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Education

SUNY Upstate <i>Ph.D.</i> Dissertation Title:	Syracuse, NY Department of Pharmacology <i>Bioinformatic Identification of Putative Regulatory Motifs</i>	2009
Johns Hopkins University <i>BS.</i>	Baltimore, MD Biomedical Engineering	2003

Research & Work Experience

<i>Assistant Professor</i>	Baker Institute/ Department of Biomedical Sciences Cornell University, Ithaca NY	July 1 st 2014-
<i>Postdoctoral Fellow</i>	Dep. Biological Statistics & Computational Biology Cornell University, Ithaca NY	2009-2014
<i>Software Developer</i>	SUNY Microarray Core Facility Syracuse, NY	2007-2008
<i>Graduate Student</i>	Department of Pharmacology, SUNY Upstate Syracuse, NY; Dr. Arkady Pertsov, Advisor	2003-2008
<i>Research Assistant</i>	Kennedy Krieger Institute, Johns Hopkins Baltimore, MD; Dr. Walter Kaufmann, Advisor	2002-2003

Distinctions & Awards

Genome Research Poster Prize: The Biology of Genomes (Cold Spring Harbor Labs)	2014
Best Poster: Reproductive Genomics Retreat, 2012, Poster Session	2012
Professional and Public Service Award: SUNY Upstate Medical University	2008
Judiciary and Ethical Committee: SUNY Upstate Medical University	2006-2008
Bausch & Lomb Honorary Science Award	1999

Open Source Software Contributions

1. Rtfbs-db. Parse TF binding motifs from public databases. Languages: R, Shell <i>GitHub</i>	2015-
2. dREG/ dREG-HD. Detection of <u>R</u> egulatory <u>E</u> lements using <u>G</u> RO-seq Data. Languages: R, C <i>GitHub</i>	2014-

3. **GroHMM**. R package for GRO-seq data analysis, HMM implementation. 2009-
Languages: R, C *Bioconductor*
4. **Affytiling**. Easy extraction of individual probes in Affymetrix tiling arrays. 2007-2016
Languages: R, C *Bioconductor*

Publications

(* equal contribution) (¥ corresponding author) (Danko lab members underlined)

Preprints Submitted for Peer-Review

1. Horibata A, Rice EJ, Zheng H, Anguish LJ, Mukai C, Marks BA, Chu T, Coonrod S¥, **Danko CG¥** (2017). RET Ligands Mediate Endocrine Sensitivity via a Bi-stable Feedback Loop with ERα. *BioRxiv*. doi: <http://biorxiv.org/content/early/2017/01/06/098848>
2. **Danko CG¥**, Wang Z, Rice EJ, Chu T, Martins AL, Tait-Wojno E, List JT, Kraus WL, Siepel A¥ (2016). Natural Selection has Shaped Coding and Non-coding Transcription in Primate CD4+ T-cells. *bioRxiv*. doi: <https://doi.org/10.1101/083212>

Peer-reviewed Publications

3. Blumberg A, Rice EJ, Kundaje A, **Danko CG**, Mishmar D (2017). Initiation of mtDNA transcription is followed by pausing, and diverge across human cell types and during evolution. *Genome Research*. Jan 3. pii: gr.209924.116. doi: 10.1101/gr.209924.116.
4. Mahat DB, Kwak H, Booth GT, Jonkers I, **Danko CG**, Patel R, Waters CT, Munson K, Core LC, Lis JT (2016). Base-Pair Resolution Genome-Wide Mapping Of Active RNA polymerases using Precision Nuclear Run-On (PRO-seq). *Nature Protocols*. Aug;11(8):1455-1476.
5. Wang Z, Martins AL, **Danko CG¥** (2016). RTFBSDB: an integrated framework for transcription factor binding site analysis. *Bioinformatics*. Jun 10. pii: btw338.
6. Mahat DB, Salamanca H Duarte FM, **Danko CG**, Lis JT (2016). Mammalian heat shock response and mechanisms underlying its genome-wide transcriptional regulation. *Molecular Cell*. Apr 7;62(1):63-78. Mar 24.
7. Welsh IC, Kwak H, Chen FL, Werner M, Shopland LS, **Danko CG**, Lis JT, Zhang M, Martin JF, Kurpios NA (2015). Embryonic gut laterality is mirrored by asymmetric chromatin architecture at the *Pitx2* locus dependent on *Pitx2* and CTCF. *Cell Reports*. Oct 13;13(2):337-49. **Cover article**
8. Chae M, **Danko CG**, Kraus WL (2015). groHMM: a computational tool for identifying unannotated and cell type-specific transcription units from global run-on sequencing data. *BMC Bioinformatics*, Jul 16;16:222.
9. Andersson R¥, Sandelin A, **Danko CG¥** (2015). A Unified Architecture of Transcriptional Regulatory Elements. *Trends in Genetics*. Jun 11. pii: S0168-9525(15)00104-3.
10. Fuda NJ, Guertin MJ, Sharma S, **Danko CG**, Martins AL, Siepel A, Lis JT (2015). GAGA Factor Maintains Nucleosome-free Promoters Allowing RNA Polymerase II Recruitment and Promoter-proximal Pausing. *PLoS Genetics*. Mar 27;11(3):e1005108.

