

## **Katherine S. Pollard**

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### **Education**

**University of California**, Berkeley, CA. M.A. and Ph.D. in Biostatistics. 1998 – 2003.

**Watson Fellowship**, “Sudden Infant Death Syndrome in three socio-political contexts: New Zealand, Indonesia, and Australia.” 1995 – 1996.

**Johns Hopkins School of Public Health**: Summer Graduate Program in Epidemiology, Baltimore, MD. 1995.

**Pomona College**, Claremont, CA. B.A. *Summa Cum Laude* in Anthropology and Mathematics. 1991 – 1995.

**Mills Summer Math Institute**, Berkeley, CA. 1994.

### **Employment**

**Associate Investigator & Associate Professor**. Gladstone Institutes, Institute for Human Genetics & Div. of Biostatistics, University of California, San Francisco, CA. 2008-present.

**Assistant Professor**. Genome Center & Dept. of Statistics, University of California, Davis, CA. 2005-2008.

**Postdoctoral Researcher**. Dept. of Biomolecular Engineering, University of California, Santa Cruz, CA. *Mentors*: David Haussler & Todd Lowe. 2003-2005.

**Postdoctoral Research Assistant**. Div. of Biostatistics, University of California, Berkeley, CA. *Mentor*: Sandrine Dudoit. 2003.

**Graduate Student Researcher**. Div. of Biostatistics, University of California, Berkeley, CA. *Mentor*: Mark van der Laan. 2000-2003.

**Summer Intern**. Microarrays Group, Chiron Corporation, Emeryville, CA. 2000.

**Summer Intern**. Clinical Trials Group, Chiron Corporation, Emeryville, CA. 1999.

**Research Assistant**. Dept. of Child Health, University of Bristol, UK. 1996-1998.

**Research Consultant**. Guy’s and St. Thomas’ United Medical and Dental Schools, London, UK. 1997.

**Research Officer**. Dept. of Child Health, University of Queensland, Australia. 1996.

**Project Coordinator**. Maori SIDS Prevention Team, University of Auckland, New Zealand. 1995.

**Research Assistant**. Dept. of Anthropology, Pomona College, Claremont, CA. 1994-1995.

## Honors & Awards

**Sophomore Math Prize**, Pomona College, Claremont, CA. 1993.

**Valedictorian, High Scholarship Prize (4.0 GPA), Math Prize, Anthropology Prize, Phi Beta Kappa Award**, Pomona College, Claremont, CA. 1995.

**Thomas J. Watson Fellowship**, Watson Foundation. 1995-1996.

**Berkeley Fellowship**, University of California, Berkeley, CA. 1998-2000.

**Evelyn Fix Memorial Prize, Chin Long Chiang Biostatistics Student of the Year**, University of California, Berkeley, CA. 2003.

**Faculty Development Award**, University of California, Davis, CA. 2007.

**Sloan Research Fellowship**, Alfred P. Sloan Foundation. 2008-2010.

## Teaching Experience

**Associate Professor**. September, 2008 – present.

University of California, Division of Biostatistics, San Francisco, CA.

- Bioinformatics & Computational Biology
- Statistical Methods for Array & Sequence Data
- Statistical Methods in Bioinformatics: Case Studies
- Quantitative Biology Seminar

**Assistant Professor**. November, 2005 – June, 2008.

University of California, Department of Statistics, Davis, CA.

- Elementary Statistics
- Categorical Data Analysis
- Statistical Methods for Bioinformatics
- Biostatistics Seminar

**Workshop Instructor**. August, 2003 – present.

- R/Bioconductor software
- DNA Microarrays
- Design of experiments
- Statistical analysis

