

# Adam C. Siepel, Ph.D.

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## PERSONAL DETAILS

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**Present position:** Chair, Simons Center for Quantitative Biology  
Professor, Watson School of Biological Sciences  
Cold Spring Harbor Laboratory

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## EDUCATION AND PROFESSIONAL QUALIFICATIONS

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### 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 24<sup>th</sup> 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, Directorate for Biological Sciences, 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

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### Journal Articles

1. Huang Y-F, Gulko B, **Siepel A**. Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. *Nat. Genet.* **49**(4):618–624, 2017.
2. Dukler N, Booth GT, Huang Y-F, Tippens N, Danko CG, Lis J, and **Siepel A**. Nascent RNA Sequencing Reveals a Dynamic Global Transcriptional Response at Genes and Enhancers to the Natural Medicinal Compound Celastrol. Preprint. *BioRxiv* 117689, 2017.
3. Flynt AS, Panzarino AM, Mondal MMH, **Siepel A**, Mohammed J, Lai EC. Deep experimental profiling of microRNA diversity, deployment, and evolution across the *Drosophila* genus. Preprint. *BioRxiv* 125997, 2017.
4. 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.
5. 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.
6. Danko CG, Wang Z, Rice EJ, Chu T, Martins AL, Wojno ET, Lis JT, Kraus LW, **Siepel A**. Natural selection has shaped coding and non-coding transcription in primate CD4+ T-cells. Preprint. *BioRxiv* 083212, 2016.
7. 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.
8. 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.
9. 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.
10. 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.
11. Mohammed J, **Siepel A**, Lai EC. Diverse modes of evolutionary emergence and flux of conserved microRNA clusters. *RNA.* **20**(12):1850–1863, 2014.
12. 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.
13. 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**, Wisely SM, Dessimoz C, Kawaoka Y, Birren BW, Lindblad-Toh K, Di Palma F, Engelhardt JF, Palermo RE, Katze MG. The draft genome sequence of the ferret (*Mustela putorius furo*) facilitates study of human respiratory disease. *Nat. Biotechnol.* **32**(12):1250–1255, 2014.

14. 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.
15. 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.
16. 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.
17. 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.
18. Freedman AH, Gronau I, Schweizer RM, Ortega-Del Vecchyo D, Han E, et al. (30 co-authors). Genome sequencing highlights the dynamic early history of dogs. *PLOS Genet.* **10**(1):e1004016, 2014.
19. Rasmussen MD, Hubisz MJ, Gronau I, **Siepel A**. Genome-wide inference of ancestral recombination graphs. *PLOS Genet.* **10**(5):e1004342, 2014.
20. 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.
21. 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.
22. 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.
23. 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.
24. 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.
25. 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.
26. 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.
27. 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.
28. 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.
29. 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.
30. Guertin MJ, Martins AL, **Siepel A**, Lis JT. Accurate prediction of inducible transcription factor binding intensities in vivo. *PLOS Genet.* **8**(3): e1002610, 2012.

