Charles G. Danko, Ph.D.   **www.dankolab.org**

Assistant Professor of Epigenetics   cgd24@cornell.edu
Baker Institute for Animal Health   dankoc@gmail.com
Hungerford Hill Rd.
Ithaca, NY 14853

Education

SUNY Upstate	Syracuse, NY	2009
Ph.D.	Department of Pharmacology	
Dissertation Title:	*Bioinformatic Identification of Putative Regulatory Motifs*	
Johns Hopkins University	Baltimore, MD	2003
B.S.	Biomedical Engineering	

Research & Work Experience

Assistant Professor of Epigenetics   July 1st 2014-
Baker Institute of Animal Health, College of Veterinary Medicine, Cornell University, Ithaca NY
Postdoctoral Fellow   2009-2014
Biological Statistics & Computational Biology, Cornell University, Ithaca NY
Software Developer   2007-2008
SUNY Microarray Core Facility, Syracuse, NY

Distinctions & Awards

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

Open Source Software Contributions

1. Rgtsvm. GPU implementation for SVMs in R (led by Zhing Wang).   2016-
   Languages: R, C/ C++   GitHub
2. Rtfbs-db. Parse TF binding motifs from public databases.   2015-
   Languages: R, Shell   GitHub
3. dREG/ dREG-HD. Detection of Regulatory Elements using GRO-seq Data.   2014-
   Languages: R, C   GitHub
4. GroHMM. R package for GRO-seq data analysis, HMM implementation.   2009-
   Languages: R, C   Bioconductor
5. Affytiling. Easy extraction of individual probes in Affymetrix tiling arrays.   2007-2016
   Languages: R, C   Bioconductor

Publications

* equal contribution, ¥ corresponding author, <u>Danko lab members</u>

Preprints Submitted for Peer-Review

1. <u>Chu T</u>, <u>Rice EJ</u>, Booth GT, Salamanca HH, <u>Wang Z</u>, Core LJ, Longo SL, Corona RJ, Chin LS, Lis JT, Kwak H¥, and **Danko CG¥** (2017). Chromatin run-on reveals nascent RNAs that differentiate normal and malignant brain tissue. *bioRxiv*: https://doi.org/10.1101/185991

2. **Danko CG¥**, <u>Choate LA</u>, Marks BA, <u>Rice EJ</u>, <u>Wang Z</u>, <u>Chu T</u>, <u>Martins AL</u>, Dukler N, Coonrod SA, Tait-Wojno E, Lis JT, Kraus WL, and Siepel A¥ (2017). Natural Selection has Shaped Coding and Non-coding Transcription in Primate CD4+ T-cells. *bioRxiv*, p.083212.

3. <u>Wang Z</u>, <u>Chu T</u>, <u>Choate LA</u>, and **Danko CG¥** (2017). Rgtsvm: Support Vector Machines on a GPU in R. arXiv preprint *arXiv*:1706.05544

4. Horibata S, <u>Rice EJ</u>, Zheng H, Anguish LJ, Mukai C, Marks BA, <u>Chu T</u>, Coonrod S¥, and **Danko CG¥** (2017). RET Ligands Mediate Endocrine Sensitivity via a Bi-stable Feedback Loop with ERα. *bioRxiv*, p. 098848.

Journal Articles

5. Dukler N, Booth GT, Huang YF, Tippens N, **Danko CG**, Lis JT, and Siepel A (2017). Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol. *Genome Research*, In press.

6. Vihervaara A, Mahat DB, Guertin MJ, <u>Chu T</u>, **Danko CG**, Lis JT, and Sistonen L (2017). Transcriptional response to stress is pre-wired by promoter and enhancer architecture. *Nature communications*, in press.

7. <u>Blumberg A</u>, <u>Rice EJ</u>, Kundaje A, **Danko CG**, and Mishmar D (2017). Initiation of mtDNA transcription is followed by pausing, and diverge across human cell types and during evolution. *Genome research, 27*(3):362-373.

