International Workshop on Machine Learning, Irvine, CA, June 1987.

Alon N, Haussler D, Welzl E. Partitioning and geometric embedding of range spaces of finite Vapnik-Chervonenkis dimension. 3rd International Conference on Computational Geometry, Waterloo, Canada, June 1987:331 40.

Blumer A, Ehrenfeucht A, Haussler D. Average sizes of suffix trees and DAWGs. 1st Montreal Conference on Combinatorics and Computer Science, University of Montreal, Canada. May 1987.

Haussler D. Learning internal disjunctive concepts. 20th Asilomar Conference on Signals, Systems and Computers, Pacific Grove, CA. November 1986.

Haussler D. Quantifying the inductive bias in concept learning. AAAI, Philadelphia, PA, August, 1986.

Haussler D, Welzl E. Range spaces and Epsilon-nets. SIAM Workshop on Computational and Discrete Geometry, Santa Cruz, CA, July 1986.

Haussler D. A methodology for assessing the learnability of knowledge structures. 1st Annual Rocky Mountain Conference on Artificial Intelligence, Boulder, CO, June 1986.

Haussler D, Welzl E. Epsilon-nets and simplex range queries. 2nd International Conference on Computational Geometry, Yorktown Heights, NY, June 1986.

Blumer A, Ehrenfeucht A, Haussler D, Warmuth M. Classifying learnable geometric concepts with the Vapnik-Chervonenkis dimension. 18th ACM Symposium on Theoretical Computational Science, Berkeley, CA, May 1986:273 82.

Bucher W, Ehrenfeucht A, Haussler D. On total regulators generated by derivation relations. Proc. 12th International Coll. Aut. Lang. Prog, Nafplion, Greece, July 1985:71 9.

Main MG, Bucher W, Haussler D. Applications of an infinite squarefree co-CFL. Proc. 12th International Coll. Aut. Lang. Prog., Nafplion, Greece, July 1985:404 12.

Blumer A, Blumer J, Ehrenfeucht A, Haussler D, McConnell R. Building the minimal DFA for the set of all subwords of a word on-line in linear time. Proc. 11th International Coll. Aut. Lang. Prog., Antwerp, Belgium, July 1984:109 18.

Blumer A, Blumer J, Ehrenfeucht A, Haussler D, McConnell R. Building a complete inverted file for a set of text files in linear time. Proceedings of the 16th ACM Symposium on Theoretical Computational Science, Washington, D.C., May 1984:349 58.

Other Publications

Daniel R. Zerbino, Benedict Paten, Glenn Hickey, David Haussler. An algebraic framework to sample the rearrangement histories of a cancer metagenome with double cut and join, duplication and deletion events. arXiv:1303.5569v1 [q-bio.GN] 22 Mar 2013.

David Haussler, David A. Patterson, Mark Diekhans, Armando Fox, Michael Jordan, Anthony D. Joseph, Singer Ma, Benedict Paten, Scott Shenker, Taylor Sittler and Ion Stoica. A Million Cancer Genome Warehouse. EECS Department, University of California, Berkeley. Technical Report No. UCB/EECS-2012-211, November 20, 2012

Roskin KM, Diekhans M, Kent, WJ, Haussler D. Score functions for assessing conservation in locally aligned regions of DNA from two species. University of California, Santa Cruz, Santa Cruz, CA Tech Report UCSC-CRL-02-30. Sep, 2002.

Haussler D. The challenge of bioinformatics. R&D Magazine. 2001 Nov;43(11):8S-SC3 (in conjunction with Scientist of the Year Award).

Kent WJ, Haussler D. GigAssembler: an algorithm for the initial assembly of the human genome working draft. UCSC-CRL-00-17, December 27, 2000.

Haussler D, Jaakkola T, Winters-Hilt S. Tradeoffs between generative and discriminative hidden Markov models. Computer Science Department, University of California, Santa Cruz, Santa Cruz, CA. 1998.

OUTSIDE PROFESSIONAL ACTIVITIES

Conferences and Meetings, Invited

2017

“Treehouse Pediatric Cancer Consortium, invited keynote speaker, Annual Stanford Center for Genomics and Personalized Medicine Symposium, Stanford, Palo Alto, CA. April

“Facilitating a culture of responsible and effective sharing of genome data,” invited speaker, BioData World Congress, BioData World Series, San Franscico. April

“The Global Alliance for Genomics and Health: Sharing Data for Genomic Medicine,” invited speaker. 2017 Sage Bionetworks Assembly: Mapping Open Ecosystems, Sage Assembly, Seattle, WA. April

“Sharing data for genomic medicine,” invited speaker, Bioinformatics for Big Data, Molecular Medicine Tri-Conference, San Francisco, CA. February

“Data Sharing in the Treehouse Childhood Cancer Initiative: The power of big data to defeat childhood cancer,” St. Baldrick’s Foundation Board Meeting, St. Baldrick’s, Montovia, CA. February

“The Global Alliance for Genomics and Health: Accessibility of Data for Medicine,” PMWC 2017 Silicon Valley, Personalized Medicine World Conference, Mountain View, CA. January

“The Global Alliance for Genomics and Health: Accessibility of Data for Medicine,” invited speaker and panelist, SU2C Scientific Summit, Stand up 2 Cancer, Santa Monica, CA. January

2016

“A public ledger to share all the world's cancer mutations,” invited speaker, Festival of Genomes, San Diego, CA. September.

“Global Sharing of Genomic Information for Precision Medicine,” invited speaker, Anschutz Medical Campus, Aurora, CO. August

“The Human Genome,” invited speaker, Commonwealth Club of California, San Francisco, CA. May 18, 2016

“Global Alliance for Genomics and Health: Genome Data Sharing,” invited speaker, Center for International Security and Cooperation, Stanford, Palo Alto, CA. May

“Global Sharing of Better and More Genomes.” Invited speaker, 13th International Congress of Human Genetics Conferenmlll, Kyoto, Japan. April

Global Sharing of Genomic Information for Precision Medicine,” invited keynote speaker, 2016 AMIA Joint Summit: Plenary Session, American Medical Informatics Association, San Francisco, CA. March

“BRCA Challenge,” invited speaker, Inaugural Precision Medicine, Molecular Medicine Tri-Conference, San Francisco, CA. March

“Cancer genomics and data sharing,” invited speaker, 2016 Future of Genomics Medicine, Scripps, La Jolla, CA. March

“Computer Science Meets Genetics in the Genome Era,” invited speaker, Special Beckman Institute Functional Genomics Center Seminar, Caltech, Pasadena, CA. March

“Global sharing of better and more genomes,” invited speaker, Advances in Genome Biology and Technology 2016, Advances in Genome Biology and Technology, Orlando, FL. February

“Global Alliance for Genomics and Health,” invited speaker, Personalized Medicine World Conference (PMWC) 2016 Silicon Valley, Personalize Medicine Worldwide Conference, International, Mountain View, CA. January

2015

“Harnessing Global Genomic Data to Defeat Cancer,” invite speaker, CARIS Scientific Board Meeting, Caris Life Sciences, Scottsdale, AZ. December

“Odyssey Into the Human Genome, invited speaker, Annual Regional Meeting, San Francisco Area Mensa, Santa Cruz, CA. November

“The Data Working Group of the Global Alliance for Genomics and Health,” invited speaker and panelist, Probabilistic Modeling in Genomics, Cold Spring Harbor, NY. October

“Harnessing Global Genomic Data for Discovery,” invited speaker, Future Sequencing Technologies and Applications, Genomics Institute of the Novartis Research Foundation, La Jolla, CA. September

“Big Data,” invited panelist, Aspen Cancer Conference Special Evening, Aspen Cancer Conference, Aspen CO. July

“Antigen Recognition Project,” invited speaker, SU2C - Google[x] Technology and Analysis Satellite Meeting, Stand up 2 Cancer, Boston, MA. July

“Federated BRCA Data Sharing: Lessons and Visions, invited speaker, BRCA Challenge, Global Alliance for Genomics and Health, Paris, France, June.