11. **Danko CG**[‡], Hyland SL, Core LJ, Martins AL, Waters CT, Lee HW, Cheung VG, Kraus WL, Lis JT[‡], and Siepel A[‡] (2015). *Accurate Identification of Active Transcriptional Regulatory Elements from Global Run-On and Sequencing Data*. **Nature Methods**. Mar 23.
12. Core LJ*, Martins AL*, **Danko CG**, Waters C, Siepel A, Lis JT (2014). *Analysis of transcription start sites from nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers*. **Nature Genetics**. Nov 10. doi: 10.1038/ng.3142. **Featured in a perspective piece**
13. Luo X, Chae M, Krishnakumar R, **Danko CG**, Kraus WL (2014). *Dynamic reorganization of the AC16 cardiomyocyte transcriptome in response to TNFalpha signaling revealed by integrated genomic analyses*. **BMC Genomics**. Feb 24;15(1):155.
14. Oxford EM, **Danko CG**, Fox P, Kornreich B, Moise NS (2014). *Change in β -catenin localization suggests involvement of the canonical Wnt pathway in Boxer dogs with arrhythmogenic cardiomyopathy*. **J Vet Intern Med**. Jan;28(1):92-101.
15. Hah N, Murakami S, Nagari A, **Danko CG**, Kraus WL (2013). *Enhancer Transcription Marks Active Estrogen Receptor Binding Sites*. **Genome Res**. May 1. PMID: 23636943.
16. **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*. **Molecular Cell**. Apr 25;50(2):212-22. **Cover article**
Featured in a perspective piece
Recommended by Faculty of 1000
17. 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**. 8(3):e60465.
18. 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.
19. Oxford EM, **Danko CG**, Kornreich BG, Maass K, Hemsley SA, Raskolnikov D, Fox PR, Delmar M, Moise NS (2011). *Ultrastructural changes in cardiac myocytes from Boxer dogs with arrhythmogenic right ventricular cardiomyopathy*. **J Vet Cardiol**, 13(2):101-13. **Cover article**
20. 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. * Equal Contribution **Featured in a perspective piece**
21. Schuster SC, et. al. (2010). *Complete Khoisan and Bantu genomes from southern Africa*. **Nature**, 18;463(7283):943-7. **Cover article**
22. **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.
23. **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.

24. 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.

Invited Publications

25. Choate LA, **Danko CG*** (2016). *Poised for development.* *Nature Genetics*. Jul 27;48(8):822-823.

Talks & Conference Participation

Invited Talks

1. **Danko CG** (2016). Mapping multiple 'layers' of gene regulation using ChRO-seq.
Host: Mike Guertin *LisFest, July 2016*
2. **Danko CG** (2016). Widespread stabilizing and positive selection govern primate enhancer evolution.
Host: Paula Cohen *NCTRI Male Res. Focus Group Meeting, April 2016*
3. **Danko CG** (2016). Glioblastoma Multiforme epigenomics through the lens of ChRO-seq.
Host: Lawrence Chin *SUNY Upstate Neuroscience Grand Rounds, Feb. 2016*
4. **Danko CG** (2015). Positive Selection in Regulatory Elements Drives Changes in Gene Expression in the Adaptive Immune System of Primate Species.
Host: Arkady Pertsov *SUNY Upstate Biomedical Sciences Retreat, 2015*
5. **Danko CG** (2014). Evolutionary Changes in Gene Expression and Regulatory Element Usage Quantified in Primate CD4⁺ T-Cells. *3CPG Annual Symposium*
6. **Danko CG** (2014). Toward a Systems Understanding of the Genetic Basis of Disease.
Baker Institute Advisory Council, Cornell Club, New York, NY
7. **Danko CG** (2014). Transcriptional Regulation through the Lens of GRO-seq.
Baker Institute Faculty Search