8. Mahat DB, Kwak H, Booth GT, Jonkers I, **Danko CG**, Patel R, Waters CT, Munson K, Core LC, and Lis JT (2016). Base-Pair Resolution Genome-Wide Mapping Of Active RNA polymerases using Precision Nuclear Run-On (PRO-seq). *Nature protocols, 11*(8):1455-1476.

9. <u>Choate LA</u>, and **Danko CG¥** (2016). Poised for development. *Nature genetics, 48*(8):822-823. Invited by the editor

10. <u>Wang Z</u>, Martins AL, and **Danko CG¥** (2016). RTFBSDB: an integrated framework for transcription factor binding site analysis. *Bioinformatics, 32*(19):3024-3026.

11. Mahat DB, Salamanca H, Duarte FM, **Danko CG**, and Lis JT (2016). Mammalian heat shock response and mechanisms underlying its genome-wide transcriptional regulation. *Molecular cell, 62*(1):63-78. Mar 24.

12. Welsh IC, Kwak H, Chen FL, Werner M, Shopland LS, **Danko CG**, Lis JT, Zhang M, Martin JF, and Kurpios NA (2015). Embryonic gut laterality is mirrored by asymmetric chromatin architecture at the Pitx2 locus dependent on Pitx2 and CTCF. *Cell reports, 13*(2): 337-349. Cover article

13. Chae M, **Danko CG**, and Kraus WL (2015). groHMM: a computational tool for identifying unannotated and cell type-specific transcription units from global run-on sequencing data. *BMC bioinformatics, 16*: 222.

14. Andersson R¥, Sandelin A, and **Danko CG¥** (2015). A unified architecture of transcriptional regulatory elements. *Trends in genetics, 31*(8):426-433.

15. Fuda NJ, Guertin MJ, Sharma S, **Danko CG**, Martins AL, Siepel A, and Lis JT (2015). GAGA factor maintains nucleosome-free regions and has a role in RNA polymerase II recruitment to promoters. *PLoS genetics, 11*(3):e1005108.

16. **Danko CG**¥, Hyland SL, Core LJ, Martins AL, Waters CT, Lee HW, Cheung VG, Kraus WL, Lis JT¥, and Siepel A¥ (2014). Accurate identification of active transcriptional regulatory elements from global run-on and sequencing data. *Nature Methods*. P.011353.

17. Core LJ*, Martins AL*, **Danko CG**, Waters C, Siepel A, and Lis JT (2014). Analysis of nascent RNA identifies a unified architecture of initiation regions at mammalian promoters and enhancers. *Nature genetics, 46*(12):1311-1320. Featured in a perspective piece

Publications Prior to Tenure Track Appointment

18. Luo X, Chae M, Krishnakumar R, **Danko CG**, and Kraus WL (2014). Dynamic reorganization of the AC16 cardiomyocyte transcriptome in response to TNFalpha signaling revealed by integrated genomic analyses. *BMC genomics, 15*(1):155.

19. Oxford EM, **Danko CG**, Fox P, Kornreich B, and Moise NS (2014). Change in β-catenin localization suggests involvement of the canonical Wnt pathway in Boxer dogs with arrhythmogenic cardiomyopathy. *Journal of veterinary internal medicine, 28*(1):92-101.

20. Hah N, Murakami S, Nagari A, **Danko CG**, and Kraus WL (2013). Enhancer Transcription Marks Active Estrogen Receptor Binding Sites. *Genome research*.

21. **Danko CG**, Hah N, Luo X, Martins AL, Core L, Lis JT, Siepel A, and Kraus WL (2013). Signaling pathways differentially affect RNA polymerase II initiation, pausing, and elongation rate in cells. *Molecular cell, 50*(2):212-222. Cover article, Featured in a perspective piece, Recommended by Faculty of 1000

22. Zeng L, Sang Chul C, **Danko CG**, Siepel A, Stanhope MJ, and Burne RA (2013). Gene Regulation by CcpA and Catabolite Repression Explored by RNA-Seq in Streptococcus mutans. *PLoS one, 8*(3):e60465.

