

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors in the order listed on Form Page 2. Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME Charles G. Danko		POSITION TITLE Postdoctoral Research Scientist, Department of Biological Statistics & Computational Biology	
eRA COMMONS USER NAME (credential, e.g., agency login) CGDANKO			
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	MM/YY	FIELD OF STUDY
Johns Hopkins University, Baltimore, MD	B.S.	9/99-6/03	Biomedical Engineering
SUNY Upstate Medical University, Syracuse, NY	Ph.D.	6/03-6/09	Bioinformatics
Cornell University, Ithaca, NY	Postdoctoral	6/09	Genomics/Bioinformatics

A. Personal Statement

I invent sophisticated computational technologies for the analysis of functional genomic “next-generation” sequencing data, and use these to develop new biological insights into the mechanisms of gene regulation. As a postdoc with Adam Siepel and W. Lee Kraus I developed a two-state hidden Markov model (HMM) to identify transcription units using Global Run-On and Sequencing (GRO-seq) data. I applied this approach to a GRO-seq data set collected following a time course of induction by 17 β -estradiol (E2) in MCF-7 cells, demonstrating that E2 responses occurs rapidly (i.e. 10 min. of treatment) and target an extensive portion of the transcriptome. I have also developed innovative new genome-wide approaches to measure the rate of transcription elongation by identifying the leading edge of a ‘wave’ of Pol II at genes up-regulated by a stimulus. My approach features an innovative combination of a three-state HMM with statistical regression techniques. As the first technology to measure polymerase speed genome-wide, this work fundamentally changes the types of scientific questions that can be addressed about transcription elongation. I also have a demonstrated history developing bioinformatics software that is widely used by the research community. As a graduate student I developed analysis software for tiling microarray data (AffyTiling), which is distributed as an extension to the popular Bioconductor package. To date, this software has been downloaded over two thousand times. As a postdoctoral trainee, I am learning to apply molecular approaches such as GRO-seq and RNA-seq to generate next-generation sequencing libraries for the study of gene regulation.

B. Positions and Honors

Positions and Employment:

- 2002–03 **Undergraduate Research Assistant.** Kennedy Krieger Institute, Center for Genetic Disorders of Cognition and Behavior, Baltimore, MD.
- 2003–09 **Graduate Student.** Department of Pharmacology, SUNY Upstate Medical University, Syracuse, NY. Dr. Arkady Pertsov, Advisor.
- 2007–09 **Software Developer.** SUNY Microarray Core Facility. Syracuse, NY.
- 2007– **Package developer/ manager** for *AffyTiling* microarray analysis software, Bioconductor.

2009– **Postdoctoral Fellow.** Department of Biological Statistics & Computational Biology. Cornell University, Ithaca NY. Dr. Adam Siepel; Dr. Lee Kraus, Joint Advisors.

Professional Societies and Public Advisory Committees:

2006–08 **Student Representative.** Judiciary and Ethical Committee, SUNY Upstate Medical University.
2008 **Programmer.** GCO2PLINK, Converts Affymetrix GCO file into PLINK format.
2010 **Instructor.** Cornell Short Read Sequencing Workshop.
2009– **Reviewer.** For *BMC Genomics* and *PLoS Computational Biology*.

Honors:

1999 **Bausch & Lomb Honorary Science Award.** Queen Anne School.
2008 **Professional and Public Service Award.** SUNY Upstate Medical University.
2009 **Postdoctoral Fellowship.** Competitive T32 in Reproductive Genomics.
2010 **Postdoctoral Fellowship.** Biological Informatics, awarded by PhRMA Foundation.
2012 **Best Poster.** Ranked 1 of 30, Reproductive Genomics Retreat Poster Session.

