Adam C. Siepel, Ph.D.

PERSONAL DETAILS

Present position:	Chair, Simons Center for Quantitative Biology Professor, Watson School of Biological Sciences Cold Spring Harbor Laboratory
Address:	Cold Spring Harbor Laboratory 2121 Koch Building One Bungtown Road Cold Spring Harbor, NY 11724–2209 (516) 367 6922 (516) 367 5501-Fax asiepel@cshl.edu http://SiepelLab.labsites.cshl.edu http://www.cshl.edu/scqb

EDUCATION AND PROFESSIONAL QUALIFICATIONS

Education

Cornell University, Ithaca, New York, B.S., Agricultural and Biological Engineering, 1994
University of New Mexico, Albuquerque, New Mexico, M.S., Computer Science, 2001
University of California, Santa Cruz, California, Ph.D., Computer Science, 2005

Professional Experience

2015 – present	Adjunct Professor, Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, NY
2014 – present	Professor, Watson School of Biological Sciences, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
2014 – present	Chair, Simons Center for Quantitative Biology, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
2014 – present	Adjunct Associate Professor, Department of Computer Science, Stony Brook University, Stony Brook, NY
2014 – present	Adjunct Professor of Computational Genomics, Institute for Computational Biomedicine, Weill Cornell Medical College of Cornell University, New York, NY
2010 – 2014	Associate Professor *(with tenure)*, Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, NY
2012 – 2013	Visiting Scientist *(during sabbatic leave from Cornell)*, European Bioinformatics Institute (EBI), Hinxton, UK
2012 – 2013	Visiting By-Fellow in Residence *(during sabbatic leave from Cornell)*, Churchill College, Cambridge University, Cambridge, UK
2006 – 2010	Assistant Professor, Department of Biological Statistics and Computational Biology, Cornell University, Ithaca, NY
2002 – 2005	Graduate Student Researcher, University of California, Santa Cruz, CA

2000 – 2001	Director of Information Technology *(acting)*, National Center for Genome Resources (NCGR), Santa Fe, NM
1997 – 2001	Software Development Group Leader, National Center for Genome Resources (NCGR), Santa Fe, NM
1996 – 1997	Bioinformatics Programmer, National Center for Genome Resources (NCGR), Santa Fe, NM
1994 – 1996	Graduate Research Assistant, HIV Database Group, Los Alamos National Laboratory (LANL), Los Alamos, NM

Honors and Awards

Distinguished Graduate Student Alumnus Award, Baskin School of Engineering, University of Santa Cruz, California, 2017.

Guggenheim Fellowship in Molecular and Cellular Biology, John Simon Guggenheim Memorial Foundation, 2012–2013.

Sloan Research Fellowship in Computational & Evolutionary Molecular Biology, Alfred P. Sloan Foundation, 2009–2011.

Packard Fellowship for Science and Engineering, David & Lucile Packard Foundation, 2007.

Microsoft Research Faculty Fellowship Program, 2007.

National Science Foundation (NSF) CAREER Award, 2007.

Graduate Research and Education in Adaptive Bio-technology (GREAT) Training Program Fellowship, University of California System-wide Biotechnology Research and Education Program (UC BREP), 2004–2005.

Achievement Rewards for College Scientists (ARCS) Scholar Award, Sponsored by ARCS Northern California Chapter, ARCS Foundation, Inc., 2003–2004.

Chancellor's Fellowship, University of California, Santa Cruz, 2002.

Editing and Review

NIH Special Emphasis Panel, National Institute of General Medical Sciences (NIGMS), Maximizing Investigators' Research Award (MIRA) Review, 2016

Peer Reviewer for the 24th FNP Prize, Foundation for Polish Science, Warsaw, Poland, 2015.

NIH Special Emphasis Panel, National Human Genome Research Institute (NHGRI), Genomic Resources, 2015.

NIH Study Section: Genomics, Computational Biology, and Technology (GCAT), 2010, 2014.

Editorial Board, *PLOS Computational Biology*, 2008–2012.

Program Committee for Research in Computational Molecular Biology (RECOMB), 2008–2010.

Editorial Board, *Genome Research*, 2007–2010.

Program Committee for Workshop on Algorithms in Bioinformatics (WABI), 2006–2008.

NSF Panelist for Directorate for Biological Sciences (BIO), 2007.

Program Committee for International Conference on Machine Learning (ICML), 2007.

Program Committee for Intelligent Systems for Molecular Biology (ISMB) / European Conference on Computational Biology (ECCB), 2004–2007.

PUBLICATIONS

Journal Articles

1. Danko CG, Choate LA, Marks BA, Rice EJ, Zhong W, Chu T, Martins AL, Dukler N, Coonrod SA, Wojno EDT, Lis JT, Kraus WL, **Siepel A**. Dynamic evolution of regulatory element ensembles in primate CD4+ T-cells. *Nat. Ecol. Evol.* **2**(3): 537-548, 2018.
2. Fang H, Huang YF, Radhakrishnan A, **Siepel A**, Lyon GJ, Schatz MC. Scikit-ribo enables accurate estimation and robust modeling of translation dynamics at codon resolution. *Cell Syst*. **6**(2): 180-191.e4, 2018.
3. Mohammed J, Flynt AS, Panzarino AM, Mondal MMH, **Siepel A**, Lai EC. Deep experimental profiling of microRNA diversity, deployment, and evolution across the *Drosophila* genus. *Genome Res.* **28**(1): 52-65, 2017.
4. Dukler N, Booth GT, Huang Y-F, Tippens N, Waters CT, Danko CG, Lis JT, and **Siepel A**. Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol. *Genome Res.* **27**: 1816-1829, 2017.
5. Kondo S, Vedanayagam J, Mohammed J, Eizadshenass S, Pang N, Kan L, Aradhya R, **Siepel A**, Steinhauer J, Lai EC. New genes often acquire male-specific functions but rarely become essential in *Drosophila*. *Genes. Dev*. **31**(18): 1841-1846, 2017.
6. Huang YF, Gulko B, **Siepel A**. Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. *Nat. Genet.* **49**(4): 618–624, 2017.
7. Freedman AH, Schweizer RM, Ortega-Del Vecchyo D, Han E, Davis BW, Gronau I, **Siepel A**, et al. (30 co-authors). Demographically-based evaluation of genomic regions under selection in domestic dogs. *PLOS Genet.* **12**(3): e1005851, 2016.
8. Kuhlwilm M, Gronau I, Hubisz MJ, de Filippo C, Prado J, Kircher M, Fu Q, Burbano HA, Lalueza-Fox C, de la Rasilla M, Rosas A, Rudan P, Brajkovic D, Kucan Z, Gusic I, Marques-Bonet T, Andres AM, Viola B, Paabo S, Meyer M, **Siepel A**, and Castellano S. Ancient gene flow from early modern humans into eastern neanderthals. *Nature.* **530**(7591): 429–433, 2016.
9. Campagna L, Gronau I, Silveira LF, **Siepel A**, Lovette IJ. Distinguishing noise from signal in patterns of genomic divergence in a highly polymorphic avian radiation. *Mol. Ecol.* **24**(16): 4238–4251, 2015.
10. Danko CG, Hyland SL, Core LJ, Martins AL, Waters CT, Lee HW, Cheung VG, Kraus WL, Lis JT, **Siepel A**. Identification of active transcriptional regulatory elements from GRO-seq data. *Nat. Methods.* **12**(5): 433–438, 2015.
11. Fuda NJ, Guertin MJ, Sharma S, Danko CG, Martins AL, **Siepel A**, Lis, JT. GAGA factor maintains nucleosome-free regions and has a role in RNA polymerase II recruitment to promoters. *PLOS Genet*. **11**(3): e1005108, 2015.
12. Gulko B, Hubisz MJ, Gronau I, **Siepel A**. A method for calculating probabilities of fitness consequences for point mutations across the human genome. *Nat. Genet.* **47**(3): 276–283, 2015.
13. Mohammed J, **Siepel A**, Lai EC. Diverse modes of evolutionary emergence and flux of conserved microRNA clusters. *RNA*. **20**(12): 1850–1863, 2014.
14. Core LJ, Martins AL, Danko CG, Waters CT, **Siepel A**, Lis JT. Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. *Nat. Genet.* **46**(12): 1311–1320, 2014.

