# **Paul Lott**

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#### **Education**

## University of California, Davis, Davis, California, 2006 - 2013

Ph.D. in Genetics, Mentor: Professor Ian Korf, Ph.D. Area of Specialization: Bioinformatics

Ph.D. Disseration Title: StochHMM: A flexible hidden Markov model framework

## University of Utah, Salt Lake City, Utah 1999-2004

B.S. in Biology, Area of Specialization: Human Genetics

## Research Experience

#### Postdoctoral Research: Genome Center, University of California, Davis

August 2013-present (Research Advisor: Dr. Luis Carvajal-Carmona)

- Identification of novel risk variants important in gastric, colorectal, thyroid, and breast cancer using NGS
- · Identification of driver mutations in gastric cancer using NGS
- · Analysis of genetic risk factors for colorectal cancer in admixed Colombian population

## Doctoral Research: Genetics Graduate Group, University of California, Davis

March 2007-August 2013 (Research Adviser: Dr. Ian Korf)

- · Development of flexible hidden Markov Model application to extend HMMs
- Designed HMM models and investigated R-loop formation in the human genome
- Development of models to classify methylated regions in the human genome

## Pre-graduate Research: Human Genetics, University of Utah, Utah

August 2005-August 2006 (Research Adviser: Dr. Victoria Lawson)

- · Investigated functional roles of MFN2 mutations leading to CMT2A disease
- Analyzed confocal microscopy images of mitochondria to determine fission and fusion rates
- Screened new patients for multiple genetic mutations associated with neurological diseases

#### June 1999-August 2005 (Research Adviser: Jean-Marc Lalouel)

- Investigating genes linked to salt-sensitive hypertension in C57BL/6 mice on chromosome 4
- Cytological and expression studies in cell lines to determine genetic contribution of ADRP to salt sensitive hypertension in C57BL/6 mice

### **Teaching Experience**

## SPRING 2007 – Teaching Assistant MCB182 Genomics

**Course content:** Information theory, Sequence alignment, Hidden Markov Models, Motif Analysis, Sequencing Technologies including next-gen sequencing, proteomics, bioinformatics

**Type of teaching:** Lead discussion sections to review and expand students' knowledge on course subjects. Presented and lead in class discussion on issues of bioethics.

#### FALL 2010 – Teaching Assistant BIS101 Genes and Gene Expression

**Course content:** Basic genetics: central dogma, principles of heredity, linkage and recombination, DNA replication. Genetic analysis, Gene regulation,

Type of teaching: Lead 3 discussion sections to review and expand students' knowledge on course subjects.

## SPRING 2013 – Teaching Assistant BIS180L Genomic Laboratory

**Course content:** Informatics, Transcriptomics, Sequence Analysis, RNA profiling and Clustering, Comparative genomics, Systems Biology, Network analysis, Proteomics

Type of teaching: Lead discussion sections and assist in computer laboratory. Develop lab tools for Galaxy Server

## **Papers**

- 1. Porter MD, Dandekar R, Lott P, Comai L, Korf I. **Ploidamatic: A copy number variant detection hidden Markov model designed for diploid next-generation sequencing data.** Bioinformatics. 2013 Under Review.
- Lott P, Korf I. StochHMM: a flexible hidden Markov model tool and C++ Library. Bioinformatics. 2013. Under Review.
- 3. Ginno PA, Lim YW, Lott P, Korf I, Chedin F. GC skew at the 5' and 3' Ends of Human Genes Links R-loop Formation to Epigenetic Regulation and Transcription Termination. Genome Res. 2013 Oct. 23(10):1590-1600.
- 4. Schroeder DI, Blair JD, Lott P, Yu HO, Hong D, Crary F, Ashwood P, Walker C, Korf I, Robinson WP, Lasalle JM. **The human placenta methylome.** Proc Natl Acad Scie. 2013 Apr. 110(15):6037-42.
- 5. Ginno PA, Lott P, Christensen HC, Korf I, Chedin F. **R-loop formation is a distinctive characteristic of unmethylated human CpG island promoters.** Molecular Cell. 2012 Mar 30;45(6):814-25. Epub 2012 Mar 1
- 6. Schroeder DI, Lott P, Korf I, LaSalle JM. Large-scale methylation domains mark a functional subset of neuronally expressed genes. Genome Res. 2011 Oct;21(10):1583-91.
- 7. Wang YZ, Yamagami T, Gan Q, Wang Y, Zhao T, Hamad S, Lott P, Schnittke N, Schwob JE, Zhou CJ. Canonical Wnt signaling promotes the proliferation and neurogenesis of peripheral olfactory stem cells during postnatal development and adult regeneration. J Cell Sci. 2011 May 1;124(Pt 9):1553-63.
- 8. Amiott EA, Lott P, Soto J, Kang PB, McCaffery JM, DiMauro S, Abel ED, Flanigan KM, Lawson VH, Shaw JM. Mitochondrial fusion and function in Charcot-Marie-Tooth type 2A patient fibroblasts with mitofusin 2 mutations. Exp Neurol. 2008 May;211(1):115-27.
- 9. Gociman B, Rohrwasser A, Hillas E, Cheng T, Hunter G, Hunter J, Lott P, Monson S, Ying J, Lalouel JM. **Response to genetic manipulations of liver angiotensinogen in the physiological range.** J Hum Genet. 2008;53(9):775-88.
- 10. Rohrwasser A, Lott P, Weiss RB, Lalouel JM. **From genetics to mechanism of disease liability.** Adv Genet. 2008;60:701-26. Review.
- 11. Gociman B, Rohrwasser A, Lantelme P, Cheng T, Hunter G, Monson S, Hunter J, Hillas E, Lott P, Ishigami T, Lalouel JM. **Expression of angiotensinogen in proximal tubule as a function of glomerular filtration rate.** Kidney Int. 2004 Jun;65(6):2153-60.

#### Conference

1. Lott P, Dunaway K, Yu K, Korf I. **StochHMM: A flexible Hidden Markov Model Framework for rapid development of HMMs.** Poster presented at Genome Informatics, Cambridge, England, UK. (2012 September)

#### Software

1. StochHMM: A flexible hidden Markov Model library and application for rapid development of HMMs. https://github.com/KorfLab/StochHMM

<u>Department/University Service</u> Genetics Graduate Group Admissions (2013)