

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-founder, Global Alliance for Genomics and Health
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

- 03/2018- Member, Inaugural National Academy of Medicine (NAM) Committee on Basic and Translational Science
- 03/2018- Consultant and external advisory committee member, The Human Cell Atlas (HCA)
- 04/2017- Member, Earth BioGenome Project (EBP) Working Group
- 09/2016- Consultant and external advisory committee member, ChanZuckerburg Initiative (CZI)
- 01/2016- Member, Secretary of Energy (SEAB) Task Force on Biomedical Sciences
- 09/2015- Vice Chair of Steering Committee, Global Alliance for Genomics and Health
- 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/Edenroc, 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 Health

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

2018- Member, National Academy of Engineering - Bioengineering

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-founder, 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: >151,000 citations, h-index 146, i10-index 276, November 9, 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.

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

Hausssler 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.

Hausssler, 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.

Hausssler 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

Toor JS, Rao AA, McShan AC, Yarmarkovich M, Nerli S, Yamaguchi K, Madejska AA, Nguyen S, Tripathi S, Maris JM, Salama SR, Hausssler D, Sgourakis NG.. A Recurrent Mutation in Anaplastic Lymphoma Kinase with Distinct Neopeptide Conformations. *Front Immunol.* 2018 Jan 30;9:99. doi: 10.3389/fimmu.2018.00099. eCollection 2018. PMID: 29441070

Jain M, Olsen HE, Turner DJ, Stoddart D, Bulazel KV, Paten B, Hausssler D, Willard HF, Akeson M, Miga KH. Linear assembly of a human centromere on the Y chromosome. *Nat Biotechnol.* 2018 Mar 19. doi: 10.1038/nbt.4109. PMID: 29553574

Casper J, Zweig AS, Villarreal C, Tyner C, Speir ML, Rosenbloom KR, Raney BJ, Lee CM, Lee BT, Karolchik D, Hinrichs AS, Haeussler M, Guruvadoo L, Navarro Gonzalez J, Gibson D, Fiddes IT, Eisenhart C, Diekhans M, Clawson H, Barber GP, Armstrong J, Hausssler D, Kuhn RM, Kent WJ. The UCSC Genome Browser database: 2018 update. *Nucleic Acids Res.* 2018 Jan 4;46(D1):D762-D769. doi: 10.1093/nar/gkx1020. PMID: 29106570

Newton Y, Novak AM, Swatloski T, McColl DC, Chopra S, Graim K, Weinstein AS, Baertsch R, Salama SR, Ellrott K, Chopra M, Goldstein TC, Hausssler D, Morozova O, Stuart JM. TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. *Cancer Res.* 2017 Nov 1;77(21):e111-e114. doi: 10.1158/0008-5472.CAN-17-0580. PMID: 29092953

Casper J, Zweig AS, Villarreal C, Tyner C, Speir ML, Rosenbloom KR, Raney BJ, Lee CM, Lee BT, Karolchik D, Hinrichs AS, Haeussler M, Guruvadoo L, Navarro Gonzalez J, Gibson D, Fiddes IT, Eisenhart C, Diekhans M, Clawson H, Barber GP, Armstrong J, Hausssler D, Kuhn RM, Kent WJ. The UCSC Genome Browser database: 2018 update. *Nucleic Acids Res.* 2017 Nov 2. doi: 10.1093/nar/gkx1020. PMID: 29106570

Newton Y, Novak AM, Swatloski T, McColl DC, Chopra S, Graim K, Weinstein AS, Baertsch R, Salama SR, Ellrott K, Chopra M, Goldstein TC, Hausssler D, Morozova O, Stuart JM. TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. *Cancer Res.* 2017 Nov 1;77(21):e111-e114. doi: 10.1158/0008-5472.CAN-17-0580. PMID: 29092953

Cancer Genome Atlas Research Network. Electronic address: wheeler@bcm.edu; Cancer Genome Atlas Research Network. Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. *Cell.* 2017 Jun 15;169(7):1327-1341.e23. doi: 10.1016/j.cell.2017.05.046. PMID: 28622513

Lincoln SE, Yang S, Cline MS, Kobayashi Y, Zhang C, Topper S, Haussler D, Paten B, Nussbaum RL. Consistency of BRCA1 and BRCA2 Variant Classifications Among Clinical Diagnostic Laboratories. *JCO Precis Oncol.* 2017 Jul;1. doi: 10.1200/PO.16.00020. Epub 2017 Apr 11. PMID: 28782058