“Bioinformatics to enable cancer immunotherapy,” invited speaker, Immunology Meeting, Stand up 2 Cancer, Boston, MA. June

“BD2K Centers of Excellence,” invited speaker Big Data in BioMedicine, Stanford University, Palo Alto, CA. May

“Odyssey into the human genome,” invited award winner, 2015 Dan David Prize, University of Tel Aviv, Tel Aviv, Israel. May

“Global Alliance for Genomics and Health,” invited speaker, 2015 TEDx Santa Cruz, April

“Calling both simple and complex mutations in cancer genome,” invited speaker, Identifying Drug Targets with Computational Genomics, 2015 Annual Meeting, American Association for Cancer Research, Philadelphia, PA. April

“Global Alliance for Genomics and Health,” invited speaker, Annual UC system-wide conference, UC Academic Business Officers Group (ABOG), Santa Cruz, CA. April

“Technology and Big Data,” invited speaker, Big Data, Genomics, and Precision Medicine Program, National Human Genome Research Institute, San Jose, CA. April

“Big Data to Knowledge (BD2K) Centers of Excellence”, invited speaker, AMIA Translational Bioinformatics Conference, San Francisco, CA. March

“Stable reference structures for human genome analysis,” invited featured speaker, Genome and Transcriptome Analysis, Molecular Medicine Tri-Conference. San Francisco, CA. February

“Global exchange of human genetic data for medicine and research,” invited keynote speaker, Bioinformatics for Big Data Track, Medicine Tri-Conference. San Francisco, CA. February

“Global Alliance for Genomics and Health,” invited speaker, Large Sequence Data Analysis & Clinical Interpretation, Personalized Medicine World Conference 2015, Mountain View, CA January

“Global exchange of human genetic data for medicine and research,” invited keynote speaker, Pacific Symposium on Biocomputing 2015, Kona, HI, January

2014

“Global exchange of human genetic data for medicine and research,” invited keynote speaker, Cold Spring Harbor Biological Data Sciences, Cold Spring Harbor, NY. November.

“Discovering and representing subclones in cancer tissues from analysis of whole genome sequencing data,” invited speaker, Tumor Heterogeneity Symposium, Stanford Cancer Institute, Palo Alto, CA. October

“Peptide Antigen Display and Recognition: a New Fusion of Genomics and Proteomics,” invited speaker, Future Opportunities for Genomic Sequencing, NHGRI, Bethesda, MD. July

Participatory Biology Panel, invited panelist, Techonomy Bio conference, Techonomy, San Jose, CA. June

“Large-scale Cancer Genomics,” invited speaker, Sadler Memorial Lecture, University of Colorado, Denver, Denver CO. May

“Large-scale Cancer Genomics,” invited speaker, 2014 BioFrontiers Symposium on Big Data, University of Colorado, Boulder, Boulder, CO. May

“Large-scale Cancer Genomics,” invited speaker, Sequence the City - Metagenomics in the Era of Big Data, IBM: Almaden Institute, San Jose, CA. May

“Large-scale Cancer Genomics,” invited speaker, AACR Annual Meeting 2014, American Association for Cancer Research, San Diego, CA. April

“Large-scale Cancer Genomics,” invited speaker, Big Data in Biology, Keystone Symposium on Molecular and Cellar Biology, San Francisco, CA. March

“Large-scale Cancer Genomics,” invited speaker, Big Data in Biology, Simons Foundation, Biotech Symposium, New York, NY. March

“Large-scale Cancer Genomics,” invited speaker, Evening Lectures in Genomics, New York Genome Center, New York, NY. March

“Cancer Genomics,” invited speaker, Bioinformatics for Big Data, 21st Molecular Medicine Tri-conference, Cambridge Healthtech Institute, San Francisco, CA. February

2013

“Cancer Genomics,” invited speaker, Global SIP Symposium: Bioinformatics and System Biology, University of Texas, Austin, TX. December.

“Comparative analysis of cortical neuron development in a stem cell model of primate neurogenesis,” invited speaker, Howard Hughes Medical Institute Scientific meeting, Howard Hughes Medical Institute, Ashburn, VA. October.

“A global alliance for genomic and clinical data,” invited keynote speaker, Beyond the Genome, BioMed Center, San Francisco, CA. October.

“Genome data in the cloud,” invited speaker, The 8th Scientific Workshop, International Cancer Genome Consortium, Toronto, Canada. October.

“Large-scale comparative genomics for cancer research,” invited speaker, Statistical Data Integration Challenges in Computational Biology: Regulatory Networks and Personalized Medicine, Banff International Research Station for Mathematical Innovation and Discovery (BIRS), Banff, Canada. August.

“Cancer Genomics,” invited speaker, Microsoft Research Faculty Summit, Microsoft, Redmond, WA. July.

“Large-scale Comparative Genomics for cancer research,” invited speaker, 2013 Human Genome Meeting and 21st International Congress of Genetics, Human Genome Organization (HUGO) and International Genetics Federation (IGF), Singapore, Singapore, April.

“Generalizations of the Fourier transform to Gelfand pairs provide a continuous time Markov model for the evolution of genomes via rearrangements and substitutions” invited speaker, Janelia Biological Sequence Analysis Conference, Howard Hughes Medical Institute, Ashburn, VA. March.

“Cancer Genomics,” invited speaker, Doc Talk lecture series, American Cancer Society, Santa Cruz, CA. February.

“Large scale Cancer Genomics analysis,” invited speaker, Pacific Symposium on Biocomputing 2013: The Future of Genome-Based Medicine, Kona, HI. January.

2012

“Benchmarking study—DNA sequence variance/rearrangement calls: algorithm comparison across centers,” invited speaker, The Cancer Genome Atlas Semi-Annual Steering Committee Meeting, The Cancer Genome Atlas, Crystal City, VA. November.

“One million cancer genomes”, invited speaker, Techonomy 2012, Techonomy, Tucson, AZ. November.

“The UCSC Cancer Genomics Hub,” invited keynote speaker, 2012 Uninex Symposium, Operating Systems Design and Implementation, Hollywood, CA. October.

“Somatic mutations in cancer as assessed by whole genome sequencing,” invited speaker, Identification and annotation of SNPs in the context of structure, function, and disease meeting, Special Interest Group (SNP-SIG), Long Beach, CA. July.

“Three periods of regulatory innovation during vertebrate evolution,” invited speaker, EMBO: Evolution in the Time of Genomics, Genetic Information Research Institute, Venice, Italy. May.

“Mutation calling,” invited speaker, The Cancer Genome Atlas Semi-Annual Steering Committee Meeting, The Cancer Genome Atlas, Houston TX. April.

“UCSC Cancer Genomics Hub,” invited speaker, The Cancer Genome Atlas Semi-Annual Steering Committee Meeting, The Cancer Genome Atlas, Houston TX. April.

“Personal cancer genomics,” invited keynote speaker, 3rd Sage Bionetworks Commons Congress, Sage Bionetworks Commons Congress, San Francisco, CA. April.

“Cancer genomics,” invited speaker, Genome Informatics Alliance 2012, Genome Informatics Alliance, Newberg OR. March.

“Benchmarking mutation calls,” invited speaker, 2012 International Cancer Genome Consortium workshop, International Cancer Genome Consortium, Cannes, France. March.

“Aspects of the evolutionary impact of retrotransposons on vertebrate genomes,” invited speaker, Genetic Information Genomic Impact, 3rd International Conference on Genomic Impact of Eukaryotic Transposable Element, Pacific Grove. February.

“Personal genomics,” invited speaker, Pacific Symposium on Biocomputing, Kona, HI. January.

2011

“Genomic analysis for pathway characterization,” invited speaker, San Antonio Breast Cancer Symposium, San Antonio, TX. December.

“Large-scale cancer genomics data analysis,” invited speaker, Enabling Cancer Research through TCGA, The Cancer Genomics Atlas, Houston, TX. November.

“CGHub: A next generation repository for next generation sequence data,” invited speaker, Enabling Cancer Research through TCGA, The Cancer Genomics Atlas, Houston, TX. November.

“Cancer genomics,” invited speaker, Howard Hughes Medical Institute, Chevy Chase, MD. November.