31. Lindblad-Toh K, Garber M, Zuk O, Lin MF, Parker BJ, et al. (63 co-authors). A high-resolution map of human evolutionary constraint using 29 mammals. *Nature*. **478**(7370): 476–482, 2011.
32. 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.
33. 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.
34. 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.
35. 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.
36. Hubisz MJ, Lin MF, Kellis M, **Siepel A**. Error and error mitigation in low-coverage genome assemblies. *PLOS One* **6**(2): e17034, 2011.
37. 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.
38. Orangutan Genome Sequencing and Analysis Consortium. Locke DP, Hillier LW, Warren WC, et al. Comparative and demographic analysis of orang-utan genomes. *Nature* **469**(7331): 529–533, 2011.
39. 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.
40. Hubisz MJ, Pollard KS, **Siepel A**. PHAST and RPHAST: Phylogenetic analysis with space/time models. *Brief. Bioinform.* **12**(1): 41–51, 2011.
41. Vinar T, Brejov B, Song G, **Siepel A**. Reconstructing histories of complex gene clusters on a phylogeny. *J. Comput. Biol.* **17**(9): 1267–1279, 2010.
42. 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, Elkahlon AG, Castelano M, Mosher DS, Sutter NB, Johnson GS, Novembre J, Hubisz MJ, **Siepel A**, Wayne RK, Bustamante CD, Ostrander EA. A simple genetic architecture underlies morphological variation in dogs. *PLOS Biol.* **8**(8): e1000451, 2010.
43. da Fonseca RR, Kosiol C, Vinar T, **Siepel A**, Nielsen R. Positive selection on apoptosis related genes. *FEBS Lett.* **584**(3): 469–476, 2010.
44. Pollard KS, Hubisz MJ, Rosenbloom KR, **Siepel A**. Detection of non-neutral substitution rates on Mammalian phylogenies. *Genome Res.* **20**(1): 110–121, 2010.
45. The MGC Project Team. Temple G, Gerhard DS, Rasooly R, Feingold EA, et al. The completion of the Mammalian Gene Collection (MGC). *Genome Res.* **19**(12): 2324–2333, 2009.
46. 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.
47. 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.
48. 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.

49. 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.
50. Miller W, Rosenbloom K, Hardison RC, Hou M, Taylor J, Raney B, Burhans R, King DC, Baertsch R, Blankenberg D, Kosakovsky P, 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.
51. **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.
52. 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.
53. ENCODE Project Consortium. Birney E, Stamatoyannopoulos JA, Dutta A, Guigo R, Gingeras T, et al. Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. *Nature* **447**(7146): 799–816, 2007.
54. Margulies EH, Cooper GM, Asimenos G, Thomas DJ, Dewey CN, **Siepel A**, Green ED, and Sidow A [42 authors]. Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. *Genome Res.* **17**(6): 760–774, 2007.
55. Rhesus Macaque Genome Sequencing and Analysis Consortium. Gibbs RA, Rogers J, Katze MG, et al. Evolutionary and biomedical insights from the rhesus macaque genome. *Science* **316**(5822): 222–234, 2007.
56. Kuhn RM, Karolchick D, Zweig AS, Trumbower H, Thomas DJ, Thakkapallayil A, Sugnet CW, Stanke M, Smith KE, **Siepel A**, Rosenbloom KR, Rhead B, Raney BJ, Pohl A, Pedersen JS, Hsu F, Hinrichs AS, Harte RA, Diekhans M, Clawson H, Bejerano G, Barber GP, Baertsch R, Haussler D, and Kent WJ. The UCSC genome browser database: update 2007. *Nucleic Acids Res.* **35**: D668–D673, 2007.
57. 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.
58. 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.
59. 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.
60. 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.
61. 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**, Smith KE, Sugnet CW, Sultan-Qurraie A, Thomas DJ, Trumbower H, Weber RJ, Weirauch

- M, Zweig AS, Haussler D, and Kent WJ. The UCSC Genome Browser Database: update 2006. *Nucleic Acids Res.* **34**: D590–598, 2006.
62. **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.
63. 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.
64. 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.
65. ENCODE Project Consortium. The ENCODE (ENCyclopedia Of DNA Elements) Project. *Science* **306**(5696): 636–640, 2004.
66. International Human Genome Sequencing Consortium. Finishing the euchromatic sequence of the human genome. *Nature* **431**: 931–945, 2004.
67. **Siepel A** and Haussler D. Phylogenetic estimation of context-dependent substitution rates by maximum likelihood. *Mol. Biol. Evol.* **21**(3):468–488, 2004.
68. **Siepel A** and Haussler D. Combining phylogenetic and hidden Markov models in biosequence analysis. *J. Comput. Biol.* **11**(2-3): 413–428, 2004.
69. Thomas JW, Touchman JW, Blakesley RW, Bouffard GG, Beckstrom-Sternberg, SM, Margulies EH, Blanchette M, **Siepel AC**, et al [71 authors]. Comparative analyses of multi-species sequences from targeted genomic regions. *Nature* **424**(6950): 788–793, 2003.
70. **Siepel AC**. An algorithm to enumerate sorting reversals for signed permutations. *J. Comput. Biol.* **10**(3-4): 575–597, 2003.
71. **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.
72. **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.
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74. 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.
75. Harger C, Skupski M, Bingham J, Farmer A, Hoisie S, Hrabner 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.
76. 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, et al. The

Genome Sequence DataBase version 1.0 (GSDB): from low pass sequences to complete genomes. *Nucleic Acids Res.* **25**(1): 18–23, 1997.