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 13;31(2):181-193. doi: 10.1016/j.ccell.2017.01.001. PMID: 28162975

Clinical Cancer Genome Task Team of the Global Alliance for Genomics and Health., Lawler M, Haussler D, Siu LL, Haendel MA, McMurry JA, Knoppers BM, Chanock SJ, Calvo F, The BT, Walia G, Banks I, Yu PP, Staudt LM, Sawyers CL. Sharing Clinical and Genomic Data on Cancer - The Need for Global Solutions. *N Engl J Med.* 2017 May 25;376(21):2006-2009. doi: 10.1056/NEJMp1612254. PMID: 28538124

Vivian J, Rao AA, Nothhaft 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, Zaraneek 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

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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: 27687569
Cancer 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

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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, Beroukhir R, Cooper L, Akbani R, Wrensch M, Haussler D, Aldape KD, Laird PW, Gutmann DH; TCGA Research Network, Nounmehr 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

Blau CA, Ramirez AB, Blau S, Pritchard CC, Dorschner MO, Schmechel SC, Martins TJ, Mahen EM, Burton KA, Komashko VM, Radenbaugh AJ, Dougherty K, Thomas A, Miller CP, Annis J, Fromm JR, Song C, Chang E, Howard K, Austin S, Schmidt RA, Linenberger ML, Becker PS, Senecal FM, Mecham BH, Lee SI, Madan A, Ronen R, Dutkowski J, Heimfeld S, Wood BL, Stilwell JL, Kaldjian EP, Haussler D, Zhu J. A Distributed Network for Intensive Longitudinal Monitoring in Metastatic Triple-Negative Breast Cancer. *J Natl Compr Canc Netw.* 2016 Jan;14(1):8-17. PMID: 26733551

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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Tucker K, Weinberger PM, Winemiller C, Zach LA, Zuna R; Cancer Genome Atlas Research Network. Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. *N Engl J Med*. 2015 Nov 4. PMID: 26536169

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Edited Journals

1996-	Associate Editor, <i>Journal of Computational Biology</i>
2005-2012	Associate Editor, <i>Public Library of Science Computational Genomics</i>
2001-2005	Editorial Board, <i>Drug Discovery Today</i>
1996-2002	Editorial Board, <i>Neural Computing Surveys</i>
1995-2002	Editorial Board, <i>Journal of Neurocomputing</i>
1993-1995	Editorial Board, <i>Journal of Artificial Intelligence Research</i>
1988-1997	Associate Editor, <i>Machine Learning</i>
1988-1997	Guest Editor, <i>Machine Learning</i> , special issue on recent theoretical directions in Machine Learning. Spring, 1988

Papers in Conference Proceedings

Morozova O, Salama SR, Bjork I, Goldstein TC, Mueller S, Sender LS, Sweet-Cordero A, Haussler D. Comparative genomic analysis for pediatric cancer patients evaluated in a California Initiative to Advance Precision Medicine Demonstration Project. American Society of Clinical Oncology. 2017 May 20. DOI: 10.1200/JCO.2017.35.15_suppl.TPS10578 Journal of Clinical Oncology 35, no. 15_suppl

Haussler D, Smuga-Otto M, Paten B, Novak AM, Nikitin S, Zueva M, Miagkov D. A Flow Procedure for the Linearization of Genome Sequence Graphs. International Conference on Research in Computational Molecular Biology. Springer, Cham. 2017 May 3. p. 34-49. DOI: 10.1007/978-3-319-56970-3_3

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Chiaromonte F, Weber RJ, Roskin KM, Diekhans M, Kent WJ, Haussler D. The share of human genomic DNA under selection estimated from human-mouse genomic alignments. Cold Spring Harbor Symposium, Quant. Biology, 2004:68:245-54.

Siepel A, Haussler D. Computational identification of evolutionarily conserved exons. Proceedings of the 8th International Conference on Research in Computational Molecular Biology, RECOMB, 2004:177-86.

Jojic V, Jojic N, Meek C, Geiger D, Siepel A, Haussler D, Heckerman D. Efficient approximations for learning phylogenetic HMM models from data. Proceedings of ISMB 2004 and Bioinformatics, 2004.

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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.

