

## **Katherine S. Pollard**

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### **Education**

**University of California**, Berkeley, CA. 1998 – 2003.

- M.A. (2000) and Ph.D. (2003) in Biostatistics.
- Honors: Berkeley Fellowship, Evelyn Fix Memorial Prize, Chin Long Chiang Biostatistics Student of the Year (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. 1991 – 1995.

- Double major: Anthropology and Mathematics, B.A. Summa Cum Laude (1995).
- Honors: Valedictorian (4.0 GPA), High Scholarship Prize, Phi Beta Kappa Award, Sigma Xi Scientific Society, Pomona College Scholar, Math Department Prize, Anthropology Department Prize, Sophomore Math Prize.

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

### **Employment**

**Associate Investigator & Associate Professor**. August, 2008 – present.  
University of California, Gladstone Institutes & Div. of Biostatistics, San Francisco, CA.

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

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

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

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

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

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

**Research Assistant.** November, 1996 – May, 1997, September, 1997 – May, 1998.  
University of Bristol Department of Child Health, Bristol, UK.

**Research Consultant.** April, 1997 – June, 1997.  
Guy's and St. Thomas' United Medical and Dental Schools, London, UK.

**Research Officer.** April – June, 1996.  
University of Queensland Department of Child Health, Australia.

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

**Research Assistant.** 1994 – 1995.  
Pomona College Anthropology Department, Claremont, CA.

## 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

## Publications

Pollard KS, Hubisz MJ, Rosenbloom KR, Siepel A (2009). *Detection of non-neutral substitution rates on mammalian phylogenies*, Genome Research, 20: 110-121.

Hsieh F, Chen S-C, Pollard KS (2009). *A nearly exhaustive search for CpG islands on whole chromosomes*, The International Journal of Biostatistics, 5(1): article 14.

Lemay DG, Lynn DJ, Martin WF, Neville MC, Casey TM, Rincon G, Kriventseva EV, Barris WC, Hinrichs AS, Molenaar AJ, Pollard KS, Maqbool NJ, Singh K, Murney R, Zdobnov EM, Tellam RL, Medrano JF, German JB, Rijnkels M (2009). *The bovine lactation genome: insights into the evolution of mammalian milk*, Genome Biology, 10: R43.

Pollard KS (2009). *What makes us human?* Scientific American, May: 44-49.

Berglund J, Pollard KS, Webster MT (2009). *Hotspots of biased nucleotide substitutions in human genes*, PLoS Biology, 7(1): e1000026.

Cozen AE, Weirauch MT, Pollard KS, Bernick DL, Stuart JM, Lowe TM (2009). *Transcriptional map of respiratory versatility in the hyperthermophilic crenarchaeon Pyrobaculum aerophilum*, Journal of Bacteriology, 191(3): 782-794.

Pollard KS, van der Laan MJ (2008). *Supervised distance matrices*, Statistical Applications in Genetics and Molecular Biology, 7(1): article 33.

Walker WL, Liao IH, Gilbert DL, Wong B, Pollard KS, McCulloch CE, Lit L, Sharp FR (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.

Holloway AK, Begun DJ, Siepel AC, Pollard KS (2008). *Accelerated sequence divergence of conserved genomic elements in Drosophila melanogaster*, Genome Research, 18: 1592-1601.

Taylor SL, Pollard KS (2008). *Evaluation of two methods to estimate and monitor bird populations*, PLoS ONE, 3(8): e3047.

Pollard KS, Serre D, Wang X, Tao H, Grundberg E, Hudson TJ, Clark AG, Frazer KA (2008). *A genome-wide approach to identifying novel human imprinted genes*, Human Genetics, 122(6): 625-634.

Taylor SL, Temple Lang D, Pollard KS (2007). *Improvements to the multiple testing package multtest*. R News, 7(3): 52-55.

Lemay DG, Neville MC, Rudolph MC, Pollard KS, German JB (2007). *Gene regulatory networks in lactation: identification of global principles using bioinformatics*, BMC Systems Biology, 1: 56.

Dreszer TR, Wall GD, Haussler D, Pollard KS (2007). *Biased clustered substitutions in the human genome: the footprints of male driven biased gene conversion*, Genome Research, 17: 1420-1430.

Magalhaes TR, Palmer J, Tomancak P, Pollard KS (2007). *Transcriptional control in embryonic Drosophila midline guidance assessed through a whole genome approach*, BMC Neuroscience, 8: 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, Haussler D (2006). *Forces shaping the fastest evolving regions in the human genome*, PLoS Genetics, 2(10).

Pollard KS, Salama SR, Lambert N, Lambot MA, Coppens S, Pedersen JS, Katzman S, King B, Onodera C, Siepel A, Kern AD, Dehay C, Igel H, Ares M Jr., Vanderhaeghen P, Haussler D (2006). *An RNA gene expressed during cortical development evolved rapidly in humans*, Nature, 443: 167-172.

Siepel A, Pollard KS, Haussler D (2006). *New methods for detecting lineage-specific selection*, Proceedings of the 10th International Conference on Research in Computational Molecular Biology: 109-205.

