

Noah Spies

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and

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Education

- 2012–
present **Stanford University School of Medicine**
Postdoctoral associate
Laboratory of Prof. Arend Sidow, Departments of Pathology and Genetics
Research focus: *evolution of structural variation*
Co-advised (since 2014) by Dr. Marc Salit, NIST
- 2006–2012 **Massachusetts Institute of Technology**
Ph.D. in Biology, June 2012
Jointly advised by Profs. David P. Bartel and Christopher B. Burge
Thesis: *Cross-regulation and interaction between eukaryotic gene regulatory processes*
- 2002–2006 **Cornell University**
Bachelor of Arts, May 2006
Cum laude in Mathematics, with a concentration in Computer Science
Cumulative GPA: 3.77

Awards

- 2016 **Best Talk Award, ISMB HiTSeq Conference**
Awarded best talk at HiTSeq, a special interest group of the ISMB conference (annual meeting of the International Society for Computational Biology) for presentation of Genome-wide Reconstruction of Complex Structural Variants using Read Clouds
- 2014–2016 **NRC/NIST Postdoctoral Fellowship**
Awarded competitive postdoctoral fellowship by the National Research Council and the National Institute of Standards and Technology for work in genomics
- 2013 **Stanford CEHG Trainee Grant**
Awarded competitive \$15,000 trainee research grant by the Stanford Center for Computational, Evolutionary and Human Genomics
- 2008 **Teresa Keng Graduate Teaching Prize**
Awarded by the MIT Biology Department for excellence in teaching 7.57: Quantitative Biology for Graduate Students

Other Research Experience

- 2004–2006 **Steve Zinder Lab, NSF Microbial Observatory, Cornell University (Ithaca, NY)**
Developed methods to characterize populations of homoacetogenic bacteria
- 2001–2002 **Karl Schmid Group, Max Planck Institute for Chemical Ecology (Jena, Germany)**
Bioinformatics internship in plant population genetics (8 months)

Teaching

- Jan 2010, 2011, 2012 **Quantitative biology workshop, MIT**
Developed and led mini-course on biostatistics with R for minority undergraduates and faculty
- 2010 **Teaching Assistant, 7.02: Introduction to Experimental Biology, MIT**
Graduate Teaching Assistant for introductory biology laboratory course for MIT undergraduates
- 2008 **Teaching Assistant, 7.57: Quantitative Biology, MIT**
Graduate Teaching Assistant for quantitative biology course for first-year graduate biology students, covering statistics, sequence analysis and systems biology
- 2005 **Computer Science 381/481 Teaching Assistant, Cornell University**
Undergraduate Teaching Assistant for (honors) theory of computing course

Service

- 2015–present **Geneticists for Diversity in Science (GDS) Volunteer**
Organize mentoring and networking events for students and postdocs in the biosciences
- 2012–2015 **49ers Academy Volunteer**
Help teach science lab classes to at-risk middle-school students in East Palo Alto charter school as part of a Stanford program
- 2010–present **Contributor to open source software**
Active member of online open source community, authoring svviz, a read visualizer for structural variants; and contributing bug reports, fixes and improvements to data science and bioinformatics tools, including freebayes, pandas and pysam
- 2010–2011 **Executive Committee, MIT Science Policy Initiative**
Helped run graduate student organization dedicated to improving engagement between scientists, engineers and policymakers, with annual budget of over \$10,000

Publications

* indicates equal author contribution

† corresponding author

- Spies N**, Weng Z, Bishara A, McDaniel J, Catoe D, Zook JM, Salit M, West RB, Batzoglou S, Sidow A. “Genome-wide reconstruction of complex structural variants using read clouds.” Preprint available on *bioRxiv*, doi:10.1101/074518.
- Zook J, Catoe D, McDaniel J, Vang L, **Spies N**, et al. 2016. “Extensive sequencing of seven human genomes to characterize benchmark reference materials.” *Scientific Data*, doi:10.1038/sdata.2016.25.
- Parikh H, Mohiyuddin M, Lam HY, Iyer H, Chen D, Pratt M, Bartha G, **Spies N**, Losert W, Zook JM, Salit M. 2016. “svclassify: a method to establish benchmark structural variant calls.” *BMC Genomics*, doi:10.1186/s12864-016-2366-2.
- Spies N**†, Zook JM, Salit M, Sidow A. 2015. “svviz: a read viewer for validating structural variants.” *Bioinformatics*, doi:10.1093/bioinformatics/btv478.
- Spies N***, Smith CL*, Rodriguez JM, Baker JC, Batzoglou S, Sidow A. 2015. “Constraint and divergence of global gene expression in the mammalian embryo.” *eLife*, doi:10.7554/eLife.05538.
- Weng Z, **Spies N**, Zhu SX, Newburger DE, Kashef-Haghighi D, Batzoglou S, Sidow A, West RB. 2015. “Cell-lineage heterogeneity and driver mutation recurrence in pre-invasive breast neoplasia.” *Genome Med*, doi:10.1186/s13073-015-0146-2.
- Sidow A, **Spies N**. 2015. “Concepts in solid tumor evolution.” Review. *Trends in Genetics*, doi:10.1016/j.tig.2015.02.001.
- Spies N**, Burge CB, Bartel DP. 2013. “3′ UTR-isoform choice has limited influence on the stability and translational efficiency of most mRNAs in mouse fibroblasts.” *Genome Res*, doi:10.1101/gr.156919.113.
- Chiang HR, Schoenfeld LW, Ruby JG, Auyeung VC, **Spies N**, Baek D, Johnston WK, Russ C, Luo S, Babiarz JE, Belloch R, Schroth GP, Nusbaum C, Bartel DP. 2010. “Mammalian microRNAs: experimental evaluation of novel and previously annotated genes.” *Genes Dev*, doi:10.1101/gad.1884710.
- Spies N***, Nielsen C*, Padgett R, Burge CB. 2009. “Biased Chromatin Signatures Around Polyadenylation Sites and Exons.” *Mol Cell*, doi:10.1016/j.molcel.2009.10.008.
- Bühler M*, **Spies N***, Bartel DP, Moazed D. 2008. “TRAMP-mediated RNA surveillance prevents spurious entry of RNAs into the *S. pombe* siRNA pathway.” *Nat Struct Mol Biol*, doi:10.1038/nsmb.1481.