15. Peng X, Alföldi J, Gori K, Eisfeld AJ, Tyler SR, Tisoncik-Go J, Brawand D, Law GL, Skunca N, Hatta M, Gasper DJ, Kelly SM, Chang J, Thomas MJ, Johnson J, Berlin AM, Lara M, Russell P, Swofford R, Turner-Maier J, Young S, Hourlier T, Aken B, Searle S, Sun X, Yi Y, Suresh M, Tumpey TM, **Siepel A**, et al. (38 co-authors). The draft genome sequence of the ferret (*Mustela putorius furo*) facilitates study of human respiratory disease. *Nat. Biotechnol*. **32**(12): 1250–1255, 2014.
16. Couger MB, Pipes L, Squina F, Prade R, **Siepel A**, Palermo R, Katze MG, Mason CE, Blood PD. Enabling large-scale next-generation sequence assembly with Blacklight. *Concurr. Comput.* **26**(13): 2157–2166, 2014.
17. Mohammed J, Bortolamiol-Becet D, Flynt AS, Gronau I, **Siepel A**, Lai EC. Adaptive evolution of testis-specific, recently evolved, clustered miRNAs in *Drosophila*. *RNA*. **20**(8): 1195–1209, 2014.
18. Wen J, Mohammed J, Bortolamiol-Becet D, Tsai H, Robine N, Westholm JO, Ladewig E, Dai Q, Okamura K, Flynt AS, Zhang D, Andrews J, Cherbas L, Kaufman TC, Cherbas P, **Siepel A**, Lai EC. Diversity of miRNAs, siRNAs, and piRNAs across 25 *Drosophila* cell lines. *Genome Res*. **24**(7): 1236–1250, 2014.
19. Arbiza L, Gottipati S, **Siepel A**, Keinan A. Contrasting X-linked and autosomal diversity across 14 human populations. *Am. J. Hum. Genet.* **94**(6): 827–844, 2014.
20. Freedman AH, Gronau I, Schweizer RM, Ortega-Del Vecchyo D, Han E, Silva PM, Galaverni M, Fan Z, Marx P, Lorente-Galdos B, Beale H, Ramirez O, Hormozdiari F, Alkan C, Vila C, Squire K, Geffen E, Kusak J, Boyko AR, Parker HG, Lee C, Tadigotla V, **Siepel A**, et al. (30 co-authors). Genome sequencing highlights the dynamic early history of dogs. *PLOS Genet.* **10**(1): e1004016, 2014.
21. Rasmussen MD, Hubisz MJ, Gronau I, **Siepel A**. Genome-wide inference of ancestral recombination graphs. *PLOS Genet.* **10**(5): e1004342, 2014.
22. Mohammed J, Flynt AS, **Siepel A**, Lai EC. The impact of age, biogenesis, and genomic clustering on *Drosophila* microRNA evolution. *RNA*. **19**(9): 1295–1308, 2013.
23. Arbiza L, Gronau I, Aksoy BA, Hubisz MJ, Gulko B, Keinan A, **Siepel A**. Genome-wide inference of natural selection on human transcription factor binding sites. *Nat. Genet.* **45**(7): 723–729, 2013.
24. Gronau I, Arbiza L, Mohammed J, **Siepel A.** Inference of natural selection from interspersed genomic elements based on polymorphism and divergence. *Mol. Biol. Evol.* **30**(5): 1159–1171, 2013.
25. Danko CG, Hah N, Luo X, Martins AL, Core L, Lis JT, **Siepel A**, Kraus WL. Signaling pathways differentially affect RNA polymerase II initiation, pausing, and elongation rate in cells. *Mol. Cell* **50**(2): 212–222, 2013.
26. Cornejo OE, Lefbure T, Bitar PD, Lang P, Richards VP, Eilertson K, Do T, Beighton D, Zeng L, Ahn SJ, Burne RA, **Siepel A**, Bustamante CD, Stanhope MJ. Evolutionary and population genomics of the cavity causing bacteria *Streptococcus mutans*. *Mol. Biol. Evol.* **30**(4): 881–893, 2013.
27. Zeng L, Choi SC, Danko CG, **Siepel A**, Stanhope MJ, Burne RA. Gene regulation by CcpA and catabolite repression explored by RNA-Seq in *Streptococcus mutans*. *PLOS One* **8**(3): e60465, 2013.
28. Ma X, Kelley JL, Eilertson K, Musharoff S, Degenhardt JD, Martins AL, Vinar T, Kosiol C, **Siepel A**, Gutenkunst RN, Bustamante CD. Population genomic analysis reveals a rich speciation and demographic history of orangutans (*Pongo pygmaeus* and *Pongo abelii*). *PLOS One* **8**(10): e77175, 2013.
29. Capra JA, Hubisz MJ, Kostka D, Pollard KS, **Siepel A**. A model-based analysis of GC-biased gene conversion in the human and chimpanzee genomes. *PLOS Genet.* **9**(8): e1003684, 2013.