Talks Selected from Abstracts

8. **Danko CG** (2016). Widespread stabilizing and positive selection govern primate enhancer evolution. *Systems Biology: Global Regulation of Gene Expression, March 2016*
9. **Danko CG** (2015). Positive Selection in Regulatory Elements Drives Changes in Gene Expression in the Adaptive Immune System of Primate Species. *SMBE 2015*
10. **Danko CG** (2012). Variation in RNA Polymerase II Transcription Rate in Human Cells.
Mountain Lake Elongation and Termination Meeting

Selected Posters

1. **Danko CG**, Martins A, Lis JT, Siepel A, Kraus WL (2014). Evolutionary Changes in Gene

Expression and Active Regulatory Element Usage Quantified in Primate CD4+ T-Cells using GRO-seq.

Biology of Genomes; Poster

Winner, Poster competition (top 3 of 324)

2. **Danko CG**, Hah N, Luo X, Martins A, Core L, Lis JT, Siepel A, Kraus WL (2012). Variation in the RNA Polymerase II Transcription Rate in Human Cells.

Reproductive Genomics Retreat; Poster

Winner, Poster competition (top 1 of 30)

3. **Danko CG**, Hah N, Kraus WL, Siepel AS. (2009). Primate-specific expansions of putative sex-hormone response elements.

Biology of Genomes; Poster

Honorable Mention, Verge poster competition

Research Support

Current

Harry N. Zweig Memorial Fund Danko (co-PI) 1/1/17-12/31/18

Functional Gene Annotation in the Horse

Genetech (CLL-13977 PO#4001955607) Danko (PI) 10/1/16-9/30/17

Understanding Resistance to Endocrine Agents in Breast Cancer Cells

Cornell University Intramural Danko (co-PI) 7/1/16-6/30/18

Development of Single Cell Sequencing Technology to Identify Paired Variable Regions of Canine B- and T-cell Receptors during Viral Infection

Research Grants in Animal Health Danko (PI) 7/1/16-6/30/18

Genetic Mapping of Canine ARVC in the English Bulldog

Walbridge Fund Chin 1/1/16-12/31/17

Cornell University Intramural Danko (co-PI) 1/1/16-12/31/17

Development of Novel Targeted Therapies for Treating Malignant Solid Tumors in Dogs

Cornell University Intramural Danko (co-PI) 12/1/15-11/31/17

Identifying the Molecular Basis of Canine Genetic Disorders and Developing Preventative Therapies

NIH-NHLBI U01 (UHL129958A) Lis (co-I) 9/1/15-8/31/20

Di-Hi-C: Creating Photo-activated X-linkers to define Nuclear Architecture

NIH-NIA R01 (2R01AG024425-11) Lee (co-I) 9/1/15-8/31/20

Genetic and Epigenetic Determinants of Longevity

Baker Institute Startup Funds Danko (PI) 7/1/14-6/30/17

Pending

NIH-NHGRI R01 Danko (PI) 9/1/16-8/31/21

Mapping RNA polymerase in tissue samples with ChRO-seq

Trainee Support

James Lewis , postdoc (Reproductive Genomics T32)	1/1/17-12/31/17
Lauren Choate , grad student (CVG scholarship)	1/1/17-12/31/17
Tinyi Chu , grad student (Croucher Foundation Fellowship)	8/1/13-7/31/16

Teaching & Mentoring

Student Advisees

Shiao-Pei Chou , <i>Genetics Genomics & Development</i>	2016-
Paul Munn , <i>Computational Biology</i>	2016-
Lauren Choate , <i>Genetics Genomics & Development</i>	2015-
Tinyi Chu , <i>Computational Biology</i>	2014-