“Cancer genomics in the TCGA TARGET and ICGC projects,” invited speaker, Translation of the cancer genome meeting, American Association for Cancer Research (AACR) San Francisco, CA. October.

“Cancer genomics,” invited speaker, Inaugural Bio-IT Cloud Summit: Cloud Computing Conference, Bio-IT World and Cambridge Healthtech Institute, La Jolla, CA. September.

“Epigenomics of stem and cancer cells: computational challenges,” invited speaker , 2011 CIRM Grantee Meetings, California Institute for Regenerative Medicine, San Francisco, CA. September.

“Cancer genomics,” keynote speaker, SIGKDD 2011Conference, Association for Computing Machinery, San Diego, CA. August.

“Cancer genomics,” invited speaker, Spring Epigenetics, Genentech, Woodside, CA. May.

“The large-scale analysis tool building perspective: The need for access to data sets, standard exchange formats, and bringing computing to the data,” invited speaker, The Collection, Storage, Management, and Distribution of Next-Generation Sequence Data, National Institutes of Health, Gaithersburg, MD. April.

“Mutation analysis,” invited speaker,” The Cancer Genome Atlas (TCGA) Semi-Annual Steering Committee Meeting, The Cancer Genome Atlas. Bethesda, MD. April.

“Cancer genomics in the TCGA project,” invited speaker, DARPA CAP3 workshop, National Cancer Institute, Bethesda, MD. April.

“Cancer genomics in the TCGA Project,” invited speaker, Conference on Systems Biology: Confronting the Complexity of Cancer, AACR/NCI, La Jolla, CA. February.

“Cancer genomics: the Next Step for SU2C,” invited speaker, Stand Up 2 Cancer Dream Team Summit, Miami, FL. January.

“Personal genomics,” invited speaker, Pacific Symposium on Biocomputing, Kona, HI. January.

2010

“Genomics and the Genome 10K Project,” invited speaker, Chance and Necessity in Evolution, International Union of Biological Sciences & Istituto per gli Studi Filosofici of Naples, Ravello, Italy. October.

“Cancer genomics and the TCGA project,” invited speaker, Molecular Diagnostics in Cancer Therapeutic Development, American Association for Cancer Research, Denver, CO. September.

“Cancer genomics data analysis,” invited speaker, Pfizer, Cancer Genomics Data Analysis, San Diego, CA. August.

“Comparative genomics and the Genome 10K Project,” invited speaker, American Genetic Association, Conservation Genomics, Hilo, HI. July.

“$1000 Genomes,” invited speaker, HiTSeq, Intelligent Systems for Molecular Biology, Boston, MA. July.

“$100 Genomes,” invited speaker, Jason Study, The MITRE Corporation, San Diego, CA. June.

“TCGA data analysis pipeline,” invited speaker, The Cancer Genome Atlas Steering Committee. Bethesda, MD. April.

“Comparative genomics for vertebrates,” invited speaker, National Human Genome Research Institute Informatics and Analysis Planning Meeting, Bethesda, MD. April.

“TCGA Data analysis and dissemination,” invited speaker, American Association for Cancer Research Annual Meeting 2010, The Cancer Genome Atlas. Washington, DC. April.

“Mapping cancer genomics data to pathways,” invited speaker, Cancer Profiling and Pathways Conference, San Francisco, CA. February.

2009

“The supercomputing challenge to decode the evolution and diversity of our genomes,” invited speaker, Supercomputing 2009 Conference, Portland, OR. November.

“Genomes in the Clouds: UCSC genomics browsers and distributed bio computation,” invited speaker, Supercomputing 2009 Conference, Portland, OR. November.

“Reconstructing the 500 million year record of evolution in the vertebrate genome,” featured lecturer, Annual Meeting of the Fellows of the California Academy of Sciences, San Francisco, CA. October.

The evolution of non-coding functional elements in our genome,” invited speaker, Evolution of the Molecular Landscape, 74th Cold Spring Harbor Symposium, Cold Spring Harbor, NY. May.

“The evolution of non-coding functional elements in our genome,” invited speaker, Harvey Mudd College, Pasadena, CA. April.

“Transposon-induced rewriting of vertebrate gene regulation,” invited speaker, AAAS Annual Meeting: Our Life and its Life: Origins and Futures, Chicago, IL. February.

“Statistical and algorithmic methods to explore evolution,” invited speaker, NIH Darwin Day, Bethesda, MD. February.

“Molecular evolution and disease,” invited speaker, HHMI Scientific Meeting: Human Disease, Genetics, Models and Progress Toward Treatments, Chevy Chase, MD. February.

“Evidence that transposons shaped vertebrate gene regulatory networks,” invited speaker, 2nd International Conference and Workshop Genomic Impact of Eukaryotic Transposable Elements, Asilomar, Monterey, CA. February.

2008

“UCSC cancer genomics browser for TCGA data,” invited speaker, TCGA Steering Committee, Washington, D.C. December.

“Non-coding RNA: Red-headed stepchild of the human genome,” invited speaker, 58th Annual Meeting of ASHG, Philadelphia, PA. November.

“Human gene predictions,” MGC-ESC Meeting, invited speaker, Rockville, MD. September.

“100 million years of evolutionary history of the human genome,” invited speaker, ISCB Conference, Toronto, CAN. July.

“100 million years of evolutionary history of the human genome,” invited speaker, 23rd Conference on AAAI-08, Chicago, IL. July.

“Computing how we became human,” invited speaker, 40th ACM Symposium on Theory of Computing, Victoria, BC. May.

“A rapidly evolved RNA gene may have played a role in the evolution of the cerebral cortex,” invited speaker, European Human Genetics Conference, Barcelona, Spain. May.

“100 million years of evolutionary history of the human genome,” plenary speaker, HapMap, Human Evolution and the Future of Life, Copenhagen, Denmark. May.

“Evolutionary genomics of the human genome,” Distinguished Lecturer, Computer Science Columbia University, New York, NY. May.

“Computing how we became human,” invited speaker, Renaissance Technologies Corporation Symposium, New York, NY. May.

“The personal genome: consequences for society,” invited speaker, 7th Annual Genome Sciences Symposium, Seattle, WA. April.

“The infinite sites model of genome evolution,” invited speaker, Gordon Conference in Molecular Evolution, Ventura, CA. February.

2007

“Reconstructing 100 million years of human evolutionary history,” honored speaker, NIH Intramural Sequencing Center’s 10th Anniversary Symposium, Bethesda, MD. October.

“Rapidly evolving non-coding regions and brain evolution,” honored speaker, 57th Annual American Society of Human Genetics Meeting, San Diego, CA. August.

“Reconstructing 100 million years of human evolutionary history,” invited speaker, Pacific Biosciences, Menlo Park, CA. July.

“Reconstructing 100 million years of human evolutionary history,” honored speaker, Vertebrate Comparative Genomics, US National Academy of Sciences and the Australian Academy of Science, Beckman Center of the National Academy of Sciences, Irvine, CA. May.

“The infinite sites model of genome evolution,” Biology of Genomes meeting, invited speaker, Cold Springs Harbor Conference, Cold Springs Harbor, NY. May.

2006

“Reconstructing 100 million years of human evolutionary history,” Johns Hopkins University, Baltimore, MD. November.

“Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome,” invited speaker, International Symposium on Genomics, Hangzhou, China. October.

“Reconstructing 100 million years of human evolutionary history,” honored speaker, Scientific Forum for Cabrillo Festival of Contemporary Music, world premiere of the Frans Lanting orchestral-photographic performance “Life: A Journey Through Time,” Santa Cruz, CA. July.

“Exploring the evolutionary history of the human genome over the last 100 million years,” keynote address, ACM SIGMOND International conference on Management of Data, Chicago, IL. June.

“Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome,” 23rd International Conference on Machine Learning (ICML), Carnegie Mellon University, Pittsburgh, PA. June.

“Ultraconserved elements, living fossil transposons, distal enhancers, and mysterious RNA genes: reconstructing the detailed evolutionary history of the human genome,” Annual Society for Molecular Biology and Evolution Meeting, Genomes, Evolution, and Bioinformatics, Arizona State University, Tempe. May.