30. Choi SC, Rasmussen MD, Hubisz MJ, Gronau I, Stanhope MJ, **Siepel A**. Replacing and additive horizontal gene transfer in *Streptococcus*. *Mol. Biol. Evol.* **29**(11): 3309–3320, 2012.
31. Kostka DA, Hubisz MJ, **Siepel A**, Pollard KS. The role of GC-biased gene conversion in shaping the fastest evolving regions of the human genome. *Mol. Biol. Evol.* **29**(3): 1047–1057, 2012.
32. Guertin MJ, Martins AL, **Siepel A**, Lis JT. Accurate prediction of inducible transcription factor binding intensities in vivo. *PLOS Genet.* **8**(3): e1002610, 2012.
33. Lindblad-Toh K, Garber M, Zuk O, Lin MF, Parker BJ, Washietl S, Kheradpour P, Ernst J, Jordan G, Mauceli E, Ward LD, Lowe CB, Holloway AK, Clamp M, Gnerre S, Alfoldi J, Beal K, Chang J, Clawson H, Cuff J, Di Palma F, Fitzgerald S, Flicek P, Guttman M, Hubisz MJ, Jaffe DB, Jungreis I, Kent WJ, Kostka D, Lara M, Martins AL, Massingham T, Moltke I, Raney BJ, Rasmussen MD, Robinson J, Stark A, Vilella AJ, Wen J, Xie X, Zody MC, Baldwin J, Bloom T, Chin CW, Heiman D, Nicol R, Nusbaum C, Young S, Wilkinson J, Worley KC, Kovar CL, Muzny DM, Gibbs RA, Cree A, Dihn HH, Fowler G, Jhangiani S, Joshi V, Lee S, Lewis LR, Nazareth LV, Okwuonu G, Santibanez J, Warren WC, Mardis ER, Weinstock GM, Wilson RK, Delehaunty K, Dooling D, Fronik C, Fulton L, Fulton B, Graves T, Minx P, Sodergren E, Birney E, Margulies EH, Herrero J, Green ED, Haussler D, **Siepel A**, et al. (86 co-authors). A high-resolution map of human evolutionary constraint using 29 mammals. *Nature.* **478**(7370): 476–482, 2011.
34. Gronau I, Hubisz MJ, Gulko B, Danko CG, **Siepel A**. Bayesian inference of ancient human demography from individual genome sequences. *Nat. Genet.* **43**(10): 1031–1034, 2011.
35. Lowe CB, Kellis M, **Siepel A**, Raney B, Clamp M, Salama SR, Kingsley D, Lindblad-Toh K, Haussler D. Three periods of regulatory innovation during vertebrate evolution. *Science* **333**(6045): 1019–1024, 2011.
36. Gottipati S, Arbiza L, **Siepel A**, Clark AG, Keinan A. Analyses of X-linked and autosomal genetic variation in population-scale whole genome sequencing. *Nat. Genet.* **43**(8): 741–743, 2011.
37. Hah N, Danko CG, Core L, **Siepel A**, Lis JT, Kraus WL. A Rapid, Extensive, and Transient Transcriptional Response to Estrogen Signaling in Breast Cancer Cells. *Cell* **145**(4): 622–634, 2011.
38. Hubisz MJ, Lin MF, Kellis M, **Siepel A**. Error and error mitigation in low-coverage genome assemblies. *PLOS One* **6**(2): e17034, 2011.
39. Yang J-S, Phillips MD, Betel D, Mu P, Sander C, Ventura A, **Siepel AC**, Chen KC, Lai EC. Widespread regulatory activity of vertebrate microRNA* species. *RNA* **17**(2): 312–326, 2011.
40. Orangutan Genome Sequencing and Analysis Consortium. Comparative and demographic analysis of orang-utan genomes. *Nature* **469**(7331): 529–533, 2011.
41. Suzuki H, Lefebure T, Hubisz MJ, Bitar PP, Lang P, **Siepel A**, Stanhope MJ. Comparative genomic analysis of the *Streptococcus dysgalactiae* species group: gene content, molecular adaptation, and promoter evolution. *Genome Biol. Evol.* **3**: 168–185, 2011.
42. Hubisz MJ, Pollard KS, **Siepel A**. PHAST and RPHAST: Phylogenetic analysis with space/time models. *Brief. Bioinform.* **12**(1): 41–51, 2011.
43. Vinar T, Brejova B, Song G, **Siepel A**. Reconstructing histories of complex gene clusters on a phylogeny. *J. Comput. Biol.* **17**(9): 1267–1279, 2010.
44. Boyko AR, Quignon P, Li L, Schoenebeck JJ, Degenhardt JD, Lohmueller KE, Zhao K, Brisbin A, Parker HG, vonHoldt BM, Cargill M, Auton A, Reynolds A, Elkahloun AG, Castelhano M, Mosher DS, Sutter NB, Johnson GS, Novembre J, Hubisz MJ, **Siepel A**, et al. (24 co-authors). A simple genetic architecture underlies morphological variation in dogs. *PLOS Biol.* **8**(8): e1000451, 2010.

45. da Fonseca RR, Kosiol C, Vinar T, **Siepel A**, Nielsen R. Positive selection on apoptosis related genes. *FEBS Lett.* **584**(3): 469–476, 2010.
46. Pollard KS, Hubisz MJ, Rosenbloom KR, **Siepel A.** Detection of non-neutral substitution rates on Mammalian phylogenies. *Genome Res.* **20**(1): 110–121, 2010.
47. The MGC Project Team. The completion of the Mammalian Gene Collection (MGC). *Genome Res.* **19**(12): 2324–2333, 2009.
48. Zhang Y, Song G, Vinar T, Green ED, **Siepel A**, Miller W. Evolutionary history reconstruction for Mammalian complex gene clusters. *J. Comput. Biol.* **16**(8): 1051–1070, 2009.
49. Holloway A, Begun D, **Siepel A**, Pollard KS. Accelerated sequence divergence of conserved genomic elements in *Drosophila melanogaster*. *Genome Res.* **18**(10): 1592–1601, 2008.
50. Wang Y, Diehl A, Wu F, Vrebalov J, Giovannoni J, **Siepel A**, Tanksley SD. Sequencing and comparative analysis of a conserved syntenic segment in the Solanaceae. *Genetics* **180**(1): 391–408, 2008.
51. Kosiol C, Vinar T, da Fonseca RR, Hubisz MJ, Bustamante CD, Nielsen R, **Siepel A**. Patterns of positive selection in six mammalian genomes. *PLOS Genet.* **4**(8): e1000144, 2008.
52. Miller W, Rosenbloom K, Hardison RC, Hou M, Taylor J, Raney B, Burhans R, King DC, Baertsch R, Blankenberg D, Kosakovsky Pond SL, Nekrutenko A, Giardine B, Harris RS, Tyekucheva S, Diekhans M, Pringle TH, Murphy WJ, Lesk A, Weinstock GM, Lindblad-Toh K, Gibbs RA, Lander ES, **Siepel A**, Haussler D, Kent WJ. 28-way vertebrate alignment and conservation track in the UCSC genome browser. *Genome Res.* **17**(12): 1797–1808, 2007.
53. **Siepel A**, Diekhans M, Brejova B, Langton L, Stevens M, Comstock CLG, Davis C, Ewing B, Oommen S, Lau C, Yu H-C, Li J, Roe BA, Green P, Gerhard DS, Temple G, Haussler D, Brent MR. Targeted discovery of novel human exons by comparative genomics. *Genome Res.* **17**(12): 1763–1773, 2007.
54. Kininis M, Chen BS, Diehl AG, Isaacs GD, Zhang T, **Siepel AC**, Clark AG, Kraus WL. Genomic analyses of transcription factor binding, histone acetylation, and gene expression reveal mechanistically distinct classes of estrogen-regulated promoters. *Mol. Cell Biol.* **27**(14): 5090–5104, 2007.
55. ENCODE Project Consortium. Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature* **447**(7146): 799–816, 2007.
56. Margulies EH, Cooper GM, Asimenos G, Thomas DJ, Dewey CN, **Siepel A**, et al. (42 co-authors). Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. *Genome Res.* **17**(6): 760–774, 2007.
57. Rhesus Macaque Genome Sequencing and Analysis Consortium. Evolutionary and biomedical insights from the rhesus macaque genome. *Science* **316**(5822): 222–234, 2007.
58. Kuhn RM, Karolchick D, Zweig AS, Trumbower H, Thomas DJ, Thakkapallayil A, Sugnet CW, Stanke M, Smith KE, **Siepel A**, et al. (25 co-authors). The UCSC genome browser database: update 2007. *Nucleic Acids Res.* **35**: D668–D673, 2007.
59. Pollard KS, Salama SR, King B, Kern AD, Dreszer T, Katzman S, **Siepel A**, Pedersen JS, Bejerano G, Baertsch R, Rosenbloom KR, Kent J, and Haussler D. Forces shaping the fastest evolving regions in the human genome. *PLOS Genet.* **2**(10): e168, 2006.
60. Pollard KS, Salama SR, Lambert N, Lambot M-A, Coppens S, Pedersen JS, Katzman S, King B, Onodera C, **Siepel A**, Kern AD, Dehay C, Igel H, Ares M, Vanderhaeghen P, and Haussler D. An

RNA gene expressed during cortical development evolved rapidly in humans. *Nature* **443**(7108): 167–172, 2006.