## Professional Memberships

**American Statistical Association**. 2002-present.

**International Society for Computational Biology**. 2005-present.

**American Society of Human Genetics**. 2012-present.

## Publications

1. K. Linblad-Toh, M. Garber, O. Zuk, B.J. Parker, S. Washieti, P. Kheradpour, J. Ernst, G. Jordan, E. Maucell, L.D. Ward, C.B. Lowe, A.K. Holloway, ... (46 others), K.S. Pollard, J.S. Pedersen, E.S. Lander, M. Kellis (2011). *A high-resolution map of human evolutionary constraint using 29 mammals*, Nature, 478: 476-482.
2. S.W. Kembel, J.A. Eisen, K.S. Pollard, J.L. Green (2011). *The phylogenetic diversity of metagenomes*, PLoS ONE, 6(8): e23214.
3. J.C. Roach, G. Glusman, R. Hubley, S.Z. Montsaroff, A.K. Holloway, D.E. Mauldin, D. Srivastava, W. Garg, K.S. Pollard, D.J. Galas, L. Hood, A.F.A. Smit (2011). *Chromosomal haplotypes by genetic phasing of human families*, The American Journal of Human Genetics, 89: 1-16.
4. S. Katzman, J.A. Capra, D. Haussler, K.S. Pollard (2011). *Ongoing GC-biased evolution is widespread in the human genome and enriched near recombination hotspots*, Genome Biology and Evolution, 3: 614-626.
5. M.D. Hirschey, T. Shimazu, J.A. Capra, K.S. Pollard, E. Verdin (2011). *SIRT1 and SIRT3 deacetylate homologous substrates: AceCSI,2 and HMGCSI,2*, Aging, 3(6): 635-642.
6. J.A. Capra, K.S. Pollard, (2011). *GC-biased in divergent sequences across the metazoans*, Genome Biology and Evolution, 3: 516-527.
7. N. Lambert, M. Lambot, A. Bilheu, V. Albert, Y. Englert, F. Libert, J. Noel, C. Sotiriou, A.K. Holloway, K.S. Pollard, V. Detours, P. Vanderhaeghen (2011). *Genes expressed in specific areas of the human fetal cerebral cortex display distinct patterns of evolution*, PLoS ONE, 6(3): e17753.
8. M.J. Hubisz, K.S. Pollard, A. Siepel (2011). *PHAST and RPHAST: phylogenetic analysis with space/time models*, Briefings in Bioinformatics, 12(1): 41-51.
9. J.K. Takeuchi, X. Lou, J.M. Alexander, H. Sugizaki, P. Delgado-Olguín, A.K. Holloway, A.D. Mori, J.N. Wylie, C. Munson, Y. Zhu, Y.Q. Zhou, R.F. Yeh, R.M. Henkelman, R.P. Harvey, D. Metzger, P. Chambon, D.Y.R. Stainier, K.S. Pollard, I.C. Scott, B.G. Bruneau (2011). *Chromatin remodeling complex dosage modulates transcription factor function in heart development*, Nature Communications, 2: article 187.
10. T.J. Sharpton, S.J. Riesenfeld, S.W. Kembel, J. Ladau, J.P. O'Dwyer, J.L. Green, J.A. Eisen, K.S. Pollard (2011). *PhylOTU: a high-throughput procedure quantifies microbial community diversity and resolves novel taxa from metagenomic data*, PLoS Computational Biology, 7(1): e1001061.
11. J.A. Capra, K.S. Pollard, M. Singh (2010). *Novel genes exhibit distinct patterns of function acquisition and network integration*, Genome Biology, 11: R127.
12. D.I. Ritter, Q. Li, D. Kostka, K.S. Pollard, S. Guo, J.H. Chuang (2010). *The importance of being cis: Evolution of orthologous fish and mammalian enhancer activity*, Molecular Biology and Evolution, 27(10): 2322-2332.
13. D. Kostka, M.W. Hahn, K.S. Pollard (2010). *Non-coding sequences near duplicated genes evolve rapidly*, Genome Biology and Evolution, 2: 518-533.