“Ultraconserved elements, living fossil transposons, distal enhancers, and mysterious RNA genes: reconstructing the detailed evolutionary history of the human genome,” inaugural speech, Broad Distinguished Lecture Series in Computational Biology, Eli & Edythe L. Broad Institute, Cambridge, MA. May.

“Feasibility of reconstructing the 100 million year history of the human genome,” Genomes and Biology, Cold Spring Harbor, NY. May.

“Applying comparative genomics to assist in the completion of the Mammalian Gene Collection,” Mammalian Gene Collection Annual Meeting, Washington, DC. April.

“The infinite sites model of genome evolution,” Workshop on Reconstruction of Ancestral Genomes, Barbados. April.

“Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome,” keynote address, 10th Annual Conference on Research in Computational Molecular Biology, Venice, Italy. March.

“Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome,” keynote address, Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY. March.

“Ultraconserved elements, living fossil transposons, and rapid bursts of change: reconstructing the uneven evolutionary history of the human genome,” Dickson Prize award talk, Carnegie-Mellon University, Pittsburg, PA. March.

“Ultraconserved elements, living fossil transposons, distal enhancers, and mysterious RNA genes: reconstructing the detailed evolutionary history of the human genome,” Integrative Graduate Education and Research Traineeships, University of Arizona, Tucson. January.

2005

“Health, medicine, and biotechnology,” keynote address, World Technology Summit, San Francisco, CA. November.

“Using evolution to explore the human genome,” honored speaker, European Bioinformatics Institute, Hinxton, UK. November.

“Using evolution to explore the human genome,” Evolutionary Genomics Meeting, The Stazione Zoologica Anton Dohrn, Naples, Italy. October.

“Using evolution to explore the human genome,” keynote address, Genome Informatics Conference, Cold Spring Harbor, NY. October.

“Using evolution to explore the human genome,” keynote address, IEEE Workshop on Computer Vision Methods for Bioinformatics, San Diego, CA. June.

“Computational reconstruction of an ancestral mammalian chromosome,” keynote address, Cold Spring Harbor Conference, Cold Spring Harbor, NY. May.

“Reconstructing an ancestral mammalian chromosome,” keynote address, Cold Spring Harbor Conference, Cold Spring Harbor, NY. May.

“Ultraconserved elements in the human genome,” European Human Genetics Conference, Prague, Czech Republic. May.

“Impact of human genome research: present and future,” Mervyn Young Memorial Lecture, University of Colorado, Boulder, Boulder, CO. April.

“Using evolution to explore the human genome,” Distinguished Engineering Alumni Award Seminar, University of Colorado, Boulder, Boulder, CO. April.

“Impact of human genome research: present and future,” honored speaker, Mervyn Young Memorial Lecture, University of Colorado, Boulder, Boulder, CO. April.

2004

“Using evolution to explore the human genome,” honored speaker, University of Washington, CSE Distinguished Lecture, Seattle, WA. December.

“Impact of human genome research: present and future,” Mervyn Young Memorial Lecture, University of Colorado, Boulder, April.

“Using evolution to explore the human genome,” Distinguished Engineering Alumni Award Seminar, University of Colorado, Boulder. April.

“Impact of human genome research: present and future,” honored speaker, Mervyn Young Memorial Lecture, University of Colorado, Boulder. April.

“Comparative genomics to identify functional elements in the human genome,” Molecular Medicine Tri-Conference, San Francisco, CA. March.

“The power of multiple vertebrate genome sequences,” Keystone Symposia, Steamboat Springs, CO. March.

“Reconstructing an ancestral mammalian genome in silico,” Gordon Research Conference in Molecular Evolution, Ventura, CA. February.

2003

“Using comparative genomics to predict functional elements in the human genome,” Distinguished Speaker Series, Sloan-Swartz Center for Theoretical Neurobiology Seminar, Colorado State University, Ft. Collins. November.

“Using comparative genomics to predict functional elements in the human genome,” 2003-04 Distinguished Seminar Series, Department of Computer Science, University of British Columbia, Canada. November.

“Using comparative genomics to predict functional elements in the human genome,” XIX International Congress of Genetics, Melbourne, Australia. July.

“Identifying functional elements in the human genome by tracing the evolutionary history of the bases: a key challenge for comparative genomics,” Intelligent Systems for Molecular Biology, Brisbane, Australia. June.

“Bioinformatics, genome evolution and the challenge of identifying functional elements in the human genome,” The Genome of Homo Sapiens. Symposium on Quantitative Biology, Cold Spring Harbor, NY. May.

“Computational genomics on mammals: sequence, function, and evolution,” Intra- and Intercellular Communication Science Meeting, Howard Hughes Medical Institute, Washington, DC. April.

“Bioinformatics, genome evolution and the challenge of identifying functional elements in the human genome,” Distinguished Science Seminar, Affymetrix, Santa Clara, CA. April.

“Computational analysis of the human and other mammalian genomes,” International Conference on Artificial Intelligence and Statistics,” Key West, FL. January.

“Computational analysis of the human and other mammalian genomes,” Oncogenomics, Phoenix, AZ. January.

2002

“Computational analysis of the human and mouse genomes,” Conference on Signals, Systems, and Computers, Asilomar Conference Center, Pacific Grove, CA. November.

“The working drafts of the human and mouse genomes,” Osong International Bio Conference, South Korea. October.

“The working drafts of the human and mouse genomes,” IBC’s Post-Genomic Bioinformatics Conference, San Francisco, CA. June.

“Assembly and initial analysis of the working draft of the human genome,” Clinical Ligand Assay Society, in conjunction with Boston Biomedica/CLAS Distinguished Scientist of the Year Award, 28th Annual Meeting, Houston, TX. May.

“Initial computational analysis of the public working drafts of the human and mouse genomes, and the long road ahead,” Genomes and Biology Conference, Cold Spring Harbor, NY. May.

“Status of the human and mouse working draft genomes, and some early comparisons,” Genes and Genomes in Health and Disease, Howard Hughes Medical Institute, Washington, DC. March.

“Status of the human genome working draft: map, assembly and web access,” Advances in Genome Biology & Technology, joint meeting with Automation in Mapping & DNA Sequencing, Marco Island, FL. February.

2001

“Overview of the human genome project and the construction of the working draft,” and “Exploring the working draft of the human genome,” NATO ASI on Artificial Intelligence and Heuristic Methods for Bioinformatics, San Miniato, Italy. October.

“Assembly and annotation of the public human genome working draft,” 13th International Genome Sequencing and Analysis Conference, San Diego, CA. October.

“Assembly and annotation of the working draft of the human genome,” Gordon Research Conference on Human Molecular Genetics, Newport, RI. August.

“The public working draft of the human genome,” keynote address, CHI Bioinformatics and Genome Research, San Francisco, CA. June.

“The public working draft of the human genome,” 33rd Annual Symposium on the Interface of Computer Science and Statistics, Costa Mesa, CA. May.

“Assembly and initial analysis of a working draft of the human genome,” New Frontiers in Structural and Computational Biology, Howard Hughes Medical Institute, Chevy Chase, MD. March.

“A working draft of the human genome,” Pacific Symposium on Biocomputing, Mauna Lani, HI. January.

2000

“Hidden Markov models, Fisher kernels and support vector machines for biosequence analysis,” Bioinformatics, Elsinore, Denmark. April.

“Computational prediction of genes and gene function from high-throughput genomics data,” Association for the Advancement of Artificial Intelligence, Washington, D.C. February.

1999

“Computational analysis of high-throughput genomics data using hidden Markov models and support vector machines,” keynote speaker, 10th Annual Genome Informatics Workshop, Tokyo. December.

“Analysis of microarray gene expression data using support vector machines,” In Silico Biology: Sequence, Structure and Function, Atlanta, GA. November.

“Combining discriminative classification methods with hidden Markov models for more effective biosequence analysis,” 8th Bioinformatics and Genome Research Conference, San Francisco, CA. June.

“Hidden Markov models and Fisher kernels for biosequence analysis,” Learning, 13th Annual Workshop, Snowbird, UT. April.

1998

“A new discriminative methodology for detecting remote protein homologies,” 1st Annual Computational Structural Biology Research Meeting, Monterey, CA. December.