77. **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

78. 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, 2017.

### Book Chapters and Review Articles

79. **Siepel A**, Arbiza L. Cis-regulatory elements and human evolution. *Curr. Opin. Genet. Dev.* **29C**: 81–89. Review, 2014.
80. **Siepel A**. Phylogenomics of primates and their ancestral populations. *Genome Res.* **19**(11): 1929–1941, 2009.
81. **Siepel A**. Darwinian alchemy: human genes from noncoding DNA. *Genome Res.* **19**(10): 1693–1695, 2009.
82. **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

83. 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 (RECOMB-CG 2009, Budapest, Hungary)*. Lecture Notes in Computer Science, **LNBI 5817**, pp. 150–163. Springer-Verlag, Berlin, Heidelberg, 2009.
84. 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.
85. 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.
86. **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.
87. 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.
88. **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.
89. **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.
90. **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.
91. 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.
92. **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: Spring 2014–2015, Fall 2015–2016.
- 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	Present
12	Yifei	Huang	Postdoc	—	2015	Present
13	Melissa	Hubisz	Grad student, PhD	—	2014	Present
14	Elizabeth	Hutton	Grad student, PhD	—	2015	Present
15	Carolin	Kosiol	Postdoc	C.D. Bustamante	2006	2008
16	Tytus	Mak	Undergrad	—	Spring 2006	Spring 2006
17	Alison	Marklein	Undergrad	—	Summer 2006	Summer 2006
18	Andre L.	Martins	Grad student, PhD	—	2007	2014
19	Jaaved	Mohammed	Grad student, PhD	E. Lai	2009	2016
20	Michael D.	Phillips	Grad student, Masters	E. Lai	2008	2010
21	Lenore	Pipes	Grad student, PhD	C. Mason	2012	Present
22	Joseph	Porter	Undergrad	—	Spring 2012	Spring 2012
23	Matthew	Rasmussen	Postdoc	—	2011	2013
24	Hirak	Sarkar	Summer Intern	—	May 2016	Aug 2016
25	Renee	Setter	Undergrad	—	Summer 2010	Fall 2010
26	Daniel	Sussman	Undergrad	—	Summer 2007	Summer 2008
27	Tomas	Vinar	Postdoc	—	2006	2008

**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 Tipples, 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**

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, “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 20, 2016.

Co-organizer of Measuring and Modeling Quantitative Sequence-function Relationships Meeting (*with Justin B. Kinney and Douglas M. Fowler*), The Banbury Center at Cold Spring Harbor Laboratory, Huntington, NY, July 5-8, 2016.