61. Bejerano G, Lowe CB, Ahituv N, King B, **Siepel A**, Salama SR, Rubin EM, Kent WJ, and Haussler D. A distal enhancer and an ultraconserved exon are derived from a novel retroposon. *Nature* **441**(7089): 87–90, 2006.
62. Pedersen JK, Bejerano G, **Siepel A**, Rosenbloom K, Lindblad-Toh K, Lander ES, Kent J, Miller W, and Haussler D. Identification and classification of conserved RNA secondary structures in the human genome. *PLOS Comput. Biol.* **2**(4): e33, 2006.
63. Hinrichs AS, Karolchik D, Baertsch R, Barber GP, Bejerano G, Clawson H, Diekhans M, Furey TS, Harte RA, Hsu F, Hillman-Jackson J, Kuhn RM, Pedersen JS, Pohl A, Raney BJ, Rosenbloom KR, **Siepel A**, et al. (27 co-authors). The UCSC Genome Browser Database: update 2006. *Nucleic Acids Res.* **34**: D590–598, 2006.
64. **Siepel A**, Bejerano G, Pedersen JS, Hinrichs AS, Hou M, Rosenbloom K, Clawson H, Spieth J, Hillier LW, Richards S, Weinstock GM, Wilson RK, Gibbs RA, Kent WJ, Miller W, and Haussler D. Evolutionarily conserved elements in vertebrate, insect, worm, and yeast genomes. *Genome Res.* **15**(8): 1034–1050, 2005.
65. Bejerano G, **Siepel AC**, Kent WJ, and Haussler D. Computational screening of conserved genomic DNA in search of functional noncoding elements. *Nat. Methods* **2**(7): 535–545, 2005.
66. International Chicken Genome Sequencing Consortium. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* **432**(7018): 695–716, 2004.
67. ENCODE Project Consortium. The ENCODE (ENCyclopedia Of DNA Elements) Project. *Science* **306**(5696): 636–640, 2004.
68. International Human Genome Sequencing Consortium. Finishing the euchromatic sequence of the human genome. *Nature* **431**: 931–945, 2004.
69. **Siepel A** and Haussler D. Phylogenetic estimation of context-dependent substitution rates by maximum likelihood. *Mol. Biol. Evol.* **21**(3):468–488, 2004.
70. **Siepel A** and Haussler D. Combining phylogenetic and hidden Markov models in biosequence analysis. *J. Comput. Biol.* **11**(2-3): 413–428, 2004.
71. Thomas JW, Touchman JW, Blakesley RW, Bouffard GG, Beckstrom-Sternberg, SM, Margulies EH, Blanchette M, **Siepel AC**, et al (71 co-authors)]. Comparative analyses of multi-species sequences from targeted genomic regions. *Nature* **424**(6950): 788–793, 2003.
72. **Siepel AC**. An algorithm to enumerate sorting reversals for signed permutations. *J. Comput. Biol.* **10**(3-4): 575–597, 2003.
73. **Siepel AC**, Steenhuis TS, Rose CW, Parlange J-Y, McIsaac GF. A simplified hillslope erosion model with vegetation elements for practical applications. *J. Hydrol.* **258**(1-4): 111–121, 2002.
74. **Siepel A**, Tolopko A, Farmer A, Steadman P, Schilkey F, Perry BD, and Beavis W. An integration platform for heterogeneous bioinformatics software components. *IBM Systems Journal* **40**(2): 570–591, 2001.
75. **Siepel A**, Farmer A, Tolopko A, Zhuang M, Mendes P, Beavis W, and Sobral B. ISYS: a decentralized, component-based approach to the integration of heterogeneous bioinformatics resources. *Bioinformatics* **17**(1): 83–94, 2001.

76. Skupski MP, Booker M, Farmer A, Harpold M, Huang W, Inman J, Kiphart D, Kodira C, Root S, Schilkey F, Schwertfeger J, **Siepel A**, Stamper D, Thayer N, Thompson R, Wortman J, Zhuang JJ, Harger C. The Genome Sequence DataBase: towards an integrated functional genomics resource. *Nucleic Acids Res.* **27**(1): 35–38, 1999.
77. Harger C, Skupski M, Bingham J, Farmer A, Hoisie S, Hraber P, Kiphart D, Krakowski L, McLeod M, Schwertfeger J, Seluja G, **Siepel A**, Singh G, Stamper D, Steadman P, Thayer N, Thompson R, Wargo P, Waugh M, Zhuang JJ, Schad PA. The Genome Sequence DataBase (GSDB): improving data quality and data access. *Nucleic Acids Res.* **26**(1): 21–26, 1998.
78. Harger C, Skupski M, Allen E, Clark C, Crowley D, Dickinson E, Easley D, Espinosa-Lujan A, Farmer A, Fields C, Flores L, Harris L, Keen G, Manning M, McLeod M, O'Neill J, Pumilia M, Reinert R, Rider D, Rohrlich J, Romero Y, Schwertfeger J, Seluja G, **Siepel A**, Schad PA. The Genome Sequence DataBase version 1.0 (GSDB): from low pass sequences to complete genomes. *Nucleic Acids Res.* **25**(1): 18–23, 1997.
79. **Siepel AC**, Halpern AL, Macken C, and Korber BTM. A computer program designed to screen rapidly for HIV type 1 intersubtype recombinant sequences. *AIDS Res. Hum. Retroviruses* **11**(11): 1413–1416, 1995.

Refereed Correspondence

80. Dukler N, Gulko B, Huang Y-F, **Siepel A**. Is a super-enhancer greater than the sum of its parts? Correspondence. *Nat. Genet.* **49**(1): 2–3, 2016.

Book Chapters and Review Articles

81. Hubisz MJ, **Siepel AC**. Chapter 11: ARGweaver. In: Dutheil J (ed.), Statistical Population Genetics. Springer, 2018. In Press.
82. **Siepel A**, Arbiza L. Cis-regulatory elements and human evolution. *Curr. Opin. Genet. Dev.* **29**C: 81–89. Review, 2014.
83. **Siepel A.** Phylogenomics of primates and their ancestral populations. *Genome Res.* **19**(11): 1929–1941, 2009.
84. **Siepel A.** Darwinian alchemy: human genes from noncoding DNA. *Genome Res.* **19**(10): 1693–1695, 2009.
85. **Siepel A** and Haussler D. Phylogenetic Hidden Markov Models. In: Nielsen R (ed.), Statistical Methods in Molecular Evolution, XII ed., pp. 325–351. Springer: New York, 2005.

Refereed Conference Papers

86. Vinar T, Brejova B, Song G, **Siepel A.** Reconstructing histories of complex gene clusters on a phylogeny. In: *Proceedings of International Workshop on Comparative Genomics. Ciccarelli FD, and Miklos I (eds.).* Comparative Genomics. RECOMB-CG 2009. Lecture Notes in Computer Science, vol. 5817. pp. 150–163. Springer, Berlin, Heidelberg, 2009.