23. Gronau I, Hubisz MJ, Gulko B, **Danko CG**, and Siepel A. (2011). Bayesian inference of ancient human demography from individual genome sequences. *Nature genetics, 43*(10):1031-1034.

24. Oxford EM, **Danko CG**, Kornreich BG, Maass K, Hemsley SA, Raskolnikov D, Fox PR, Delmar M, and Moïse NS (2011). Ultrastructural changes in cardiac myocytes from Boxer dogs with arrhythmogenic right ventricular cardiomyopathy. *Journal of veterinary cardiology, 13*(2):101-113. Cover article

25. Hah N*, **Danko CG***, Core L, Waterfall JJ, Siepel A, Lis JT, and Kraus WL (2011). A rapid, extensive, and transient transcriptional response to estrogen signaling in breast cancer cells. *Cell, 145*(4):622-634. Featured in a perspective piece

26. Schuster SC et al. (2010). Complete Khoisan and Bantu genomes from southern Africa. *Nature, 463*(7283):943-947. Cover article

27. **Danko CG**, and Pertsov AM (2009). Identification of gene co-regulatory modules and associated cis-elements involved in degenerative heart disease. *BMC medical genomics, 2*(1):31.

28. **Danko CG**, McIlvain VA, Qin M, Knox BE, and Pertsov AM (2007). Bioinformatic identification of novel putative photoreceptor specific cis-elements. *BMC bioinformatics, 8*(1):407.

29. 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. *Journal of child neurology, 18*(10):675-682.

Seminars & Talks

2017   "Transcriptional regulation through the lens of ChRO-seq", Baker Institute Seminar Series, Cornell University, Ithaca, NY. 3rd year review seminar

2017   "Mapping transcriptional regulation at multiple layers using ChRO-seq", International Society for Animal Genetics, Dublin, Ireland. Workshop keynote

2017   "Widespread stabilizing and positive selection govern primate enhancer evolution", Department of Ecology & Evolutionary Biology, Cornell University, Ithaca, NY.

2017   "Natural Selection has Shaped Coding and Non-coding Transcription in Primate CD4+ T-cells", Enhanceropathies, Banbury Center of Cold Spring Harbor laboratory, NY.

2016   "Mapping multiple 'layers' of gene regulation using ChRO-seq", LisFest, Cornell University, Ithaca, NY.

2016   "Widespread stabilizing and positive selection govern primate enhancer evolution", National Centers for Translational Research in Reproduction and Infertility Male Research Focus Group Meeting, Cornell University, Ithaca, NY.

2016   "Glioblastoma Multiforme epigenomics through the lens of ChRO-seq", SUNY Upstate Neuroscience Grand Rounds, Syracuse, NY.

2015   "Positive Selection in Regulatory Elements Drives Changes in Gene Expression in the Adaptive Immune System of Primate Species", SUNY Upstate Biomedical Sciences Retreat, Syracuse, NY.

2014   "Evolutionary Changes in Gene Expression and Regulatory Element Usage Quantified in Primate CD4+ T-Cells", 3CPG Annual Symposium, Cornell University, Ithaca, NY.

2014   "Toward a Systems Understanding of the Genetic Basis of Disease", Baker Institute Advisory Council, Cornell Club, New York, NY.

2014   "Transcriptional Regulation through the Lens of GRO-seq", Baker Institute Faculty Search, Ithaca, NY.

Selected from Abstracts

2017   "Chromatin run-on reveals nascent RNAs that differentiate normal and malignant brain tissue", Mechanisms of Eukaryotic Transcription, Cold Spring Harbor Laboratory, NY.

2016   "Widespread stabilizing and positive selection govern primate enhancer evolution", Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor Laboratory, NY.

2015   "Positive Selection in Regulatory Elements Drives Changes in Gene Expression in the Adaptive Immune System of Primate Species". Society for Molecular Biology and Evolution, Vienna, Austria.