“Statistical methods in biosequence analysis: discriminative vs. generative models,” 2nd Annual Conference on Computational Genomics, Reston, VA. November.

“Models and methods in biosequence analysis,” International Conference on Problems in Biophysics, Moscow. June.

“Hidden Markov models for protein families,” Structure-Function Based Genomics Symposium, London, England. April.

1997

“Statistical genome analysis: hidden Markov methods,” Newton Seminar, Isaac Newton Institute, Cambridge, England. October.

“A brief look at some machine learning problems in genomics,” keynote lecture, 10th International Conference on Computational Learning Theory, Vanderbilt University, Nashville, TN. July.

“Design of the Genie genefinder,” Finding Genes: Computational Analysis of DNA Sequences, Cold Spring Harbor, NY. March.

1996

“VC dimension, covering numbers and worst-case prediction of individual sequences,” ICMS Workshop on the Vapnik-Chervonenkis Dimension, Edinburgh, Scotland. September.

“Using hidden Markov models for biosequence analysis,” keynote lecture, 4th International Conference on Intelligent Systems in Molecular Biology, St. Louis, MO. June.

1995

“Using hidden Markov models to search biosequence databases,” Workshop on Knowledge, Discovery and Database Mining, Montreal, Canada. August.

“Hidden Markov and related statistical models: how they have been applied to biosequence analysis,” Workshop on Uncertainty in Artificial Intelligence, Montreal, Canada. August.

“Hidden Markov models in biosequence analysis,” Workshop on Biosequence Analysis, Aspen Center for Physics, Aspen, CO. June.

“Prediction, data compression and metric dimension,” 11th ACM Symposium on Computational Geometry, Vancouver, Canada. June.

“Hidden Markov models for proteins,” DIMACS Workshop on Sequence Based Methods for Protein Folding, Rutgers, NJ. March.

“Bounds on the mutual information between a parameter and a sequence of conditionally independent observations,” Workshop on Theory of Neural Networks, Pohang, Korea. February.

1994

“Hidden Markov models for multiple alignments and database search for proteins,” Meeting on Critical Assessment of Techniques for Protein Structure Prediction, Asilomar Conference Center, Pacific Grove, CA. December.

“Using stochastic context-free grammars to fold, align and model homologous RNA sequences,” Workshop on the Fusion of Molecular Biology and Knowledge Information Processing, Tokyo, Japan. December.

1993

“Hidden Markov models and beyond,” Macromolecules, Genes and Computers: Chapter Three, Waterville, NH. August.

“On-line prediction: models from computational learning theory and statistics,” Learning Days in Jerusalem Conference, Jerusalem, Israel. May.

1992

“How to use expert advice,” 6th Conference on Neural Information Processing Systems, post-meeting workshop on Bayesian Methods, Vail, CO.

“Hidden Markov models for protein families,” 6th Conference on Neural Information Processing Systems, post-meeting workshop on hidden Markov Models, Vail, CO.

“Hidden Markov models for protein families” and “Bayes Methods for Prediction,” Workshop on Supervised Learning, Santa Fe, NM.

“How well do Bayes Methods work for on-line prediction of +1,-1 values?” 3rd NEC Symposium on Computation and Cognition, Princeton, NJ.

1991

“How well do Bayes methods work?” 5th Conference on Neural Information Processing Systems, post-meeting workshop on Bayesian methods, Vail, CO.

“Uniting the VC and TLS theories of generalization,” Neural Networks for Computing, Snowbird, UT. April.

“Computational learning theory,” 3rd Woodward Conference on Modeling Complex Phenomena, San Jose, CA. April.

1990

“Learnability and the metric dimension: decision theoretic generalizations of the PAC learning model,” 1st International Workshop on Algorithmic Theory, Tokyo, Japan. October.

“Probably approximately correct learning,” National Conference, Association for the Advancement of Artificial Intelligence, Boston, MA. July.

1989

“Complexity issues in learning from random examples,” Annual Meeting of the Society for Industrial and Applied Mathematics, Mini-symposium on Neural Computing, San Diego, CA. July.

“Bounds on sufficient training set size when learning from random examples,” Neural Networks for Computing, Snowbird, UT. April.

“Probably approximately correct learning,” Discovery and Learning: Philosophical and Computational Perspectives, Pittsburgh, PA. April.

“Generalization in neural networks: a computational learning theory perspective,” Annual Meeting of the American Association for the Advancement of Science, San Francisco, CA. January.

1988

“Theoretical results in machine learning,” 5th International Conference on Machine Learning, Ann Arbor, MI. June.

Talks and Presentations at Colleges and Universities, Invited speaker

2017

“Data Driven Solutions for Silicon Valley: A Conversation with Distinguished Leaders,” invited panelist, UCSC/Silicon Valley Regional Data Trust, San Jose, CA. January

2016

“Can we find the genetic changes that make us human?,” invited speaker, Original Thinkers Series, University of California, Santa Cruz, Washington DC. November

“Genomes and cancer,” invited speaker, UCSC Faculty Research Seminar, University of California, Santa Cruz, CA. November

“Can we find the genetic changes that make us human?, ” invited speaker, UCSC BME 280B Seminar Series, University of California, Santa Cruz, CA. November

“Genomes and cancer,” invited speaker, The Pebble Beach & Tennis Club, University of California, Santa Cruz, Pebble Beach, CA. November

“Genomes,” invited speaker, UCSC Emeriti Association, University of California, Santa Cruz, CA. October

“Cancer Genomics,” invited speaker, Bioethics guest lecture, University of California, Santa Cruz, CA. October

“Can we decode cancer?” invited speaker, UCSC Silicon Valley Open House, University of California, Santa Cruz, Santa Clara, CA. September

“California Kids Cancer Comparison project,” invited keynote speaker, University of California Computing Services Meeting, University of California, Santa Cruz, CA. July

“Global Alliance for Genomics and Health,” invited speaker, 17th Bioengineering Institute of California Symposium, University of California, San Francisco, CA. June

“California Kids Cancer Comparison project,” invited speaker, Treehouse Event, University of California, Santa Cruz, Santa Cruz, CA. June

“Odyssey,” invited speaker, Silicon Valley Original Thinkers, University of California, Santa Cruz, Palo Alto, CA. May

“Molecular characterization for diagnoses and treatment,” invited speaker, Computational Cancer Biology workshop, Simons Institute, UC Berkeley. February

2015

“Elementary mathematics behind phenomena like the evolution of life,” invited speaker, Mathematics Colloquium, University of California Santa Cruz. October.

“Genomics and Cancer,” invited speaker, BME280B seminar, University of California Santa Cruz. October.

“Odyssey Into the Human Genome,” invited speaker, UCSC - Santa Cruz County Estate Planning Council breakfast, University of California, Santa Cruz. October

“Harnessing Global Genomic Data,” invited speaker, UCSC BioEngineering Symposium, University of California, Santa Cruz. June

“Global Alliance for Genomics and Health,” invited speaker, UCSC Dean’s club dinner, University of California, Santa Cruz, Los Gatos. April

2014

“Cancer Genomics,” invited speaker, BME280B seminar, University of California Santa Cruz. November.

“New hypothesis about the evolution of human brain size,” invited speaker, Computational Approaches to Evolution, The Simons Institute for the Theory of Computing, University of California, Berkeley. March

“Creating (and Mapping to) a Universal Reference Genome,” invited speaker, Computation-Intensive Probabilistic and Statistical Methods for Large-Scale Population Genomic, The Simons Institute for the Theory of Computing, University of California, Berkeley. February

“Large-scale Cancer Genomics,” invited speaker, Cancer Genomics Symposium, Berkeley Training Program: Genomics and Computational Biology, University of California, Berkeley. January.

2013

“The quest to conquer cancer: Computer geeks to the rescue,” invited speaker, 21st Century Club members annual lunch, University of California Santa Cruz. November.

“Genome evolution and cancer genomics,” invited speaker, BME280B seminar, University of California Santa Cruz. October.

“The quest to conquer cancer: Computer geeks to the rescue!” invited speaker, Local Roots, Global Impact, University of California Santa Cruz. October.