Thesis Committee

Ying Qiao , <i>Genetics Genomics & Development (Koren)</i>	2016-
Kara Rode , <i>Biochemistry, Molecular & Cell Biology (Lis)</i>	2016-
Shing Hu , <i>Comparative Biomedical Sciences (Kurpios)</i>	2016-
Brooke Marks , <i>Biological & Biomedical Sciences (Coonrod)</i>	2016-
Charles Liang , <i>Computational Biology (Yu)</i>	2016-
Ian Rose , <i>Genetics Genomics & Development (Nikitin)</i>	2015-
Lina Bagepalli , <i>Biochemistry, Molecular & Cell Biology (Lis)</i>	2015-
Michelle White , <i>Biological & Biomedical Sciences (Boyko)</i>	2015-
Anyimilehidi Mazo-Vargas , <i>Entomology (Reed)</i>	2015-
Nate Tippens , <i>Tri-I Computational Biology & Medicine (Lis, Yu)</i>	2015-
Noah Dukler , <i>Tri-I Computational Biology & Medicine (Siepel)</i>	2015-
Digbijay Mahat , <i>Biochemistry, Molecular & Cell Biology (Lis)</i>	2014-
Joo Hyun Im , <i>Genetics Genomics & Development (Lazzaro)</i>	2014-
Wenke Wang , <i>Biochemistry, Molecular & Cell Biology (Lee)</i>	2014-

A-exam Committees

Anyimilehidi Mazo-Vargas , <i>Entomology (Reed)</i>	2016
Ian Rose , <i>Genetics Genomics & Development (Nikitin)</i>	2016
Tina Tran , <i>Biochemistry, Molecular & Cell Biology (Schimenti)</i>	2016
Jacob Merle , <i>Genetics Genomics & Development (Grimson)</i>	2016
Lina Bagepalli , <i>Biochemistry, Molecular & Cell Biology (Lis)</i>	2016
Lauren Choate , <i>Genetics Genomics & Development (Danko)</i>	2016
Michelle White , <i>Biological & Biomedical Sciences (Boyko)</i>	2016
Noah Dukler , <i>Tri-I Computational Biology & Medicine (Siepel)</i>	2015

Ravi Patel , <i>Genetics Genomics & Development (Grimson)</i>	2015
Joo Hyun Im , <i>Genetics Genomics & Development (Lazzaro)</i>	2014
Wenke Wang , <i>Biochemistry, Molecular & Cell Biology (Lee)</i>	2014

Teaching

Molecular Basis of Disease (BioMG4390, Danko, Kwak)	2017-
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Guest Teaching

Precision and genomic medicine (BME6120, De Vlaminck)	2016
Problems in Genetics & Development (BioMG7810)	2015-2016
Computational Genetics & Genomics (BTRY4840/6840, Williams)	11/5/2015
3CPG Short Read Sequencing Workshop	2010

Intra- & Extramural Service

Intramural Service

Bio-IT Advisory Board <i>Advisory board to the Bio-IT core facility.</i>	2016-
Admissions Committee <i>Tri-I grad program in computational biology & medicine</i>	2016-
Admissions Committee <i>Genetics Genomics & Development graduate program</i>	2016-
GG&D Recruitment Faculty Coordinator <i>Organizes GG&D recruitment.</i>	2016
Bio Honors Thesis Review <i>Lydia Lam</i>	2016
BBS Recruitment Organizer <i>Baker visit</i>	2016
Admissions Committee <i>Computational Biology Graduate Program</i>	2015-
Awards Committee <i>Rank LPS/ Wellnitz Paper Awards (GG&D program)</i>	2015
Faculty Search in Computational Genomics <i>Molecular Biology & Genetics</i>	2014-2015

Reviewing Activity (Academic Journals)

<i>Genome Research</i>	<i>BMC Bioinformatics</i>
<i>Molecular Biology & Evolution</i>	<i>BMC Genomics</i>
<i>Nature Protocols</i>	<i>PLoS One</i>
<i>Nature Genetics</i>	<i>Cell</i>
<i>Bioinformatics</i>	<i>Mol. Cancer Res.</i>
<i>PLoS Computational Biology</i>	