2012   "Variation in RNA Polymerase II Transcription Rate in Human Cells", Post-initiation Activities of RNA Polymerases: 2012 Transcription meeting, Mountain Lake, VA.

Selected Posters

2014   "Evolutionary Changes in Gene Expression and Active Regulatory Element Usage Quantified in Primate CD4+ T-Cells using GRO-seq.", Biology of Genomes; Cold Spring Harbor, NY. Winner, Poster competition (top 3 of 324)

2012   "Variation in the RNA Polymerase II Transcription Rate in Human Cells", Cornell Reproductive Genomics Retreat, Ithaca, NY. Winner, Poster competition (top 1 of 30)

2009   "Primate-specific expansions of putative sex-hormone response elements", Biology of Genomes; Cold Spring Harbor, NY; CVG/ Verge retreat. Honorable Mention, Verge

Research Support

Current

R01 HG009309-01 (Danko)   02/01/17-01/31/22
Mapping RNA polymerase in tissue samples with ChRO-seq
National Institutes of Health (NHGRI)
   The major goal of this project is to develop a suite of molecular and computational technologies that allow researchers to directly measure transcriptional regulation of genes, enhancers, and lincRNAs in limited clinical isolates.
   Role: PI
   Project Direct costs: $1,225,000

Harry N. Zweig Memorial Fund (Antczak, Danko)   01/01/17-12/31/18
Functional Gene Annotation in the Horse
Harry N. Zweig Memorial Fund for Equine Research
   The major goal is to identify the functional genes in horses.
   Role: Co-PI
   Project Direct costs: $124,746
   Danko Lab Direct costs: $64,633

CLL-13977 PO#4001955607 (Danko)   10/01/16-09/30/17
Understanding Resistance to Endocrine Agents in Breast Cancer Cells
Genentech, Inc.
   The goal of this project is to examine RNA Polymerase II distribution on genes in the breast   cancer cell line MCF7 after a variety of different treatments.
   Role: PI
   Project Direct costs: $46,016

I3081 Canine Research Grants in Animal Health (multiple Baker PIs)   12/01/15-11/30/17
Identifying the Molecular Basis of Canine Genetic Disorders and Developing Preventative Therapies.
Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University
   The major goal of this project is to develop research resources that aid in mapping DNA sequences causally responsible for genetic diseases in the domestic dog, and to develop   strategies to prevent diseases by selective breeding or genetic engineering.
   Role: Co-PI
   Project Direct costs: $216,173

I3203 Canine Research Grants in Animal Health (multiple Baker PIs)   07/01/16-06/30/18
Development of Single Cell Sequencing Technology to Identify Paired Variable Regions of Canine B- and T-cell Receptors during Viral Infection
Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University
    The goal is to development single-cell sequencing in dogs.
    Role: PI
    Project Direct costs: $240,000

I3080 Canine Research Grants in Animal Health (multiple Baker PIs)   01/01/16-12/31/17
Development of Novel Targeted Therapies for Treating Malignant Solid Tumors in Dogs.
Baker Institute for Animal Health, College of Veterinary Medicine, Cornell University
    The major goal of this project is to identify novel mediators of malignant solid tumors in dogs; carry out pre-clinical trials to test the ability of targeted inhibitors in preventing progression of these tumors; and to use Tethered Enzyme Technology (TET) to develop a Point of Care testing device for screening/early diagnosis and monitoring of disease progression via the analysis of known tumor biomarkers and those identified through this project.
    Role: Co-PI
    Project Direct costs: $240,000

I3110 Cornell Research Grants Program in Animal Health (Danko)   07/1/16-06/30/18
Genetic Mapping of Canine ARVC in the English Bulldog
Cornell University College of Veterinary Medicine
    The goal is to identify the genetic basis of canine ARVC in the English Bulldog and Boxer
    Role: PI
    Direct costs: $100,000

Walbridge Fund (Chin)   01/01/16-12/31/17
    The goal is to analyze a cohort of ~80 glioblastoma specifmens using ChRO-seq.
    Role: PI
    Project Direct Costs: $50,000