14. S. Katzman, A.D. Kern, K.S. Pollard, S.R. Salama, D. Haussler (2010). *GC-biased evolution near human accelerated regions*, PLoS Genetics, 6(5): e1000960.
15. S.L. Taylor, K.S. Pollard (2010). *Composite interval mapping to identify quantitative trait loci for point-mass mixture phenotypes*, Genetics Research, 92: 39-53.
16. K.S. Pollard, M.J. Hubisz, K.R. Rosenbloom, A. Siepel (2009). *Detection of non-neutral substitution rates on mammalian phylogenies*, Genome Research, 20: 110-121.
17. F. Hsieh, S.-C. Chen, K.S. Pollard (2009). *A nearly exhaustive search for CpG islands on whole chromosomes*, The International Journal of Biostatistics, 5(1): article 14.
18. D.G. Lemay, D.J. Lynn, W.F. Martin, M.C. Neville, T.M. Casey, G. Rincon, E.V. Kriventseva, W.C. Barris, A.S. Hinrichs, A.J. Molenaar, K.S. Pollard, N.J. Maqbool, K. Singh, R. Murney, E.M. Zdobnov, R.L. Tellam, J.F. Medrano, J.B. German, M. Rijnkels (2009). *The bovine lactation genome: insights into the evolution of mammalian milk*, Genome Biology, 10:R43.
19. K.S. Pollard (2009). *What makes us human?* Scientific American, May: 44-49 (cover story).
20. J. Berglund, K.S. Pollard, M.T. Webster (2009). *Hotspots of biased nucleotide substitutions in human genes*, PLoS Biology, 7(1): e1000026.
21. S.L. Taylor, K.S. Pollard (2009). *Hypothesis tests for point-mass mixture data with application to omics data with many zero values*, Statistical Applications in Genetics and Molecular Biology, 8(1): article 8.
22. A.E. Cozen, M.T. Weirauch, K.S. Pollard, D.L. Bernick, J.M. Stuart, T.M. Lowe (2009). *Transcriptional map of respiratory versatility in the hyperthermophilic crenarchaeon Pyrobaculum aerophilum*, Journal of Bacteriology, 191(3): 782-794.
23. K.S. Pollard, M.J. van der Laan (2008). *Supervised distance matrices*, Statistical Applications in Genetics and Molecular Biology, 7(1): article 33.
24. W.L. Walker, I.H. Liao, D.L. Gilbert, B. Wong, K.S. Pollard, C.E. McCulloch, L. Lit, F.R. Sharp (2008). *Empirical Bayes accommodation of batch-effects in microarray data using identical replicate reference samples: Application to RNA expression profiling of blood from Duchenne muscular dystrophy patients*, BMC Genomics, 9: 494.
25. A.K. Holloway, D.J. Begun, A. Siepel, K.S. Pollard (2008). *Accelerated sequence divergence of conserved genomic elements in Drosophila melanogaster*, Genome Research, 18: 1592-1601.
26. S.L. Taylor, K.S. Pollard (2008). *Evaluation of two methods to estimate and monitor bird populations*, PLoS ONE, 3(8): e3047.
27. K.S. Pollard, D. Serre, X. Wang, H. Tao, E. Grundberg, T.J. Hudson, A.G. Clark, K. Frazer (2008). *A genome-wide approach to indentifying novel-imprinted genes*, Human Genetics, 122(6): 625-634.
28. S.L. Taylor, D. Temple Lang, K.S. Pollard (2007). *Improvements to the multiple testing package multtest*, R News 7(3): 52-55.
29. D.G. Lemay, M.C. Neville, M.C. Rudolph, K.S. Pollard, J.B. German (2007). *Gene regulatory networks in lactation: identification of global principles using bioinformatics*, BMC Systems Biology, 1: 56.