“Cancer Genomics,” invited keynote address, Chemical and Systems Biology Department, Stanford, Santa Cruz, CA. September.

“Big data and new models needed to study DNA variation in cancer,” invited speaker, Oxford Big Data in Biomedicine Conference, Stanford University, Palo Alto, CA. May.

“Big data and new models needed to study DNA variation in evolution and cancer,” invited speaker, Frontiers in Interdisciplinary Biosciences, Stanford University, Palo Alto, CA. May.

“Big data and new models needed to study DNA variation in evolution and cancer,” invited speaker, Simons institute: Visions of Computing, Simons institute, UC Berkeley, CA. April.

“Cancer Genomics,” invited plenary speaker, 2013 Information Theory and applications Workshop, University of California San Diego, San Diego CA. February.

“Cancer Genomics,” invited speaker, Nanobiotechnology Seminar Series, Stanford University, Palo Alto, CA. January.

2012

“Genomics” invited speaker, Bioethics class lecture, University of California Santa Cruz. November.

“The UCSC Cancer Genomics Hub,” invited keynote speaker, 2012 Nature/Institute of Genomic Medicine Annual 2012 Symposium, UCSD Institute of Genomic Medicine, University of California, San Diego. November.

“Genomics gets personal,” invited keynote speaker, Genomics Gets Personal: Property, Persons, Privacy, University of California Santa Cruz and California Institute for Quantitative Biosciences (QB3), San Francisco, CA. September.

“The UCSC Cancer Genomics Hub,” invited speaker, Research Review Day, University of California Santa Cruz. September.

“Cancer Genomics,” invited speaker, The 80th Birthday Symposium for Andrzej Ehrenfeucht, Distinguished Professor of Computer Science, University of Colorado, Boulder. September.

“Cancer Genomics,” invited speaker, Simons Institute for the Theory of Computing, University of California, Berkeley. July.

“Analysis of cancer genomics,” Machine Learning Summer School, University of California, Santa Cruz. July.

“Cancer genomics,” invited speaker, Human Genomics, Upper Division, Stanford University, Palo Alto, CA. May.

“Cancer Genomics,” invited keynote speaker, 30 Years of Computational Biology at USC, University of Southern California, Los Angeles, CA. March.

“Cancer Genomics,” invited speaker, Santa Cruz Philosophical Society’s Dinner and a Lecture series, Santa Cruz Philosophical Society, Santa Cruz. March.

2011

“Cancer Genomics,” invited speaker, Caltech General Biology Seminar Series, Pasadena, CA. December.

“The evolution of non-coding functional elements in our genome,” invited speaker, Evolutionary Genomics, Institute for Pure and Applied Mathematics (IPAM), University of California, Los Angeles. November.

“Cancer Genomics in the TCGA TARGET and ICGC projects,” invited speaker, Sanford Statistics Seminar, Stanford University, Palo Alto, CA. November.

“Cancer Genomics,” invited speaker, Wellcome Trust Sanger Institute, Cambridge, UK. October.

“Cancer Genomics,” invited speaker and honoree, Weldon Memorial Prize, Oxford University, Oxford, UK. October.

“At the dawn of personalized medicine," invited speaker, Santa Cruz Foundation Forum, University of California, Santa Cruz. October.

“Cancer Genomics in the TCGA, TARGET, and ICGC projects,” plenary speaker, Research review Day, University of California, Santa Cruz. October.

“Cancer and evolutionary genomics,” invited speaker, Next-generation Sequencing Technology & Algorithms for Primary Data Analysis, Institute for Pure and Applied Mathematics (IPAM), University of California, Los Angeles. October.

“Cancer genomics and the TCGA project,” invited speaker, Evolution and Cancer Conference, University of California, San Francisco. June.

“Cancer Genomics,” invited speaker, AMP Lab Summer Retreat, University of California, Berkeley, Santa Cruz, CA May.

“Cancer Genomics,” plenary speaker, Theory of Computation as a Lens on the Sciences, Computer Science Division, University of California, Berkeley. May.

“Cancer Genomics in the TCGA project,” invited speaker, Integrative Cancer Biology Program, Center for Cancer Systems Biology, Stanford University, Palo Alto, CA. April.

2010

“Cancer Genomics data analysis,” invited speaker, Moore’s UCSD Cancer Center, Translational Onocology Symposium, San Diego, CA. August

“Cactus graphs for genome comparisons,” invited speaker, CASB-16, University of California, San Diego. May.

”Rearranging genomes,” invited speaker, RECOMB be 2010, University of California, San Diego. May.

“The Genome 10K Project: a genetic map of 10,000 species,” invited speaker, UCSC Women's Club, University of California, Santa Cruz. March.

2009

“Cancer Genomics: the informatics of discovery from billions of measurements,” featured speaker, Biomedical Sciences Seminar Series, University of California, San Francisco. October.

“Molecular evolution and cancer genetics,” invited speaker, Bioethics class lecture, University of California, Santa Cruz. October.

“Molecular evolution and cancer genetics,” invited speaker, Cancer Genetics Program Meeting, University of California, San Francisco. September.

“Molecular evolution and cancer genetics,” keynote speaker, 8th Annual International Conference on Computational Systems Bioinformatics, Stanford University, Palo Alto, CA. August.

“100 million years of evolutionary history of the human genome,” invited speaker, Jon Postel Distinguished Lecture, University of California, Los Angeles. January.

2008

“The Human Genome Project: 100 years of Human Evolution,” invited speaker, Bioethics class lecture, University of California, Santa Cruz. October.

“A rapidly evolved RNA gene may have played a role in the evolution of cerebral cortex,” invited speaker, Anatomy, Development, and Evolution of the Brain, University of California, Santa Barbara. April.

2007

“The Human Genome Project,” invited speaker, Bioethics class lecture, University of California, Santa Cruz. October.

“Reconstructing the evolutionary history of the human genome,” Frontiers in Biology seminar series, Stanford University, Palo Alto, CA. May.

“A rapidly evolved RNA gene may have played a role in the evolution of the cerebral cortex,” honored speaker, UCSD Project for Explaining the Origin of Humans Symposium, La Jolla, CA. March.

2006

“Reconstructing the evolutionary history of the human genome,” 3rd University of California, Santa Cruz/QB3 Symposium of Bioinformatics, Santa Cruz, CA. December.

“Reconstructing 100 million years of human evolutionary history,” Center for Algorithmic and System Biology Algorithmic Biology Meeting, University of California, San Diego, La Jolla, CA. November.

“Reconstructing 100 million years of human evolutionary history,” invited speaker, Beckman Center for Molecular and Genetic Medicine at Stanford, Palo Alto, CA. October.

“Exploring the evolutionary history of the human genome over the last 100 million years,” Human Evolution Symposium, University of California, San Francisco, CA. May.

“Ultraconserved elements, living fossil transposons, distal enhancers, and mysterious RNA genes: reconstructing the detailed evolutionary history of the human genome,” Institute for Pure and Applied Mathematics, University of California, Los Angeles. January.

“Exploration of the Human Genome,” invited speaker, Bioethics class lecture, University of California, Santa Cruz. January.

2005

“Using evolution to explore the human genome,” invited speaker, Computational and Genomic Biology Seminar Series, University of California, Berkeley. November.

“Using evolution to explore the human genome,” honored speaker, UC System-Wide Bioengineering Symposium, University of California, Santa Cruz. June.

2004

“Using evolution to explore the human genome,” National Academy of Science Sackler Colloquium, Stanford University, Palo Alto, CA. October.

“Comparing the human, chimp, mouse and rat genomes: using evolution to predict functional elements in the human genome,” Chemistry and Genomics Seminar, Stanford University, Palo Alto, CA. March.

“Comparing the human, chimp, mouse and rat genomes: using evolution to predict functional elements in the human genome,” Sali Labs, University of California, San Francisco, CA. January.

2002

“Initial computational analysis of the public working drafts of the human and mouse genomes, and the long road ahead,” Workshop on Theory of Computation and the Sciences, Berkeley, CA. May.

2000

“A working draft of the human genome,” Biomedical Computation at Stanford, Stanford University, Palo Alto, CA. October.