Schneider KL, Pollard KS, Baertsch R, Pohl A, Lowe TM (2006). *The UCSC Archaeal Genome Browser*, Nucleic Acids Research, 34, Database issue: D407–D410.

The Chimpanzee Sequencing and Analysis Consortium (2005). *Initial sequence of the chimpanzee genome and comparison with the human genome*, Nature, 437: 69-97.

Salomonis NG, Cotte N, Zambon AC, Pollard KS, Vranizan K, Doniger SW, Dolganov G, Conklin BR (2005). *Identifying genetic networks underlying myometrial transition to labor*, Genome Biology, 6:R12.

Pollard KS, Birkner MD, Dudoit S, van der Laan MJ (2005). *Test statistics null distributions in multiple testing: simulation studies and applications to genomics*. Journal de la Société Française de Statistique, 146 (1-2), Numéro double spécial Statistique et Biopuces: 77-115.

Pollard KS, van der Laan MJ (2005). *Cluster analysis of genomic data with applications in R*, in Bioinformatics and Computational Biology Solutions Using R and Bioconductor. Gentleman R, Carey V, Huber W, Irizarry R, Dudoit S (Editors). Springer (Statistics for Biology and Health Series): 209-229.

Pollard KS, Dudoit S, van der Laan MJ (2005). *Multiple testing procedures and applications to genomics*, in Bioinformatics and Computational Biology Solutions Using R and Bioconductor. Gentleman R, Carey V, Huber W, Irizarry R, Dudoit S (Editors). Springer(Statistics for Biology and Health Series): 251-272.

van der Laan MJ, Dudoit S, Pollard KS (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.

van der Laan MJ, Dudoit S, Pollard KS (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.

Dudoit S, van der Laan MJ, Pollard KS (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.

Pollard KS, van der Laan MJ (2004). *Choice of a null distribution in resampling-based multiple testing*, *Journal of Statistical Planning and Inference*, 125, Special issue for the Third International Conference on Multiple Comparisons: 85-100.

van der Laan MJ, Pollard KS (2003). *A new algorithm for hybrid hierarchical clustering with visualization and the bootstrap*. *Journal of Statistical Planning and Inference*, 117: 275-303.

Pollard KS, van der Laan MJ (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.

van der Laan MJ, Pollard KS, Bryan J (2003). *A new partitioning around medoids algorithm*. *Journal of Statistical Computation and Simulation*, 73(8): 575-584.

Pollard KS, van der Laan MJ (2003). *Statistical inference for two-way clustering of gene expression data*, in *Nonlinear Estimation and Classification*. Denison DD, Hansen MH, Holmes C, Mallick B, Yu B (Editors). Springer Verlag: 305-320.

Pollard KS, van der Laan MJ (2002). *New methods for identifying significant clusters in gene expression data*. *Proceedings of JSM 2002, Biometrics Section*.

Pollard KS, van der Laan MJ (2002). *A method to identify significant clusters in gene expression data*. *Proceedings of SCI 2002, Volume II*: 318-325.

Pollard KS, van der Laan MJ (2002). *Statistical inference for two-way clustering of gene expression data*. *Mathematical Biosciences*, 176(1): 99-121.

Bryan J, Pollard KS, van der Laan MJ (2002). *Paired and unpaired comparison and clustering with gene expression data*. *Statistica Sinica*, 12(1): 87-110.

Nelson EAS, Taylor BJ, ICCPS Study Group (2001). *International child care practices study: infant sleep position and parental smoking*. *Early Human Development*, 64: 7-20.

Nelson EAS, Taylor BJ, ICCPS Study Group (2001). *International child care practices study: infant sleep environment*. *Early Human Development*, 62: 43-55.

Pollard K, Fleming P, Young J, Sawczenko A, Blair P (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.

Fleming PJ, Blair P, Pollard K, Platt MW, Leach C, Smith I, Berry PJ, Golding, J (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.

ICCPS Study Group, Nelson EAS, Taylor BJ (1999). *International child care practices study: methods and study population*. Early Human Development, 55: 149-168.

Pollard KS, Armstrong D, Bartholomew J (1997). *Assessing the impact of redevelopment on the health status of Liddle Ward*. Report prepared for the Lambeth, Southwark and Lewisham Health Authority.

Pollard KS, Leach C, Blair P, Sawczenko A, Young J, Fleming PJ (1997). *Does failure to use a soother increase the risk of SIDS? Epidemiological and physiological studies*. Pediatric Pulmonology, 24(6): 451.

## Software Projects

PAMSIL (stand alone C program)

R/Bioconductor Packages: *hopach* and *multtest*

<http://www.bioconductor.org/>

<http://www.r-project.org/>

UCSC Genome Browsers

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

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

## Grants

### Active

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 \*

NIH R01

*What made us human?*

Role: PI (Adam Siepel, co-PI)

2008-2012

\$864,000

Gordon & Betty Moore Foundation

*Integrating evolutionary, ecological and statistical approaches to metagenomics*

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

2008-2011

\$1,791,500

Sloan Research Fellowship in Computational & Evolutionary Molecular Biology

Role: PI

2009-2011

\$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

### Completed

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: 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.