C. Publications (* Denotes equal contribution):

1. Jarrar MH, **Danko CG**, Reddy S, Lee YJ, Bibat G, Kaufmann WE. (2003). MeCP2 expression in human cerebral cortex and lymphoid cells: immunochemical characterization of a novel higher-molecular-weight form. *J Child Neurol*, 18(10):675-82.
2. **Danko CG**, McIlvain VA, Qin M, Knox BE, Pertsov AM. (2007). Bioinformatic identification of novel putative photoreceptor specific *cis*-elements. *BMC Bioinformatics*, Oct 22;8(1):407
3. **Danko CG**, Pertsov AM. (2009). Identification of co-regulatory modules and associated *cis*-elements involved in degenerative heart disease. *BMC Medical Genomics*, 28;2:31.
4. Schuster SC, Miller W, Ratan A, Tomsho LP, Giardine B, Kasson LR, Harris RS, Petersen DC, Zhao F, Qi J, Alkan C, Kidd JM, Sun Y, Drautz DI, Bouffard P, Muzny DM, Reid JG, Nazareth LV, Wang Q, Burhans R, Riemer C, Wittekindt NE, Moorjani P, Tindall EA, **Danko CG**, Teo WS, Buboltz AM, Zhang Z, Ma Q, Oosthuysen A, Steenkamp AW, Oostuisen H, Venter P, Gajewski J, Zhang Y, Pugh BF, Makova KD, Nekrutenko A, Mardis ER, Patterson N, Pringle TH, Chiaromonte F, Mullikin JC, Eichler EE, Hardison RC, Gibbs RA, Harkins TT & Hayes VM. (2010). Complete Khoisan and Bantu genomes from southern Africa. *Nature*, 18;463(7283):943-7.
5. Hah N*, **Danko CG***, Core L, Waterfall JJ, Siepel A, Lis JT, Kraus WL. (2011). A rapid, extensive, and transient transcriptional response to estrogen signaling in breast cancer cells. *Cell*, 13;145(4):622-34.
6. Oxford EM, **Danko CG**, Kornreich BG, Maass K, Hemsley SA, Raskolnikov D, Fox PR, Delmar M, Moïse NS. (2011). Ultrastructural changes in cardiac myocytes from Boxer dogs with arrhythmogenic right ventricular cardiomyopathy. *J Vet Cardiol*, 13(2):101-13.
7. Gronau I, Hubisz MJ, Gulko B, **Danko CG**, Siepel A. (2011). Bayesian inference of ancient human demography from individual genome sequences. *Nature Genetics*, 18;43(10):1031-4.
8. Zeng L, Sang Chul C, **Danko CG**, Siepel A, Stanhope MJ, Burne RA. (2013). Gene Regulation by CcpA and Catabolite Repression Explored by RNA-Seq in *Streptococcus mutans*. *PLoS One*. 2013;8(3):e60465.
9. **Danko CG**, Hah N, Luo X, Martins AL, Core L, Lis JT, Siepel A, Kraus WL. (2013). Signaling Pathways Differentially Affect RNA Polymerase II Initiation, Pausing, and Elongation Rate in Cells. *Mol Cell*. 2013 Apr 25;50(2):212-22.
10. Hah N, Murakami S, Nagari A, **Danko C**, Kraus WL. (2013). Enhancer Transcripts Mark Active Estrogen Receptor Binding Sites. *Genome Res*. May 1.

D. Research Support:

Completed Research Support

T32 HD052471-01A1

Roberson (PI)

01/05/09-01/05/11

Genomic evaluation of binding sequence variation in a sex-hormone dependent transcription factor.

The goal is to develop analytical and informatic methods to evaluate the role of motif sequence variation in the direct targets of a sex-hormone dependent transcription factor, estrogen receptor alpha.

Role: Postdoctoral Fellow

PhRMA Foundation Fellowship in Biological Informatics

Danko (PI)

12/01/10-11/30/12

Exploring the Direct Estrogen-Regulated Transcriptome using a Multidisciplinary Approach.

My objective is to use GRO-seq, a novel short read sequencing based approach that identifies the location and orientation of engaged polymerase, to determine the direct targets of estrogen receptor alpha.

Role: PI