1998

“Using hidden Markov models for biosequence analysis: recent tests and new methods,” Understanding the Genome: Technological and Mathematical Challenges, Mathematical Sciences Research Institute, Berkeley, CA. May.

1996

“Hidden Markov Models for Biosequence Analysis,” Workshop on Theoretical and Computational Biology, Lawrence Berkeley National Laboratory, Berkeley, CA. August.

1991

“Information theory, VC dimension and the Bayesian approach to machine learning,” Workshop on Computational Learning Theory and Natural Learning Systems, Berkeley, CA. September.

UNIVERSITY SERVICE

Service to the University

05/2010	Chair, review committee, Biomedical Informatics Degree Program, University of California, San Francisco
2006	Panel member, Life Sciences Division Review Committee, Lawrence Berkeley National Laboratory
2000-	Scientific co-director, California Institute for Quantitative Biosciences (QB3)
1998-	Member, UC System-Wide Life Science Informatics Working Group

Other Service to the Campus

2011-2016	Director, Cancer Genomics Hub, UC Santa Cruz
2008-2012	Director, Institute for the Biology of Stem Cells, UC Santa Cruz
2005-	Director, Training Program in the Systems Biology of Stem Cells, UC Santa Cruz

1999- Director, UCSC Center for Biomolecular Science and Engineering

Current Postdoctoral Scholars and Doctoral Students

2016- Jason Fernandes, Postdoctoral Scholar, Investigating the regulation of transposable elements by primate-specific transcription factors

2015- John Vivian, Doctoral Student, Large Scale Cancer Genome Analysis

2015- Audrey Musselman-Brown, Doctoral Student,

2015- Charles Markello, Doctoral Student,

2013- Joel Armstrong, Doctoral Student,

2013- Arjun Rao, Doctoral Student, Precision Immunotherapy for Cancer treatment

2013- Ian Fiddles, Doctoral Student, Comparative genome annotation

2013- Adam Novak, Doctoral Student, Comparing methods for aligning multiple genomes and developing computer algorithms to map changes in ambiguous areas of the genome

2013- Olena Morozova, Postdoctoral Scholar, California Institute for Regenerative Medicine (CIRM) Fellow, Applying integrative genomics and bioinformatics approaches to study cancers of the nervous system

2012- Karen Hayden-Miga, Postdoctoral Scholar, Developing a comprehensive map of centromere sequencing variation across a large number of individuals from distinct populations

2010- Andrew Field, Doctoral Student, California Institute for Regenerative Medicine (CIRM) Fellow, Regulation of cortical neuron development from embryonic stem cells, focusing on the role ncRNAs play in this process

2006- Mark Diekhans, Doctoral Student, Cancer genomics hub, computational gene finding, UCSC Mammalian Gene Collection project (read about Mark's work on the Consensus Coding Sequence gene set in UCSC Currents) and the database of the Genome 10K Project

Previous Postdoctoral Scholars

2011 to 2014 Maximilian Haeussler, European Molecular Biology Organization (EMBO) Fellow, currently Assistant Research Scientist, UC Santa Cruz Genomics Institute, University of California, Santa Cruz, CA

2011 to 2014 Adam Ewing, currently research fellow, the Mater Medical Research Institute and honorary fellow, the University of Queensland

2009 to 2014 Frank Jacobs, currently Assistant Professor at the Swammerdam Institute for Life Sciences (SILS), University of Amsterdam, The Netherlands

2011 to 2013 Glenn Hickey, currently postdoctoral scholar, currently Assistant Research Scientist, UC Santa Cruz Genomics Institute, University of California, Santa Cruz, CA

2010 to 2013 Daniel Zerbino, currently Regulation Team Leader, Ensembl, EBI, UK

2007 to 2012 Benedict Paten, currently Assistant Research Scientist, Comparative Genomics UC Santa Cruz Genomics Institute, University of California, Santa Cruz, CA

2010 to 2011 Charlie Vaske, currently Chief Scientific Officer, Five3 Genomics, Santa Cruz, CA

2006 to 2011 Jing Zhu, currently Assistant Research Scientist, Cancer Genomics, UC Santa Cruz Genomics Institute, University of California, Santa Cruz, CA

2006 to 2010 Jason Underwood, currently Principal Scientist, Pacific Biosciences, Menlo Park, CA

2007 to 2009 Jian Ma, currently Associate Professor, Computational Biology School of Computer Science, Carnegie Mellon, Pittsburgh PA

2006 to 2009 Ting Wang, Helen Hay Whitney Fellow, currently Principal Investigator, Associate Professor of Genetics, Associate Professor of Computer Science and Engineering, Washington University in St. Louis, MO

2006 to 2007 Mario Stanke, currently Associate Professor, Institute for Mathematics and Computer Science, University of Greifswald, Germany

2005 to 2008 Andrew Kern, currently Assistant Professor, Genetics, Rutgers University, NJ

2005 to 2006 Chen-Hsiang Yeang, currently Associate Research Fellow, the Institute of Statistical Science, Academia Sinica, Taipei, Taiwan

2004 to 2007 Jakob Skou Pedersen, currently Associate Professor, Clinical Medicine and Bioinformatics Research Centre (BiRC), University of Aarhus, Denmark

2003 to 2007 Gill Bejerano, currently Associate Professor of Developmental Biology, Associate Professor of Computer Science, Associate Professor of Pediatrics (Medical Genetics), Stanford University, Palo Alto, CA

2003 to 2005 Katherine Pollard,(Co-supervised by Todd Lowe), currently Lead Scientist and Senior Investigator, Gladstone Institute, Professor, Division of Biostatistics, University of California, San Francisco School of Medicine, CA

2003 to 2004 Brian Lucena, currently Assistant Professor, Mathematics, American University, Cairo

2002 to 2004 Terry Furey, currently Assistant Professor, Genetics, University of North Carolina

2002 to 2003 Mathieu Blanchette, currently Assistant Professor, Computer Science, McGill University, Montreal, Canada

2000 to 2001 Rune Lyngsoe, currently Research Developer, Undisclosed Company, Oxford, UK, Oxford University, UK

1998 to 1999 Bill Noble, currently Professor, Computer Sciences and Engineering, University of Washington, Seattle, WA

1998 Tommi Jaakkola, currently Professor, Electrical Engineering & Computer Science, MIT

1996 to 1998 Betty Lazareva, currently an Independent Biotechnology Professional

1992 Anders Krogh, Postdoctoral Scholar, currently Professor, Computational and RNA Biology, University of Copenhagen, Denmark

Previous Doctoral Students

2009 to 2015 Amie Radenbaugh, Doctoral Student, Identification of DNA and RNA mutations in cancer using High-Throughput Sequencing Data, currently on Bioinformatics Scientist, NantOmics, Santa Cruz, CA

2008 to 2015 Tracy Ballinger, Doctoral Student, Characterizing insertions in cancer genomes to look for evidence of retrotransposition in tumors, currently Bioinformatician Research Fellow, Colin Semple's lab, Institute of Genetics and Molecular Medicine, Edinburgh, Scotland

2010 to 2014 Mia Gifford, Doctoral Student, “Emergence of drug resistance in cancer” currently on sabbatical

2008 to 2014 Dent Earl, “Evaluations and Application of the three A’s of Genomics: Assembly, Alignment, Annotation,” currently Software engineer, Google, Mountain View, CA

2008 to 2014 Ngan Nguyen, “Immunogenomics, Database of the Genome 10K Project,” currently bioinformatics scientist, Atreca, San Carlos, CA

2006 to 2014 David Greenberg, “An evolutionary arms race between zinc finger proteins and retrotransposons in ape genomes,” currently Senior Scientist, Pacific Biosciences, Menlo Park, CA