87. Zhang Y, Song GT, Vinar T, Green ED, **Siepel A**, Miller W. Reconstructing the evolutionary history of complex human gene clusters. *In: Proceedings of 12th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2008, Singapore)*. Lecture Notes in Computer Science, **LNBI 4955,** pp. 29–49. Springer, Heidelberg, Berlin, 2008.
88. Sobral BWS, Mangalam H, **Siepel A**, Mendes P, Pecherer R, and McLaren G. Bioinformatics for rice resources. In: Goode JA and Chadwick D (eds). Novartis Foundation Symposium 236, Rice Biotechnology: Improving Yield, Stress Tolerance and Grain Quality. pp. 59–84, John Wiley & Sons, Ltd., Chichester, UK, 2001.
89. **Siepel A**, Pollard KS, and Haussler D. New methods for detecting lineage-specific selection. In: Proceedings of the 10th Annual International Conference Research on Research in Computational Molecular Biology (RECOMB 2006, Venice, Italy). Lecture Notes in Computer Science, **LNBI 3909**, pp. 190–205. Springer-Verlag, Heidelberg, Berlin, 2006.
90. Jojic V, Jojic N, Meek C, Geiger D, **Siepel A**, Haussler D, and Heckerman D. Efficient approximations for learning phylogenetic HMM models from data. In: Proceedings of the Twelfth International Conference on Intelligent Systems for Molecular Biology / Third European Conference on Computational Biology (ISMB/ECCB 2004, Glasgow, Scotland, UK); and *Bioinformatics.* **20**(Suppl. 1): i161–i168, 2004.
91. **Siepel A** and Haussler D. Computational identification of evolutionarily conserved exons. In: Proceedings of the Eighth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2004, San Diego, CA). pp. 177–186, ACM Press, New York, NY. 2004.
92. **Siepel A** and Haussler D. Combining phylogenetic and hidden Markov models in biosequence analysis. In: Proceedings of the Seventh Annual International Conference on Research in Computational Molecular Biology (RECOMB 2003, Berlin, Germany). pp. 277–286, ACM Press, New York, NY, 2003.
93. **Siepel A**. An algorithm to enumerate all sorting reversals. In: Proceedings of the Sixth Annual International Conference on Computational Molecular Biology (RECOMB 2002, Washington D.C.), pp. 281–290, ACM Press, New York, NY, 2002.
94. Moret BME, **Siepel AC**, Tang J, and Liu T. Inversion Medians Outperform Breakpoint Medians in Phylogeny Reconstruction from Gene-Order Data. In: Guigó R, Gusfield D (eds). Algorithms in Bioinformatics (WABI 2002, Rome, Italy). Lecture Notes in Computer Science, vol 2452. Springer, Heidelberg, Berlin, 2002.
95. **Siepel AC** and Moret BME. Finding an Optimal Inversion Median: Experimental Results. In: *Proceedings of the First International Workshop on Algorithms in Bioinformatics. Gascuel O, Moret BME (eds)*. (WABI 2001, Aarhus, Denmark). Lecture Notes in Computer Science, vol 2149. Springer, Heidelberg, Berlin, 2001.

Teaching

Quantitative Biology I, II, and Genetics & Genomics Course Lecturer, Watson School of Biological Sciences, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY: 2014–present.

Graduate Special Topics in Biometry & Statistics: Genomics of Gene Regulation [BTRY 6940] *(with John Lis)*, Cornell University*,* Ithaca, NY: Spring 2014.

Probabilistic Graphical Models [BTRY 4790/6790 and CS 4782/6782], Cornell University, Ithaca, NY: Fall 2008, 2010, 2013.

Computational Genetics & Genomics [BTRY 4840/6840], Cornell University, Ithaca, NY: Fall 2006–2007, 2009, 2011.

Graduate-level Biometry & Statistics Course: Applied Bioinformatics [BTRY 6700] *(with Jason Mezey, Alon Keinan, and Haiyuan Yu)*, Cornell University, Ithaca, NY, Fall 2010–2011.

Summer Course in Evolutionary Genomics: Computational Genomics (three-day module), Kunming Institute of Zoology (KIZ), Chinese Academy of Sciences, Kunming, China, August 2011.

Comparative Genomics/Molecular Evolution (three-day module) *(with Spencer Muse)*, Summer Institute in Statistical Genetics, School of Public Health, University of Washington, Seattle, Washington, June 2008–2010.

Graduate-level Biometry & Statistics Course: Topics in Computational Genomics [BTRY 7200], Cornell University, Ithaca, NY, Spring 2006–2010.

Trainees

list	First	Last	Type	Joint Mentor	Start	End
1	Leonardo	Arbiza	Postdoc	A. Keinan	2010	2013
2	Amit	Blumberg	Postdoc	—	2016	Present
3	Bronislava	Brejova	Postdoc	—	2006	2008
4	Sang Chul	Choi	Postdoc	—	2010	2013
5	Omar	Cornejo	Postdoc	C.D. Bustamante	2009	2010
6	Charles	Danko	Postdoc	W.L. Kraus	2009	2014
7	Alexandra	Denby	Undergrad	—	2006	2008
8	Adam	Diehl	Grad student, Masters	—	2006	2010
9	Noah	Dukler	Grad student, PhD	—	2014	Present
10	Ilan	Gronau	Postdoc	—	2009	2014
11	Brad	Gulko	Grad student, PhD	—	2010	2017
12	Yifei	Huang	Postdoc	—	2015	Present
13	Melissa	Hubisz	Grad student, PhD	—	2014	Present
14	Hussein	Hijazi	Postdoc	—	2018	Present
15	Elizabeth	Hutton	Grad student, PhD	—	2015	Present
16	Carolin	Kosiol	Postdoc	C.D. Bustamante	2006	2008
17	Tytus	Mak	Undergrad	—	Spring 2006	Spring 2006
18	Alison	Marklein	Undergrad	—	Summer 2006	Summer 2006
19	Andre L.	Martins	Grad student, PhD	—	2007	2014
20	Jaaved	Mohammed	Grad student, PhD	E. Lai	2009	2016
21	Michael D.	Phillips	Grad student, Masters	E. Lai	2008	2010
22	Lenore	Pipes	Grad student, PhD	C. Mason	2012	2017
23	Joseph	Porter	Undergrad	—	Spring 2012	Spring 2012
24	Matthew	Rasmussen	Postdoc	—	2011	2013
25	Hirak	Sarkar	Summer Intern	—	May 2016	Aug 2016
26	Renee	Setter	Undergrad	—	Summer 2010	Fall 2010
27	Daniel	Sussman	Undergrad	—	Summer 2007	Summer 2008
28	Tomas	Vinar	Postdoc	—	2006	2008

29	Yixin	Zhao	Postdoc	—	2018	Present

Thesis Committees

Current

Talitha Forcier, Ph.D., Watson School of Biological Sciences, Cold Spring Harbor Laboratory.
Stephanie Hyland, Ph.D., Tri-Institute Computational Biology and Medicine (CBM) program.
Laraib Malik, Ph.D., Computer Science, Stony Brook University.
Monica Ramstetter, Ph.D., Computational Biology, Cornell University.
Hirak Sarkar, Ph.D., Computer Science, Stony Brook University.
Avi Srivastava, Ph.D., Computer Science, Stony Brook University.
Nathaniel Tippens, Ph.D., Tri-Institute Computational Biology and Medicine (CBM) program.

