

# Dent A. Earl ([dearl@soe.ucsc.edu](mailto:dearl@soe.ucsc.edu))

Department of Biomolecular Engineering  
Jack Baskin School of Engineering  
University of California, Santa Cruz  
1156 High Street  
Santa Cruz, CA 95064

Email: [dearl@soe.ucsc.edu](mailto:dearl@soe.ucsc.edu)  
URL: <http://users.soe.ucsc.edu/~dearl/>  
Github: <https://github.com/dentearl/>

## Education

Ph.D. Bioinformatics, University of California, Santa Cruz, expected September 2014.  
Internship, Software Engineering, Google Inc, June – September 2013.  
M.S. Bioinformatics, University of California, Santa Cruz, 2010.  
M.A. Biology, University of California, Los Angeles, 2008.  
B.A. Biology, University of California, Santa Cruz, 2001.

## Research Interests

Population Genomics. Evolutionary Biology. Data Visualization. Big Data.

## Current Projects

“Building infrastructure for Google Genomics,” with [David Konerding \(dek@google.com\)](mailto:David.Konerding@Google.com).  
“Alignathon, a whole genome alignment collaborative competition,” with [Dr. David Haussler](mailto:Dr.David.Haussler).  
“The 100-way whole genome alignment,” with [Dr. Benedict Paten](mailto:Dr.Benedict.Paten), [Dr. Glenn Hickey](mailto:Dr.Glenn.Hickey) and [Dr. David Haussler](mailto:Dr.David.Haussler).

## Teaching Experience

### University of California, Santa Cruz

Teaching Assistant, [Introduction to Biotechnology](#), Winter 2013.  
Teaching Assistant, [Computational Genomics](#), Winter 2010, Winter 2011.  
Teaching Assistant, Genetics, Winter 2009.

## University of California, Los Angeles

Teaching Assistant, [Population Genetics](#), Spring 2007, Spring 2008.

Teaching Assistant, [Introduction to Life Sciences](#), Fall 2005, Winter 2006, Fall 2006, Fall 2007.

Teaching Assistant, [Computational and Theoretical Population Biology](#), Spring 2006.

Teaching Assistant, [Evolution](#), Fall 2004.

## Publications

### Google Scholar Citations

Ewing, A.D., Ballinger, T.J. Earl, D. et al. (2013) **Retrotransposition of gene transcripts leads to structural variation in mammalian genomes** *Genome Biology*. vol 14:R22. doi: [10.1186/gb-2013-14-3-r22](https://doi.org/10.1186/gb-2013-14-3-r22).

Bradnam, K.R. et al. (2013) **Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species** *arXiv.org*. url: <http://arxiv.org/abs/1301.5406>.

Earl, D. and vonHoldt, B.M. (2012) **STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method.** *Conservation Genetics Resources*. vol 4 (2) pp. 359-361. doi: [10.1007/s12686-011-9548-7](https://doi.org/10.1007/s12686-011-9548-7).

Earl, D. et al. (2011) **Assemblathon 1: A competitive assessment of de novo short read assembly methods.** *Genome Research*. vol. 21 (12) pp. 2224-41 doi: [10.1101/gr.126599.111](https://doi.org/10.1101/gr.126599.111).

Paten B., Earl D., et al. (2011) **Cactus: Algorithms for genome multiple sequence alignment.** *Genome Research*. 21: 1512-1528. doi: [10.1101/gr.123356.111](https://doi.org/10.1101/gr.123356.111).

vonHoldt B.M., Pollinger J.P., Earl D., et al. (2011) **A genome-wide perspective on the evolutionary history of enigmatic wolf-like canids.** *Genome Research*. 21: 1294-1305. doi: [10.1101/gr.116301.110](https://doi.org/10.1101/gr.116301.110).

Paten B., Diekhans M., Earl D., et al. (2010) **Cactus graphs for genome comparisons.** In *Research in Computational Molecular Biology*, Ed: Berger B. Springer Berlin, Heidelberg. doi: [10.1007/978-3-642-12683-3\\_27](https://doi.org/10.1007/978-3-642-12683-3_27).

Vaske C.J., Benz S.C., Sanborn J.Z., Earl D., et al. (2010) **Inference of patient-specific pathway activities from multi-dimensional cancer genomics data using PARDIGM.** *Bioinformatics*. 26(12):i237-i245 doi: [10.1093/bioinformatics/btq182](https://doi.org/10.1093/bioinformatics/btq182).

## Computer Skills

Programming languages: Python, C, R.

Graphics: Adobe Illustrator, Python matplotlib, R.

Operating systems: Linux, MacOS.

Other: Unit testing, analysis pipelines, compute clusters, SQL, Django, Heroku, L<sup>A</sup>T<sub>E</sub>X, HTML, CSS, Bash, Gnu Make.

Erdős: 3, via David Haussler.

Last updated: July 17, 2014  
<http://www.soe.ucsc.edu/~dearl/>