2008 to 2013	Ted Goldstein, “Tools for Extracting Actionable Medical Knowledge from Genomic Big Data,” currently Research Associate, MedBook Biomolecular Engineering, University of California, Santa Cruz, CA
2006 to 2013	Chris Szeto, “Discovery of clinically relevant molecular signatures in cancer,” currently Consultant, Five3 Genomics, Santa Cruz, CA
2007 to 2012	Stephen Benz, “Sample-specific cancer pathway analysis using PARADIGM,” currently Chief Executive Officer, Five3 Genomics, Santa Cruz, CA
2005 to 2012	Zack Sanborn “Tumor vs. Matched-Normal Sequencing Analysis and Data Integration,” currently Chief Technology Officer, Five3 Genomics, Santa Cruz, CA
2004 to 2011	Courtney Onodera, UCSC Predoctoral CIRM Scholar, “Characterization of Transcriptional Enhancers in the Human and Mouse Genomes,” currently Bioinformatics Scientific Programmer/Analyst, Genomic Medicine Initiative, University of California, San Francisco, CA
2004 to 2010	Craig Lowe, “The contribution of mobile elements to regulatory innovations on the human lineage,” currently Postdoctoral Scholar, David Kingsley lab, Howard Hughes Medical Institute, Stanford University, Palo Alto, CA
2004 to 2010	Solomon Katzman, “Evolutionary Forces at Work in the Human Genome,” currently High-Throughput Sequencing Analyst, UC Santa Cruz Genomics Institute, University of California, Santa Cruz, CA
2002 to 2010	Krishna Roskin, “Past, present, and future of sequence alignment,” currently Post-Doctoral Fellow, Scott Boyd lab, Department of Pathology, Stanford University School of Medicine, Palo Alto, CA
2002 to 2010	Robert Baertsch, “Burst of exapted human retrogenes not found in mouse and improved methods for identifying retrocopies,” currently Software Programer on contract basis
2003 to 2009	Brian Raney, “Reconstructing Ancestral Genomes: A case study of small inversions on the human lineage since the eutherian explosion,” currently Software Developer, Genome Browser Project, UC Santa Cruz Genomics Institute, University of California, Santa Cruz
2002 to 2005	Adam Siepel, “Comparative mammalian genomics : models of evolution and detection of functional elements,” Professor and Director of the $50M Simons Center, Cold Spring Harbor Laboratory
2001 to 2007	Yontao Lu, “Identification and analysis of psuedogenes in the human and mouse genomes”, Bioinformatics Scientist, Affymetrix, Santa Clara, CA
2001 to 2006	Daryl Thomas, “Using variation and constraint to understand functional elements in the human genome,” currently Associate Director, Life Technologies, Carlsbad, CA
1999 to 2005	Charles Sugnet, “Discovery and detection of alternative splicing,” currently Sr Bioinformatics Engineer, Ion Torrent, South San Francisco, CA
1999 to 2003	Hui Wang, “Splice variant chip design and variant-based expression analysis,” currently Bioinformatics/Biostatistics Head, HTG Molecular Diagnostics, Tucson, AZ
1998 to 2002	Terry Furey, ARCS Scholar, “Analysis and annotation of the draft human genome sequence,” currently Assistant Professor, Genetics, University of North Carolina, Chapel Hill, NC
1997 to 2003	Stephen Winters-Hilt, “Machine learning methods for channel current cheminformatics, biophysical analysis, and bioinformatics,” currently Visiting Associate Professor, Computer Science and Biology, Connecticut College
1995 to 2000	Melissa Cline, “Protein sequence alignment reliability: prediction and measurement,” currently Project Scientist, Molecular, Cell, & Developmental Biology, UC Santa Cruz Genomics Institute, University of California, Santa Cruz, CA
1994 to 2003	David Kulp, “Protein-coding gene structure prediction using generalized hidden Markov models,” co-founder of Neomorphic, which was acquired by Affymetrix; currently Assistant Professor, Computer Science, University of Massachusetts, Amherst

1999 Michael Brown, “RNA modeling using stochastic context-free grammars,” currently a research scientist in the biotech industry

1997 Kimmen Sjölander, “A Bayesian-information theoretic method for evolutionary inference in proteins,” currently Associate Professor, Bioengineering, University of California, Berkeley, Berkeley, CA. Won a U.S. Presidential Early Career Award in Science and Engineering

1993 Yoav Freund, “Data filtering and distribution modeling algorithms for machine learning,” currently Professor, Computer Science &Engineering, University of California, San Diego, La Jolla, CA, won Gödel Prize for 2003

1992 Phil Long, “Towards a more comprehensive theory of learning in computers,” currently Research Scientist, Google, Mountain View, CA

1990 Giulia Pagallo, “Adaptive decision tree algorithms for learning from examples,” currently Software Manager, Apple Computer, Cupertino, CA

1990 Alexander Milosavljevic, “Categorization of macromolecular sequences by minimal length encoding,” currently Associate Professor, Molecular and Human Genetics, Baylor College of Medicine, Houston, TX

1989 Nick Littlestone, “Mistake bounds and logarithmic linear-threshold learning algorithms,” currently Computer Programmer, Patternlanguage.com, Berkeley, CA

1985 Janet Blumer, “Algorithms for the directed acyclic word graph and related structures”

M.S. Theses Supervised

2012 Jeffrey Long

2011 Chris Wilks, “Exploiting MAINE/FAIRE Experimental Data for Gene-Finding in Plasmodium falciparum Using Random Forests,” currently PhD student, Johns Hopkins University: Home, Baltimore, Maryland

2006 Timothy Dreszer, “Biased Clustered Substitutions in the Human Genome: Sex, Gambling and Non-Darwinian Evolution”

2002 Matt Xia, “Study of molecular evolution by comparison of vertebrate genomes,” currently Software Engineer, Life Technologies

2002 Wei Wu (project option), currently Associate Research Professor, Lane Center for Computational Biology, Carnegie-Mellon

2002 Rachel Bevan (project option)

2002 Trevor Bruen (project option), currently Assistant Professor, St. Francis Xavier College, Canada

2001 Fan Shen (project option), currently Bioinformatics Scientist, Affymetrix, Santa Clara, CA

2000 Albion Baucom, “Protein structure and function prediction: tools and techniques,” currently Systems Architect, Genentech, San Francisco, CA

2000 Rachel Karchin, “Classifying G-protein coupled receptors with support vector machines,” Associate Professor, Department of Biomedical Engineering, John Hopkins University, Baltimore, MD

1999 David Lin, “Deriving reliable intron and splice site evidence from ESTs to improve gene finding,” currently Senior Director, Informatics and Automation, Complete Genomics, Mountain View, CA

1995 Brad Gulko, “Using phylogenetic Markov trees to detect conserved structure in RNA multiple alignments,” currently Doctoral Student, Computer Science Department, Cornell University, Ithaca, NY

1994 Rebecca Underwood, “Stochastic context-free grammars for modeling three spliceosomal small nuclear ribonucleic acids”

1994 Anne Urban, “Hidden Markov models in characterization, discrimination and alignment of the Helicase family of proteins”

1989 Jeanne Rich, “Training an animated arm to reach for objects in space using a neural network”

1988 Jean Cailton, “Constrained backpropogation: an algorithm for learning in artificial neural networks”

Senior Theses Supervised/Undergraduate Awards

2002 Krishna Roskin, Huffman Prize, currently Post-Doctoral Fellow, Scott Boyd lab, Pathology, Stanford University, Palo Alto, CA

1995 David Konerding, currently Director of Genomics, Google, Mountain View, CA

1995 Jesse Reklaw (received the Chancellor’s award for undergraduate research)

RESEARCH INTERESTS

Bioinformatics, genomics, computational genomic data analysis, molecular evolution and comparative genomics, genomic and clinical data sharing and standards, cancer genomics, neurodevelopment, stem cell research, immunogenomics, information theory, pattern recognition, machine learning, artificial intelligence, information theory, theoretical computer science

RECENT TEACHING INTERESTS

Computational genomics, comparative genomics, cancer genomics

COURSES TAUGHT

Current courses:

Cancer Genomics Seminar

Comparative Genomics Seminar

Computational Genomics

Previous courses:

Bioinformatics and Genomics Seminar

Bioinformatics

The Nature of Computation: Introduction to Computer Science Introduction to Programming

Abstract Data Types

Discrete Mathematics

Data Structures and Algorithms

Probabilistic Algorithms and Average Case Complexity

Theory of Automata and Formal Languages

Theory of Computation

Artificial Intelligence

Machine Learning

Neural Computation