- Co-organizer of 1st Probabilistic Modeling in Genomics Conference (ProbGen15), *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, *inaugural meeting (with Joe Pickrell and Barbara Engelhardt, et al)*, New York Genome Center, New York, NY, Jan 2015.
- 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
Computational methods for human genomic data integration: demography, selection, and functional potential.	A. Siepel, CSHL	NIH / NIGMS R01 GM102192	1,722,155	1/1/13 – 12/31/17
Factor-general characterization of dynamic transcriptional stress responses.	A. Siepel, CSHL J. Lis, Cornell	NIH / NHGRI R01 HG007070	1,011,632 <i>NCE to 5/31/17</i>	9/1/13 – 5/31/17
Continued development and maintenance of the PHAST software for comparative genomics.	A. Siepel, CSHL	NIH / NHGRI R01 HG008161	576,000	4/24/15 – 1/31/18
New York Center for Collaborative Research in Common Disease Genomics.	R.B. Darnell, NYGC <u>Subawd Co-I:</u> A. Siepel, CSHL	NIH / NHGRI UM1 HG008901	21,557 <i>Subawd only</i>	1/14/16 – 11/30/17
Collaborative Research: NSFDEB–BSF: Quantifying genomic porosity in non-model radiations.	A. Siepel, CSHL I. 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
Packard Fellowship for Science and Engineering in Biological Sciences	A. Siepel, Cornell	David & Lucile Packard Found. 2007–31762	825,000 <i>NCE to 8/31/14</i>	9/1/07 – 8/31/14
Evolutionary genomics and population genetics of pathogenic streptococci.	M. Stanhope, Cornell. <u>Co-I's:</u> A. Siepel, Cornell, C.D. Bustamante, Cornell, R. Burne, U. Florida	NIH / NIAID R01 AI073368	2,252,000	7/1/08 – 6/30/13
Coordinate gene regulation in animal cells. ( <i>Administrative Supplement</i> )	J. Lis, Cornell. <u>Co-I:</u> A. Siepel, Cornell	NIH / NIGMS R01 GM025232	1,137,000	4/1/09 – 3/31/13
What made us human?	K.S. Pollard, Gladstone Institutes, UCSF. <u>Co-I:</u> A. Siepel, Cornell	NIH / NIGMS R01 GM082901	274,000 <i>A. Siepel Subawd only</i>	9/1/08 – 8/31/12
NSF CAREER Award: Models of evolution and discovery of functional elements in mammals and <i>Drosophila</i> .	A. 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 <i>lump sum</i>	2007
Prediction of novel human protein-coding genes using cross-species alignments and phylogenetic hidden Markov models.	D. Haussler, UCSC. <u>Subawd PI:</u> A. Siepel, Cornell	NIH / NCI Subawd 22XS013A	159,000 <i>Subawd only</i>	5/15/06 – 11/14/07

### **Invited Conference and Symposium Lectures**

- Revolutionizing Next-Generation Sequencing (2<sup>nd</sup> Edition) [*Rngs2*], VIB Tools & Technologies Conference, Flanders Meeting & Convention Center, Antwerp, Belgium, March 20-21, 2017.
- Genomics & Systems Biology VII Conference, New York University Abu Dhabi (NYUAD) Campus Conference Center, Saadiyat Island, Abu Dhabi, United Arab Emirates, February 7-9, 2017.
- 66<sup>th</sup> Annual Meeting of the American Society of Human Genetics (ASHG), Vancouver Convention Centre, Vancouver, BC, Canada, October 18-22, 2016.
- 2nd Probabilistic Modeling in Genomics Conference (ProbGen16), Department of Statistics, University of Oxford, UK, September 12-14, 2016.
- ICQG5, 5th International Conference in Quantitative Genetics, Monona Terrace Community and Convention Center, Madison, WI, June 12-17, 2016
- Conference on 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.
- 11<sup>th</sup> [BC]<sup>2</sup> Basel Computational Biology Conference, Basel, Switzerland, July 2013.
- Biology of Genomes Conference, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, May 2013.
- Biology of Genomes Conference, 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.
- Society for Molecular Biology & Evolution (SMBE) Annual Meeting, Iowa City, IA, June 2009.
- 22<sup>nd</sup> Annual Meeting on the Biology of Genomes [*session chair*], Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, May 2009.
- 8<sup>th</sup> Annual Computational Molecular Biology Symposium, Carnegie Mellon University, Pittsburgh, PA, April 2009.
- 10<sup>th</sup> Annual Advances in Genome Biology and Technology (AGBT) Meeting, 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.
- 8<sup>th</sup> International Bioinformatics 2006 Conference, Society for Bioinformatics in the Nordic Countries (SocBIN), Aarhus, Denmark, June 2006.
- 19<sup>th</sup> 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.