Completed

B. Arman Aksoy, Ph.D., Tri-Institute Computational Biology and Medicine (CBM) program, 2015.
Samuel Arbesman, Ph.D., Computational Biology, Cornell University, 2008.
Tara Baxter, M.S., Genetics and Development, Cornell University, 2014.
Jeremiah Degenhardt, Ph.D., Computational Biology, Cornell University, 2010.
Feng Gao, Ph.D., Computational Biology, Cornell University 2016.
Gabriel Hoffman, Ph.D., Genetics and Development, Cornell University, 2013.
Haley Hunter-Zinck, Ph.D., Tri-Institute Computational Biology and Medicine (CBM) program, 2014.
Helgi Ingolfsson, Ph.D., Tri-Institute Computational Biology and Medicine (CBM) program, 2010.
Hayan Lee, Ph.D., Computer Science, Stony Brook University, 2015.
Aaron Lenfestey, Ph.D., Computer Science, Cornell University, qualified 2009.
Maria Nattestad, Ph.D., Watson School of Biological Sciences, Cold Spring Harbor Laboratory, 2017.
Yogesh Saletore, Ph.D., Tri-Institute Computational Biology and Medicine (CBM) program, 2015.
Solomon Shenker, Ph.D., Tri-Institute Computational Biology and Medicine (CBM) program, 2016.
Molly Shook, Ph.D., Genetics and Development, Cornell University, qualified 2009.
Nick Stepankiw, Ph.D., Biochemistry, Molecular & Cell Biology (BMCB), Cornell University, 2016.
Paula Tataru, Ph.D., Aarhus University, Aarhus, Denmark, 2015.
Xu Wang, Ph.D., Genetics and Development, Cornell University, 2011.
Katherine Wilkins, Ph.D., Computational Biology, Cornell University, 2016.
Erin Wissink, Ph.D., Genetics and Development, Cornell University, left committee 2014.
Wendy Wong, Ph.D., Biometry, Cornell University, 2006.
Chun-Nam Yu, Ph.D., Computer Science, Cornell University, 2010.

Other Service

Guest Speaker at the Annual Meeting of the “NHGRI Genome Sequencing Program (GSP)”, Bethesda, MD, April 2018.

Guest Member of the Editorial Committee Planning Meeting for the “*2019 Annual Review of Genomics and Human Genetics*”, New York, NY, January 2018.

Co-organizer of New York Area Population Genomics Workshop (NYPG18), *(with Casey Brown, Barbara Engelhardt, Joe Pickrell, Molly Przeworski, Matt Rockman)*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, January 2018.

Co-organizer of New York Area Meeting in Quantitative Biology (NYQB17): "Making Use of Emerging Technologies" *(with Alex Krasnitz, Neville Sanjana, Rahul Satija, and Olga Troyanskaya)*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, August 2017.

Advisory Board Member, School of Engineering Bioinformatics, New York University, New York, NY, 2015–present.

Admissions Committee, Watson School of Biological Sciences (WSBS), Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 2015–present.

Graduate Field Membership, Genetics Program, Stony Brook University, Stony Brook, NY, 2015–present.

Graduate Field Membership, Physiology, Biophysics and Systems Biology Program, Weill Cornell Medical College of Cornell University, New York, NY, 2015–present.

Graduate Student Admissions Committee, Tri-Institutional MD-PhD Training Program in Computational Biology & Medicine, Cornell University, Ithaca, NY, 2006–present.

Developer of freely available software package: "PHAST (PHylogenetic Analysis with Space/Time models)" *[> 2500 downloads]*, 2003–present.

Contributor to UC Santa Cruz Genome Browser (Conservation, ExoniPhy, DLESS, and Positive Selection tracks), 2003–present.

Co-organizer of New York Area Meeting in Quantitative Biology (NYQB16): "Computational and Statistical Genomics: Applications to Disease", inaugural meeting *(with Christina Leslie, Bud Mishra, Joe Pickrell, and Olga Troyanskaya)*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, July 2016.

Co-organizer of the Banbury Center meeting: "Measuring and Modeling Quantitative Sequence-function Relationships" *(with Justin B. Kinney and Douglas M. Fowler)*, at Cold Spring Harbor Laboratory, Huntington, NY, July 2016.

Co-organizer of 1st Probabilistic Modeling in Genomics Conference, *inaugural meeting (with Barbara Engelhardt and Thomas* Mailund*)*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, October 2015.

Co-organizer of New York Area Population Genomics Workshop (NYPG15), *inaugural meeting (with Barbara Engelhardt, Joe Pickrell, Molly Przeworski, Matt Rockman, et al.)*, New York Genome Center, New York, NY, January 2015.

Co-organizer of "Biological Sequence Analysis and Probabilistic Models" workshop *(with Anders Krogh, Gerton Lunter, Gilean McVean, Molly Przeworski, Richard Durbin, and Thomas Mailund)*, Merton College, Oxford, UK, July 2014.

Director of Graduate Studies, Graduate Field of Computational Biology, Cornell University, Ithaca, NY, 2011–2014.

Endorsement Committee for Cornell University Nominees of the Churchill Scholarship, Ithaca, NY, 2009–2014.

Associate Director, Center for Comparative and Population Genomics, Cornell University, Ithaca, NY, 2008–2014.

Advisory Committee, Weill Institute for Cell and Molecular Biology, Cornell University, Ithaca, NY, 2007–2014.

Graduate Field Membership, Cornell University, Ithaca, NY, 2006–2014:
  Statistics, 2013–2014.
  Applied Math, 2009–2014.
  Computational Biology, Biometry, Computer Science, and Genetics & Development, 2006–2014.

Faculty Search Committees, Cornell University, Ithaca, NY, 2007–2014:
  Biological Statistics and Computational Biology, 2008, 2012 *[chair]*, and 2014 *[chair]*.
  Computer Science, 2007–2009, 2012.
  Molecular Biology and Genetics, 2008, 2012.
  Department of Biological Statistics and Computational Biology (BSCB) / Weill Institute, 2008.

Faculty Advisor for Information Technology, Life Sciences Core Laboratories Center, Cornell University, Ithaca, NY, 2008–2012.

Faculty Senate, College of Agriculture and Life Sciences, Cornell University, Ithaca, NY, 2008–2011.

Participation in International Genomics Consortia, 2003–2011:
  Orangutan Sequencing and Analysis Consortium, 2008–2011.
  2x Mammals Sequencing and Analysis Consortium, 2008–2011.
  Mammalian Gene Collection (MGC) Project, 2004–2009.
  Rhesus Macaque Sequencing and Analysis Consortium, 2006–2007.
  ENCyclopedia Of DNA Elements (ENCODE) Consortium, 2004–2007.
  International Human Genome Sequencing Consortium, 2004.
  International Chicken Genome Sequencing Consortium, 2003–2004.

Strategic Planning Working Group for Research, Scholarship and Creativity, Cornell University, Ithaca, NY, 2009.

Advisory Committee for Primate Genome Sequencing, National Human Genome Research Institute (NHGRI) of NIH, Bethesda, MD, 2007–2009.

Undergraduate Biology Curriculum Task Force, Cornell University, Ithaca, NY, 2007–2008.