30. T.R. Dreszer, G.D. Wall, D. Haussler, K.S. Pollard (2007). *Biased clustered substitutions in the human genome: the footprints of male driven biased gene conversion*, Genome Research, 17: 1420-1430.
31. T.R. Magalhaes, J. Palmer, P. Tomancak, K.S. Pollard (2007). *Transcriptional control in embryonic Drosophila midline guidance assessed through a whole genome approach*, BMC Neuroscience, 8: 59.
32. K.S. Pollard, S.R. Salama, B. King, A.D. Kern, T. Dreszer, S. Katzman, A. Siepel, J.S. Pedersen, G. Bejerano, R. Baertsch, K.R. Rosenbloom, J. Kent, D. Haussler (2006). *Forces shaping the fastest evolving regions in the human genome*, PLoS Genetics, 2(10): e168.
33. K.S. Pollard, S.R. Salama, N. Lambert, M.A. Lambot, S. Coppens, J.S. Pedersen, S. Katzman, B. King, C. Onodera, A. Siepel, A.D. Kern, C. Dehay, H. Igel, M. Ares, Jr., P. Vanderhaeghen, D. Haussler (2006). *An RNA gene expressed during cortical development evolved rapidly in humans*, Nature, 443: 167-172.
34. A. Siepel, K.S. Pollard, D. Haussler (2006). *New methods for detecting lineage-specific selection*, Proceedings of the 10th International Conference on Research in Computational Molecular Biology: 190-205.
35. K.L. Schneider, K.S. Pollard, R. Baertsch, A. Pohl, T.M. Lowe (2006). *The UCSC Archaeal Genome Browser*, Nucleic Acids Research; 34, Database issue: D407-D410.
36. The Chimpanzee Sequencing and Analysis Consortium (2005). *Initial sequence of the chimpanzee genome and comparison with the human genome*. Nature, 437: 69-87.
37. N.G. Salomonis, N. Cotte, A.C. Zamboni, K.S. Pollard, K. Vranizan, S.W. Doniger, G. Dolganov, B.R. Conklin (2005). *Identifying genetic networks underlying myometrial transition to labor*. Genome Biology, 6: R12.
38. K.S. Pollard, S. Dudoit, M.J. van der Laan (2005). *Multiple Testing Procedures: R multtest Package and Applications to Genomics in Bioinformatics and Computational Biology Solutions Using R and Bioconductor*, R. Gentleman, V. Carey, W. Huber, R. Irizarry, S. Dudoit (Editors). Springer (Statistics for Biology and Health Series), pp. 251-272.
39. K.S. Pollard, M.J. van der Laan (2005). *Cluster Analysis of Genomic Data in Bioinformatics and Computational Biology Solutions Using R and Bioconductor*, R. Gentleman, V. Carey, W. Huber, R. Irizarry, S. Dudoit (Editors). Springer (Statistics for Biology and Health Series), pp. 209-229.
40. K.S. Pollard, M.D. Birkner, S. Dudoit, M.J. van der Laan (2005). *Test statistics null distributions in multiple testing: simulation studies and applications to genomics*. Numéro double spécial Statistique et Biopuces, Journal de la Société Française de Statistique, Vol. 146(1-2): 77-115.
41. M.D. Birkner, K.S. Pollard, S. Dudoit, M.J. van der Laan (2005). *Multiple testing procedures and applications to genomics*. U.C. Berkeley Division of Biostatistics Working Paper Series. Working Paper 168.
42. M.J. van der Laan, S. Dudoit, K.S. Pollard (2004). *Augmentation procedures for control of the generalized family-wise error rate and tail probabilities for the proportion of false positives*. Statistical Applications in Genetics and Molecular Biology, 3(1): article 15.

43. M.J. van der Laan, S. Dudoit, K.S. Pollard (2004). *Multiple testing. Part II. Step-down procedures for control of the family-wise error rate*. *Statistical Applications in Genetics and Molecular Biology*, 3(1): article 14.
44. S. Dudoit, M.J. van der Laan, K.S. Pollard (2004). *Multiple testing. Part I. Single-step procedures for control of general type I error rates*. *Statistical Applications in Genetics and Molecular Biology*, 3(1): article 13.
45. K.S. Pollard, M.J. van der Laan (2004). *Choice of null distribution in resampling-based multiple testing*. *Journal of Statistical Planning and Inference*, 125: 85-100.
46. M.J. van der Laan, K.S. Pollard, J. Bryan (2003). *A new partitioning around medoids algorithm*. *Journal of Statistical Computation and Simulation*, 73(8): 575-584.
47. K.S. Pollard, M.J. van der Laan (2003). *Multiple testing for gene expression data: an investigation of null distributions with consequences for the permutation test*. *Proceedings of the 2003 International MultiConference in Computer Science and Engineering, METMBS'03 Conference*: 3-9.
48. K.S. Pollard, M.J. van der Laan (2002). *Resampling-based multiple testing: Asymptotic control of type I error and applications to gene expression data*. U.C. Berkeley Division of Biostatistics Working Paper Series. Working Paper 121.
49. K.S. Pollard, M.J. van der Laan (2002). *New methods for identifying significant clusters in gene expression data*. 2002 Proceedings of the American Statistical Association, Biometrics Section.
50. K.S. Pollard, M.J. van der Laan (2002). *A method to identify significant clusters in gene expression data*. *Proceedings of SCI 2002, Vol. II*: 318-325.
51. K.S. Pollard, M.J. van der Laan (2002). *Statistical inference for simultaneous clustering of gene expression data*, in **Nonlinear Estimation and Classification**, D.D. Denison, M.H. Hansen, C. Holmes, B. Mallick, B. Yu (Editors). Springer-Verlag, pp. 305-320.
52. J. Bryan, K.S. Pollard, M.J. van der Laan (2002). *Paired and unpaired comparison and clustering with gene expression data*. *Statistica Sinica*, 12(1): 87-110.
53. K.S. Pollard, M.J. van der Laan (2002). *Statistical inference for simultaneous clustering of gene expression data*. *Mathematical Biosciences*, 176(1): 99-121.
54. M.J. van der Laan, K.S. Pollard (2001). *Hybrid clustering of gene expression data with visualization and the bootstrap*. *Journal of Statistical Planning and Inference*, 2003, 117: 275-303.
55. E.A.S Nelson, B.J. Taylor, ICCPS Study Group (2001). *International child care practices study: infant sleep position and parental smoking*. *Early Human Development*, 64: 7-20.
56. E.A.S. Nelson, B.J. Taylor, ICCPS Study Group (2001). *International child care practices study: infant sleep environment*. *Early Human Development*, 62: 43-55.
57. K.S. Pollard, P.J. Fleming, J. Young, A. Sawczenko, P. Blair (1999). *Night-time non-nutritive sucking in infants aged 1 to 5 months: relationship with infant state, breastfeeding, and bed- versus room-sharing*. *Early Human Development*, 56(2-3):185-204.
58. P.J. Fleming, P. Blair, K.S. Pollard, M.W. Platt, C. Leach, I. Smith, P.J. Berry, J. Golding (1999). *Pacifier use and sudden infant death syndrome: results from the CESDI/SUDI case control study*. *Archives of Disease in Childhood*, 81(2): 112-116.