Haussler D, Krogh A, Brown M, Mian IS, Sjölander K. Protein modeling with hidden Markov models: an analysis of globins. 26th Hawaii Systems Conference, January 1993. [Awarded best paper in AI methods in biotechnology track].

Cesa-Bianchi N, Freund Y, Helmbold D, Haussler D, Schapire R, Warmuth M. How to use expert advice, (extended abstract), 25th ACM Symposium on Theoretical Computer Science (STOC), 1993:382-91.

Haussler D, Krogh A. DNA Alignment and clustering. Neural Networks for Computing, Snowbird, UT, Sandi von Pier (ed), AT&T Bell Laboratories, Crawfords Corner Road, Rm. 4E-422, Holmdel, NJ 07733. April 7, 1992.

Haussler D, Barron A. How well do Bayes methods work for on-line prediction of +1,-1 values? 3rd NEC Symposium on Computation and Cognition, Princeton, NJ, 1992.

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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Opper M, Haussler D. Calculation of the learning curve of Bayes optimal classification algorithm for learning a perceptron with noise. 4th Workshop on Computational Learning Theory (COLT), Santa Cruz, CA, August 1991:75-87.

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Haussler D, Long P. A generalization of Sauer's lemma. Southeastern Conference on Combinatorics, Graph Theory and Computing, Baton Rouge, LA, February 1991.

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.

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

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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.

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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.

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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

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Novak AM, Hickey G, Garrison E, Blum S, Connelly A, Dilthey A, Eizenga J, Elmohamed, MA Saleh, Guthrie S, Kahles A, Keenan S, Kelleher J, Kural D, Li H, Lin MF, Miga K, Ouyang N, Rakocevic G, Maciek Smuga-Otto M, Alexander Wait Zaranek AW, Richard Durbin R, Gil McVean G, Haussler D, Paten B. Genome Graphs. Cold Spring Harbor Labs Journals. bioRxiv. 2017 Jan 1. 101378. doi:https://doi.org/10.1101/101378

Hiranuma N, Liu J, Song C, Goldsmith J, Dorschner M, Pritchard C, Burton K, Mahen E, Blau S, Senecal F, Monsky W, Parker S, Schmechel S, Allison S, Gadi VK, Salama SR, Radenbaugh A, Goldman M, Johnsen J, Heimfeld S, Komashko V, LaMadrid-Hermannfeldt M, Duan Z, Benz S, Soon-Shiong P, Haussler D, Zhu J, Ruzzo W, Noble W, Blau CA. Cis-Compound Mutations are Prevalent in Triple Negative Breast Cancer and Can Drive Tumor Progression. Cold Spring Harbor Labs Journals. bioRxiv 2016 January 1. 085316. doi: <https://doi.org/10.1101/085316>

Lincoln S, Cline M, Yang S, Kobayashi Y, Topper S, Haussler D, Paten B, Nussbaum. What Have Public Databases Taught Us About Variant Classification? The Example of BRCA1 and BRCA2. The journal of molecular diagnostics. Elsevier Science Inc. 2016 November 1. vol:18 iss:6 pg:949.

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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

2018

"The California Kids Cancer Comparison Project," invited plenary keynote speaker, 25th anniversary Molecular Medicine Tri-Conference, San Francisco. February

"The Human Genome Graph," invited speaker, PMWC 2018 Silicon Valley, Personalized Medicine World Conference, Mountain View. January

2017

"The California Kids Cancer Comparison: harnessing the power of big data to benefit single patients in California ... and now, around the world," invited keynote speaker, 2017 California Initiative to Advance Precision Medicine conference, California Initiative to Advance Precision Medicine La Jolla, CA. October

"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 Francisco. 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, Monrovia, 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 Conference, 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," invited 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 Cellular 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 2011 Conference, 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, CO. April.

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

"Impact of human genome research: present and future," honored speaker, Mervyn Young Memorial Lecture, University of Colorado, 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, CO. 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 gene finder," 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

2018

"Genomics at UCSC," invited speaker, UC's Council for Vice Chancellors for Research (COVCR), University of California, Santa Cruz, CA. March

2017

"Genome evolution: battling transposons," invited speaker, Fall BME 280, University of California, Santa Cruz, CA. November

"Genomics at UCSC," invited speaker, Bioethics BME 80G, University of California, Santa Cruz, CA. October

"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 Oncology 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

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