U01HL129958 (Lis, Henning, Zipfel, Ozer, Danko)   09/01/15-08/31/20
Di-Hi-C: Creating Photo-activated X-linkers to define Nuclear Architecture
National Institutes of Health
    The goal of this proposal is to develop a method that can reveal the organization of DNA in nucleus with unprecedented resolution, and thus inform us about the mechanics of how genes are misregulated to produce disease conditions and how effective therapies could be developed.
    Role: Co-I
    Danko Lab Direct Costs: $340,000

2R01AG024425-11 (Lee, Danko)   09/01/15-08/31/20
Genetic and Epigenetic Determinants of Longevity
National Institutes of Health
   The goal of this proposal is to develop a method that can reveal the organization of DNA in
   nucleus with unprecedented resolution, and thus inform us about the mechanics of how genes
   are misregulated to produce disease conditions and how effective therapies could be
   developed.
   Role: Co-I
   Danko Lab Direct Costs: $45,161

Teaching & Mentoring

Cornell Graduate Field Memberships

Comparative Biomedical Sciences (CBS)	2014-
Computational Biology (CB)	2014-
Genetics, Genomics, and Development (GG&D)	2014-

Technical Staff

Edward J. Rice (laboratory manager)	2014-
Zhong Wang, Ph.D. (programmer)	2015-

Postdoctoral Fellows

Amit Blumberg, Ph.D. (joint with Adam Siepel)   2017-

Mridusmita Saikia, Ph.D. (joint with Elia Tait-Wojno & Iwijn De Vlaminck)   2016-

James Lewis, Ph.D.   2016-
   Reproductive Genomics T32

Graduate Students

Adriana Alexander, Comparative Biomedical Sciences (joint with Paula Cohen) 2017-
   NSF predoctoral fellowship, SUNY McNair Diversity Fellowship

Shiao-Pei Chou, Genetics, Genomics & Development   2016-

Paul Munn, Computational Biology   2016-

Lauren Choate, Genetics, Genomics & Development   2015-
   Center for Vertebrate Genomics fellowship

Tin Yi Chu, Computational Biology   2014-
   Croucher Foundation Fellowship

Rotation Students

Albert Vill, Genetics, Genomics & Development	2016
Charles Liang, Computational Biology	2016
Eamon Collins, Biomedical Engineering	2016
Kofi Gyan, Tri-Institutional Program for Computational Biology & Medicine	2016
Coryandar Gilvary, Tri-Institutional Program for Computational Biology & Medicine	2016

Andrew Wiens, Computer Science	2016
Dania Villarnovo, Comparative Biomedical Sciences	2015
Blaine Harlan, Genetics, Genomics & Development	2015
Ian Rose, Genetics, Genomics & Development	2015
Xiatong Yao, Tri-Institutional Program for Computational Biology & Medicine	2015
Yu-Ling (Linda) Lan, Genetics, Genomics & Development	2015
Alyssa Wetterau, Comparative Biomedical Sciences	2014

Undergraduate/ Post Baccalaureate Students

Connor Musick, Undergraduate	2017-
Marlena Holter, VIP Student	2017
Gavisha Waidyaratne, Postbac	2017
Madison Ramsey, Undergraduate	2017-
Kai Chun "Katie" Lin, Cornell Abroad	2016
Shuting Jin, Leadership student	2015
Alice Wang, Undergraduate	2015-2016