Biology of Genomes Conference, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, May 2004.

### **Invited Seminars and Workshops**

Bioinformatics Seminar Series, University of California, Los Angeles, February 27, 2017.

Mathematical Biology Seminar Series, University of Pennsylvania, Philadelphia, PA, January 23, 2017.

Quantitative Biology Seminar Series, University of California, Berkeley, October 5, 2016.

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

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

Campus-wide Lecture Series, “April is Math Awareness Month”, Departments of Mathematical Sciences and Computer Science, Worcester Polytechnic Institute (WPI), Worcester, MA, April 2016.

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

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

Biostatistics and Medical Informatics (BMI) Seminar Series, University of Wisconsin-Madison, Madison, WI, September 2015.

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

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

Paleobiology Seminar Series, Department of Anatomical Sciences, Stony Brook University School of Medicine, Stony Brook, NY, April 2015.

Workshop: From Genome Function to Biomedical Insight: ENCODE and Beyond, *organized by the National Human Genome Research Institute (NHGRI)*, Natcher Conference Center, NIH Campus, Bethesda, MD, March 2015.

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.

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

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

Organismic and Evolutionary Biology (OEB) Seminar Series, College of Natural Sciences, University of Massachusetts, Amherst, MA, September 2014.

Institute for Computational Biomedicine (ICB) Seminar Series, Weill Cornell Medical College of Cornell University, New York, NY, September 2014.

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

Institut de Biologie Computationnelle (IBC), Université Montpellier 2, Montpellier, France, June 2014.

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

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

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

Invited Seminar: Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, December 2013.

Department of Human Genetics, University of Chicago, Chicago, IL, November 2013.

Center for Bioinformatics Research, School of Informatics and Computing, Indiana University, Bloomington, IN, September 2013.

Wellcome Trust Centre for Human Genetics, University of Oxford, England, UK, May 2013.

Cambridge Statistics Initiative (CSI) One-day Meeting 2013, Centre for Mathematical Sciences (CMS), University of Cambridge, England, UK, April 2013.

Workshop: Biological Sequence Analysis and Probabilistic Models (*organized by A. Siepel, K. Pollard, and S. Eddy*), Janelia Farm Research Campus, Ashburn, VA, March 2013.

European Bioinformatics Institute (EBI), European Molecular Biology Laboratory (EMBL), Hinxton, England, UK, February 2013.

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

Universite Claude Bernard Lyon 1 (UCBL), Villeurbanne, Lyon, France, January 2013.

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

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

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

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

Evolutionary Studies (EvoS) Program Seminar Series, Binghamton University, State University of New York (SUNY), Binghamton, NY, December 2011.

Evolutionary Genomics Seminar Series, Phyloseminar.org (*online phylogenetics seminar*), 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, 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.

Center for Algorithmic and Systems Biology (CASB) Meeting of twenty leading experts in bioinformatics (CASB-20), University of California, San Diego, CA, May 2010.

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

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



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

Bioinformatics Seminar Series, University of California, Los Angeles, CA, January 2010.

National Human Genome Research Institute (NHGRI), Bethesda, MD, March 2009.

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

NIH Mammalian Gene Collection (MGC) Program, External Steering Committee Meeting (*final meeting*), National Institutes of Health (NIH), Rockville, MD, September 2008.

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

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

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

Evolutionary Genetics Seminar Series, University of California, Davis, CA, May 2008.

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

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

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

Microsoft Research, Redmond, WA, March 2008.

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

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

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

Workshop: Synthesizing Computational Resources for Cis-regulatory Molecular Evolution, National Evolutionary Synthesis Center (NESCent), Durham, NC, March 2007.

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

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

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

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

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

Entomology Seminar Series, College of Agriculture and Life Sciences, Cornell University, Ithaca, NY, January 2006.

Biochemistry and Molecular Biology (BMB) Seminar Series, Pennsylvania State University, University Park, PA, April 2005.

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

Department of Computer Science, University of California, Berkeley, CA, February 2005.

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

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

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

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