Research Support

CURRENT

Program and/or Project Title	PI, Institution	Source, Grantor #	Total Award	Award Period
Evolutionary Human Genomics: Demography, Natural Selection, and Transcriptional Regulation	Siepel, CSHL	NIH / NIGMS R35 GM127070	$ 2,396,075	3/1/18 – 2/28/23
Continued development and maintenance of the PHAST software for comparative genomics.	Siepel, CSHL	NIH / NHGRI R01 HG008161	$ 576,000 *NCE to 1/31/19*	4/24/15 – 1/31/19
Collaborative Research: NSFDEB–BSF: Quantifying genomic porosity in non-model radiations.	Siepel, CSHL Lovette, Cornell	NSF / BIO DEB1555769	$ 197,334	3/1/16 – 2/28/19

COMPLETED

Program and/or Project Title	**PI, Institution**	**Source, Grantor #**	**Total Award**	**Award Period**
Computational methods for human genomic data integration: demography, selection, and functional potential.	Siepel, CSHL	NIH / NIGMS R01 GM102192	$ 1,722,155	1/1/13 – 12/31/17
New York Center for Collaborative Research in Common Disease Genomics.	Darnell, NYGC Subawd Co-I: Siepel, CSHL	NIH / NHGRI UM1 HG008901	$ 32,500 *Subawd only*	1/14/16 – 11/30/17
Factor-general characterization of dynamic transcriptional stress responses.	Siepel, CSHL Lis, Cornell	NIH / NHGRI R01 HG007070	$ 1,011,632 *NCE to 5/31/17*	9/1/13 – 5/31/17
Packard Fellowship for Science and Engineering in Biological Sciences	Siepel, Cornell	David & Lucile Packard Found. 2007–31762	$ 825,000 *NCE to 8/31/14*	9/1/07 – 8/31/14
Evolutionary genomics and population genetics of pathogenic streptococci.	Stanhope, Cornell. Co-I's: Siepel, Cornell, Bustamante, Cornell, Burne, U. Florida	NIH / NIAID R01 AI073368	$ 2,252,000	7/1/08 – 6/30/13
Coordinate gene regulation in animal cells. *(Administrative Supplement)*	Lis, Cornell. Co-I: Siepel, Cornell	NIH / NIGMS R01 GM025232	$ 1,137,000	4/1/09 – 3/31/13
What made us human?	Pollard, Gladstone Institutes, UCSF. Co-I: Siepel, Cornell	NIH / NIGMS R01 GM082901	$ 274,000 *A. Siepel Subawd only*	9/1/08 – 8/31/12
NSF CAREER Award: Models of evolution and discovery of functional elements in mammals and *Drosophila*.	Siepel, Cornell	NSF / BIO DBI 0644111	$ 645,870	3/1/07 – 2/29/12
Sloan Research Fellowship in Molecular Biology	A. Siepel, Cornell	Alfred P. Sloan Foundation	$ 50,000	2009 – 2011
Microsoft Research Faculty Fellowship Program	A. Siepel, Cornell	Microsoft Research	$ 200,000 *lump sum*	2007
Prediction of novel human protein-coding genes using cross-species alignments and phylogenetic hidden Markov models.	D. Haussler, UCSC. Subawd PI: A. Siepel, Cornell	NIH / NCI Subawd 22XS013A	$ 159,000 *Subawd only*	5/15/06 – 11/14/07

Invited Conference and Symposium Lectures

50th Anniversary of the Neutral Theory of Molecular Evolution, Society for Molecular Biology and Evolution Conference (SMBE 2018), Yokohama, Japan, July 2018.

13th Systems Biology: Global Regulation of Gene Expression Conference, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, March 2018.

Conference on Genome Informatics, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, November 2017.

Keynote Lecture, 3rd Probabilistic Modeling in Genomics Conference (ProbGen17), Aarhus University, Denmark, September 2017.

Revolutionizing Next-Generation Sequencing (2nd Edition), Antwerp, Belgium, March 2017.

Genomics & Systems Biology VII Conference, New York University Abu Dhabi, Saadiyat Island, Abu Dhabi, United Arab Emirates, February 2017.

66th Annual Meeting of the American Society of Human Genetics (ASHG), Vancouver, BC, Canada, October 2016.

2nd Probabilistic Modeling in Genomics Conference (ProbGen16), University of Oxford, UK, September 2016.

5th International Conference in Quantitative Genetics (ICQG5), Madison, WI, June 2016

Genome Informatics, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, October 2015.

Society for Molecular Biology & Evolution (SMBE) Annual Meeting, Vienna, Austria, July 2015.

Twelfth RECOMB Satellite Conference on Comparative Genomics (RECOMB-CG), Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, October 2014.

Mathematical and Computational Evolutionary Biology, Laboratoire d'Informatique, de Robotique et de Microélectronique de Montpellier (LIRMM), Montpellier, France, June 2014.

11th Basel Computational Biology Conference $[BC]^2$, Basel, Switzerland, July 2013.

26th Annual Meeting on The Biology of Genomes, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, May 2013.

24th Annual Meeting on The Biology of Genomes, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, May 2011.

Second RECOMB Satellite Conference on Bioinformatics Education (RECOMB-BE), University of California, San Diego, La Jolla, CA, May 2010.

Annual Meeting of the Society for Molecular Biology & Evolution (SMBE), Iowa City, IA, June 2009.

22nd Annual Meeting on The Biology of Genomes *[session chair]*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, May 2009.

8th Annual Computational Molecular Biology Symposium, Carnegie Mellon University, Pittsburgh, PA, April 2009.

10th Annual Advances in Genome Biology and Technology (AGBT), Marco Island, FL, February 2009.

Frontiers of Evolutionary Biology *(one-day workshop)*, Pennsylvania State University, State College, PA, October 2008.

Packard Foundation 20th Anniversary Fellows Reunion, Park City, UT, September 2008.

Biomedical Engineering Society (BMES) Annual Meeting, Chicago, IL, October 2006.

8th International Bioinformatics 2006 Conference, Society for Bioinformatics in the Nordic Countries (SocBIN), Aarhus, Denmark, June 2006.

19th Annual Meeting on The Biology of Genomes, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, May 2006.

First International Conference on Phylogenomics, Sainte-Adele, Quebec, Canada, March 2006.

17th Annual Meeting on The Biology of Genomes, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, May 2004.

Invited Seminars and Workshops

National Laboratory of Genomics for Biodiversity (LANGEBIO Cinvestav), "Advanced Genomics Unit Seminar", Irapuato, Mexico, February 2018.

International Laboratory for Human Genome Research (LIIGH-UNAM), "Horizons in Genomic Research Seminar", National University of Mexico (UNAM), Queretaro, Mexico, February 2018.

Charles Bronfman Institute for Personalized Medicine (IPM), "2017-2018 Monthly Seminar Series", Icahn School of Medicine at Mt. Sinai, New York, NY, December 2017.

Banff International Research Station (BIRS) for Mathematical Innovation and Discovery, "Challenges and Synergies in the Analysis of Large-Scale Population-Based Biomedical Data Workshop", Casa Matemática Oaxaca (CMO), Oaxaca, Mexico, November 2017.

Laufer Center for Physical and Quantitative Biology, "Laufer Center Seminar Series", Stony Brook University, Stony Brook, NY, October 2017.

Carnegie Mellon – University of Pittsburgh "Computational Biology PhD Program", Pittsburgh, PA, September 2017.

UCLA, "Bioinformatics Seminar", Los Angeles, February 2017.

University of Pennsylvania, "Mathematical Biology Seminar", Philadelphia, PA, January 2017.

UC Berkeley, "Quantitative Biology Seminar", Berkeley, CA, October 2016.

Cornell University, "Mechanisms of Transcription: Pausing to Celebrate John Lis", Ithaca, NY, July 2016.

The Banbury Center, "Measuring and Modeling Quantitative Sequence-function Relationships", Cold Spring Harbor Laboratory, Huntington, NY, July 2016.

Worcester Polytechnic Institute, "April is Math Awareness Month", Departments of Mathematical Sciences and Computer Science, Worcester, MA, April 2016.