Thesis Committee Membership

Alex Cheng, Biomedical Engineering (De Vlaminck)	2017-
Kara Rode, Biochemistry, Molecular & Cell Biology (Lis)	2016-
Shing Hu, Comparative Biomedical Sciences (Kurpios)	2016-
Brooke Marks, Biological & Biomedical Sciences (Coonrod)	2016-
Charles Liang, Computational Biology (Yu)	2016-
Ian Rose, Genetics Genomics & Development (Nikitin)	2015-
Lina Bagepalli, Biochemistry, Molecular & Cell Biology (Lis)	2015-
Michelle White, Biological & Biomedical Sciences (Boyko)	2015-
Anyimilehidi Mazo-Vargas, Entomology (Reed)	2015-
Nate Tippens, Tri-I Computational Biology & Medicine (Lis, Yu)	2015-
Noah Dukler, Tri-I Computational Biology & Medicine (Siepel)	2015-
Digbijay Mahat, Biochemistry, Molecular & Cell Biology (Lis)	2014-2017
Joo Hyun Im, Genetics Genomics & Development (Lazzaro)	2014-
Wenke Wang, Biochemistry, Molecular & Cell Biology (Lee)	2014-

A-exam Committee Membership

Tinyi Chu, Computational Biology (Danko)	2017
Kara Rode, Biochemistry, Molecular & Cell Biology (Lis)	2017
Paul Munn, Computational Biology (Danko)	2017
Charles Liang, Computational Biology (Yu)	2017
Qiliang "Andy" Ding, Genetics Genomics & Development (Kroen, Clark)	2017
Anyimilehidi Mazo-Vargas, Entomology (Reed)	2016
Ian Rose, Genetics Genomics & Development (Nikitin)	2016
Tina Tran, Biochemistry, Molecular & Cell Biology (Schimenti)	2016
Jacob Merle, Genetics Genomics & Development (Grimson)	2016
Lina Bagepalli, Biochemistry, Molecular & Cell Biology (Lis)	2016

Lauren Choate, Genetics Genomics & Development (Danko)	2016
Michelle White, Biological & Biomedical Sciences (Boyko)	2016
Noah Dukler, Tri-I Computational Biology & Medicine (Siepel)	2015
Ravi Patel, Genetics Genomics & Development (Grimson)	2015
Joo Hyun Im, Genetics Genomics & Development (Lazzaro)	2014
Wenke Wang, Biochemistry, Molecular & Cell Biology (Lee)	2014

Workshops/ Short Courses

3CPG Short Read Sequencing Workshop	2010

Undergraduate Curriculum

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

Graduate Curriculum

Precision and Genomic Medicine (BME6120, De Vlaminck) – guest lecture	2016
Problems in Genetics & Development (BioMG7810)	2015-2017
Computational Genetics & Genomics (BTRY4840/6840, Williams) – guest lecture	2015

Administrative Experience

Intramural Service

Institute of Biotechnology, Core facilities @ Cornell, Member of Advisory Board	2017-
Bio-IT Core Facility, Chair of the Advisory Board	2017-
Tri-I Graduate Program in Computational Biology & Medicine, Member of Admissions Committee	2016-
Genetics Genomics & Development graduate program, Member of Admissions Committee	2016-
CVM Strategic Planning, Member of Research & Graduate Education Committee	2016-2017
Bio-IT Core Facility, Member of Advisory Board	2016-2017
Center for Vertebrate Genomics, Shared Resources Committee Member	2016-
GG&D graduate program, Faculty Coordinator for Recruitment	2016
Undergraduate Thesis Review, Bio Honors Lydia Lam	2016
BBS Recruitment, Co-Organizer Baker visit	2016
Computational Biology Graduate Program, Member Admissions Committee	2015-2016
Baker Institute Seminar Series, Coordinator	2015
LPS/ Wellnitz Paper Awards (GG&D program), Awards Committee Rank	2015
Computational Genomics Molecular Biology & Genetics, Faculty Search Committee	2014-2015

Extramural Service

4DN Consortium Annual Meeting, Abstract Reviewer	2017
4DN Consortium Annual Meeting, Organizing Committee	2017
4DN Consortium, Data Analysis Working Group	2016-

***Ad Hoc* Journal Reviews**

Genome Research	BMC Bioinformatics

Molecular Biology & Evolution

BMC Genomics

Nature Protocols

PLoS One

Nature Genetics

Cell

Nucleic Acids Research

Mol. Cancer Res.

PLoS Computational Biology

Bioinformatics

PCI Evolutionary Biology

Trends in Genetics

Nature Communications