59. ICCPS Study Group, E.A.S. Nelson, B.J. Taylor (1999). *International child care practices study: methods and study population*. Early Human Development, 55: 149-168.
60. K.S. Pollard, D. Armstrong, J. Bartholomew (1997). *Assessing the impact of redevelopment on the health status of Liddle Ward*. Report prepared for the Lambeth, Southwark and Lewisham Health Authority.
61. K.S. Pollard, C. Leach, P. Blair, A. Sawczenko, J. Young, P.J. Fleming (1997). *Does failure to use a soother increase the risk of SIDS? Epidemiological and physiological studies*. Pediatric Pulmonology, 24(6): 451.

## Software Projects

### Statistical Programming

Clustering Algorithms

*hopach*

<http://cran.fhcrc.org/web/packages/hopach/index.html>

*pamsil*

<http://docpollard.org/pamsil.tar.gz>

Multiple Hypothesis Testing Procedures

*multtest*

<http://cran.fhcrc.org/web/packages/multtest/index.html>

### Genome Browsers

<http://genome.ucsc.edu/>

<http://archaea.ucsc.edu/>

### Comparative Genomics

Phylogenetic Analysis with Space/Time Models (PHAST)

<http://compgen.bscb.cornell.edu/phast/>

<http://cran.r-project.org/web/packages/rphast/index.html>

### Metagenomics

Operational Taxonomic Units

*PhylOTU*

<https://github.com/sharpton/PhylOTU>

Simulations

*MetaPASSAGE*

<https://github.com/sriesenfeld/MetaPASSAGE>

## Grants

### Active

NIH R01

*What made us human?*

Role: PI (Adam Siepel, co-PI)

2008-2012

\$864,000 \*

NSF/DMS

*Exploring the niche space of human microbiome functions through convex geometry and evolutionary genomics*

Role: PI

2011-2013

\$789,809

NIH U01

*The epigenetic landscape of heart development*

Role: PI (jointly with Benoit Bruneau, Bruce Conklin, Deepak Srivastava, Shinya Yamanaka, and Laurie Boyer)

2009-2014

\$4,429,581

### Completed

Gordon & Betty Moore Foundation

*Integrating evolutionary, ecological and statistical approaches to metagenomics*

Role: PI (jointly with Jonathan Eisen and Jessica Green)

2008-2012

\$1,791,500

Sloan Research Fellowship in Computational & Evolutionary Molecular Biology

Role: PI

2009-2010

\$45,000

UCSF Program for Breakthrough Biomedical Research (PBBR) Integrative Research Award

*In vivo characterization of the vertebrate regulatory code*

Role: PI (jointly with Nadav Ahituv)

2009-2010

\$197,387

UC Davis Faculty Development Award

Role: PI

2007-2008

\$16,000

NIH Individual National Research Service Award

*Defining the Topography of Gene Expression (#1 F32 GM070249-01)*

Role: PI (Postdoctoral Fellow)

2003-2005  
\$39,700

University of California Discovery Grant  
*Computationally Intensive Statistical Inference for Microarray Based Drug Discovery* (#LSI00-10050)  
Role: Graduate student researcher (PI: Mark J. van der Laan)  
2001-2003  
\$334,000

\* Dollar amounts are total direct costs for the funding period.