Renaissance Technologies, "Monthly Colloquium Series", East Setauket, NY, January 2016.

Center for Quantitative Biology, "Mathematics and the Quest for Fundamental Principles of Biology Workshop", University of Utah, Salt Lake City, UT, December 2015.

Biostatistics and Medical Informatics (BMI), "BMI Department Seminars", University of Wisconsin-Madison, Madison, WI, September 2015.

Simons Institute for the Theory of Computing, "Evolutionary Biology and the Theory of Computing Reunion Workshop", UC Berkeley, CA, July 2015.

Computational Biology Center (cBio), "Annual Scientific Retreat", Memorial Sloan-Kettering Cancer Center, Norwalk, CT, May 2015.

Stony Brook School of Medicine, "Paleobiology Seminar Series", Stony Brook University, Stony Brook, NY, April 2015.

NHGRI, "From Genome Function to Biomedical Insight: ENCODE and Beyond", Bethesda, MD, March 2015.

Barbados Workshop: "Understanding non-coding DNA through intra- and inter-species epigenomic variation", *(organized by G. Bourque and T.M. Pastinen)*, McGill University, Bellairs Research Institute, Holetown, Barbados, January 2015.

Rutgers University, "Genetics Department Seminar", Piscataway, NJ, November 2014.

Computer Science Departmental Colloquium, “Topics in Modern Computer Science”, Stony Brook University, Stony Brook, NY, October 2014.

University of Massachusetts, “Organismic and Evolutionary Biology”, Amherst, MA, September 2014.

Weill Cornell Medical College of Cornell University, “Institute for Computational Biomedicine”, New York, NY, September 2014.

Merton College, “Workshop on Biological Sequence Analysis and Probabilistic Models”, *(organized by G. Lunter, T. Mailund, A. Siepel, G. McVean, R. Durbin, A. Krogh, and M. Przeworski)*, Oxford, UK, July 2014.

University of Montpellier 2, “Computational Biology Institute (IBC)”, Montpellier, France, June 2014.

Duke University, “Computational Biology & Bioinformatics Program”, Durham, NC, April 2014.

Harvard School of Public Health, “Department of Biostatistics Colloquium”, Boston, MA, March 2014.

University of Pennsylvania, “Bioinformatics Forum”, Philadelphia, PA, February 2014.

Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, December 2013.

University of Chicago, “Department of Human Genetics Seminar Series”, Chicago, IL, November 2013.

Indiana University, “Center for Bioinformatics Research” Seminar Series, Bloomington, IN, September 2013.

University of Oxford, “Wellcome Trust Centre for Human Genetics Seminar Series”, UK, May 2013.

Centre for Mathematical Sciences, “Cambridge Statistics Initiative Seminar”, University of Cambridge, Cambridge, UK, April 2013.

Co-organizer of “Biological Sequence Analysis and Probabilistic Models Workshop” *(with Katherine Pollard, and Sean Eddy)*, Janelia Farm Research Campus, Ashburn, VA, March 2013.

European Bioinformatics Institute (EMBL-EBI), Hinxton, UK, February 2013.

Microsoft Research Ltd., Cambridge, UK, February 2013.

Universite Claude Bernard Lyon 1, Lyon, France, January 2013.

Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, December 2012.

Aarhus University, “Bioinformatics Research Centre”, Denmark, November 2012.

University of Copenhagen, “Bioinformatics Centre”, Department of Biology, Denmark, October 2012.

Emory University, “Population Biology, Ecology, and Evolution (PBEE) Graduate Program”, Atlanta, GA, February 2012.

“Evolutionary Studies (EvoS) Program”, SUNY Binghamton, NY, December 2011.

“Evolutionary Genomics Seminar Series” *(online phylogenetics seminar),* Phyloseminar.org, May 2011.

Vienna Graduate School of Population Genetics, Department of Biomedical Sciences, University of Veterinary Medicine, Vienna, Austria, March 2011.

Comenius University, Bratislava, Slovakia, March 2011.

University of Geneva, Switzerland, March 2011.

“BioMaPS Summer School: New Directions in Evolutionary and Population Genetics”, Rutgers University, Piscataway, NJ, June 2010.

“Gene histories versus species histories Workshop,” Bertinoro, Italy, May 2010.

Computational Center for Algorithmic and Systems Biology, "Meeting of Twenty Leading Experts in Bioinformatics (CASB-20)", UC San Diego, San Diego, CA, May 2010.

Mathematical Biosciences Institute, "Inference in Stochastic Models for Sequence Evolution Workshop", Columbus, OH, February 2010.

Syracuse University, Physics Department, Syracuse, NY, January 2010.

"Cross-campus Epigenomics Seminar Series", Weill Cornell Medical College of Cornell University, New York, NY, January 2010.

UCLA, "Bioinformatics Seminar Series", Los Angeles, CA, January 2010.

National Human Genome Research Institute, Bethesda, MD, March 2009.

Cornell University, "Applied Math Colloquium", Ithaca, NY, October 2008.

"Mammalian Gene Collection (MGC), "Final External Steering Committee Meeting", Rockville, MD, September 2008.

ISMB 2008 Special Interest Group, "Genome-scale Pattern Analysis in the Post-ENCODE Era", Toronto, Ontario, Canada, July 2008.

"Microsoft Research Faculty Summit", Redmond, WA, July 2008.

Cornell University, "Tree Thinking at Cornell" Symposium, Laboratory of Ornithology, Ithaca, NY, May 2008.

UC Davis, "Evolutionary Genetics Seminar Series", Davis, CA, May 2008.

Stanford University, Department of Developmental Biology, Stanford, CA, May 2008.

University of Washington, Department of Genome Sciences, Seattle, WA, March 2008.

University of Washington, Department of Statistics, Seattle, WA, March 2008.

Microsoft Research, Redmond, WA, March 2008.

University of Toronto, Centre for Cellular and Biomolecular Research, Toronto, Canada, October 2007.

University of Copenhagen, Center for Comparative Genomics, Denmark, June 2007.

3rd Barbados Workshop on Computational Gene Regulation, McGill University, Bellairs Research Institute, Holetown, Barbados, April 2007.

NESCent Workshop on *cis*-regulatory molecular evolution, National Evolutionary Synthesis Center, Durham, NC, March 2007.

Cornell University, Department of Molecular Biology and Genetics, Ithaca, NY, September 2006.

Computational and Statistical Genomics Workshop, Banff International Research Station, Banff, Canada, July 2006.

1st Barbados Workshop on Paleogenomics, McGill University, Bellairs Research Institute, Holetown, Barbados, April 2006.

McGill University, Centre for Bioinformatics, Montreal, Quebec, Canada, March 2006.

Pennsylvania State University, Center for Comparative Genomics and Bioinformatics, University Park, PA, February 2006.

Cornell University, Department of Entomology, Ithaca, NY, January 2006.

Pennsylvania State University, Department of Biochemistry and Molecular Biology, University Park, PA, April 2005.

New York University, Department of Biology and Courant Institute, New York, NY, March 2005.

UC Berkeley, Department of Computer Science, Berkeley, CA, February 2005.

Cornell University, Department of Computer Science and Department of Biological Statistics and Computational Biology, Ithaca, NY, February 2005.

Pennsylvania State University, Department of Statistics, University Park, PA, February 2005.

University of Washington, Department of Genome Sciences, Seattle, WA, January 2005.

Stanford University, Department of Computer Science, Stanford, CA, October 2003.