

Charles G. Danko, Ph.D.

Assistant Professor of Epigenetics
Baker Institute for Animal Health
Hungerford Hill Rd.
Ithaca, NY 14853

www.dankolab.org

cgd24@cornell.edu

dankoc@gmail.com

Education

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

Research & Work Experience

Robert N. Noyce Assistant Professor in Life Science and Technology	2019-
Baker Institute of Animal Health, College of Veterinary Medicine, Cornell University, Ithaca NY	
Assistant Professor	2014-2019
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

Robert N. Noyce Assistant Professorship in Life Science and Technology	2019
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 Zhong Wang). Languages: R, C/ C++ GitHub	2016-
2. Rtfbs-db. Parse TF binding motifs from public databases. Languages: R, Shell GitHub	2015-
3. dREG/ dREG-HD. Detection of Regulatory Elements using GRO-seq Data. Languages: R, C GitHub/ http://dreg.dnasequence.org	2014-
4. GroHMM. R package for GRO-seq data analysis, HMM implementation. Languages: R, C Bioconductor	2009-

- | | |
|--|--------------|
| 5. Affytiling. Easy extraction of individual probes in Affymetrix tiling arrays. | 2007-2016 |
| Languages: R, C | Bioconductor |

Publications

* equal contribution, ¥ corresponding author, Danko lab members

Preprints

1. Ray J*, Munn PR*, Vihervaara A, Ozer A¥, **Danko CG¥**, Lis JT¥ (2019). Chromatin conformation remains stable upon extensive transcriptional changes driven by heat shock. *bioRxiv*: <https://doi.org/10.1101/527838>
2. Wang Z, Chu T, Choate LA, **Danko CG¥** (2017). Rgtsvm: Support Vector Machines on a GPU in R. *arXiv*: <https://arxiv.org/abs/1706.05544>

Journal Articles

3. van der Burg KRL, Lewis JJ, Martin A, Nijhout HF, **Danko CG**, Reed RD¥ (2019). Contrasting roles of transcription factors spineless and EcR in the highly dynamic chromatin landscape of butterfly wing metamorphosis. *Cell Reports*. Apr 23;27(4):1027-1038.e3.
4. Webb LM, Oyesola OO, Fruh SP, Kamynina E, Still KM, Patel RK, Peng SA, Cubitt RL, Grimson AW, Grenier JK, Harris TH, **Danko CG**, Tait Wojno E¥ (2019). The Notch signaling pathway promotes basophil responses during helminth induced - type 2 inflammation. *Journal of Experimental Medicine*. Apr 11. pii: jem.20180131.
5. Chou S, **Danko CG¥** (2019). AlleleHMM: a data-driven method to identify allele-specific differences in distributed functional genomic marks. *Nucleic Acids Research*. Mar 28. pii: gkz176. doi: 10.1093/nar/gkz176.
6. Wang Z, Chu T, Choate LA, **Danko CG¥** (2019). Identification of regulatory elements from nascent transcription using dREG. *Genome Research*. Feb;29(2):293-303. doi: 10.1101/gr.238279.118.
7. Saikia M, Burnham P, Keshavjee SH, Wang MFZ, Moral-Lopez P, Hinchman MM, **Danko CG**, Parker JSL, De Vlaminck I¥ (2019). Simultaneous multiplexed amplicon sequencing and transcriptome profiling in single cells. *Nature Methods*. Jan;16(1):59-62.
8. Chu T, Wang Z, Chou S, **Danko CG¥** (2018). Discovering transcriptional regulatory elements from run-on and sequencing data using the web-based dREG gateway. *Current Protocols in Bioinformatics*. e70. doi: 10.1002/cpbi.70
9. Chu T, Rice EJ, Booth GT, Salamanca HH, Wang Z, Core LJ, Longo SL, Corona RJ, Chin LS, Lis JT, Kwak H¥, **Danko CG¥** (2018). Chromatin run-on and sequencing maps the transcriptional regulatory landscape of glioblastoma multiforme. *Nature Genetics*. Nov;50(11):1553-1564.
10. Blumberg A, **Danko CG**, Kundaje A, Mishmar D¥ (2018). A common pattern of DNase-I footprinting throughout the human mtDNA unveils clues for a chromatin-like organization. *Genome Research*. Aug;28(8):1158-1168.
11. Horibata S, Rice EJ, Zheng H, Mukai C, Chu T, Marks BA, Coonrod SA¥, **Danko CG¥** (2018). A bi-stable feedback loop between GDNF, EGR1, and ER α contributes to endocrine resistant breast cancer. *PLoS One*. Apr 3;13(4):e0194522.

12. Horibata S, [Rice EJ](#), Mukai C, Marks BA, Sams LK, Zheng H, Anguish LJ, Coonrod SA, [Danko CG](#) (2018). ER-positive breast cancer cells are poised for RET-mediated endocrine resistance. *PLoS One*. Apr 2;13(4):e0194023.
13. Birkenheuer CH, [Danko CG](#), Baines JD (2018). Herpes Simplex Virus 1 Dramatically Alters Loading and Positioning of RNA Polymerase II on Host Genes Early in Infection. *J Virol*. 2018 Feb 7. pii: JVI.02184-17. doi: 10.1128/JVI.02184-17.
14. [Danko CG](#), [Choate LA](#), Marks BA, [Rice EJ](#), [Wang Z](#), [Chu T](#), [Martins AL](#), Dukler N, Coonrod SA, Tait-Wojno E, Lis JT, Kraus WL, Siepel A (2018). Dynamic Evolution of Regulatory Element Ensembles in Primate CD4+ T Cells. *Nature Ecology & Evolution*. Mar;2(3):537-548. **Featured in a perspective piece**
15. Meyers-Wallen VN, Boyko AR, [Danko CG](#), Grenier JK, Mezey JG, Hayward JJ, Shannon LM, Gao C, Shafquat A, [Rice EJ](#), Pujar S, Eggers S, Ohnesorg T, Sinclair AH (2017) XX Disorder of Sex Development is associated with an insertion on chromosome 9 and downregulation of RSPO1 in dogs (*Canis lupus familiaris*). *PLoS One*. Oct 20;12(10):e0186331.
16. Dukler N, Booth GT, Huang YF, Tippens N, [Danko CG](#), Lis JT, Siepel A (2017). Nascent RNA sequencing reveals a dynamic global transcriptional response at genes and enhancers to the natural medicinal compound celastrol. *Genome Research*, Oct 12. doi: 10.1101/gr.222935.117.
17. Vihervaara A, Mahat DB, Guertin MJ, [Chu T](#), [Danko CG](#), Lis JT, Sistonen L (2017). Transcriptional response to stress is pre-wired by promoter and enhancer architecture. *Nature communications*, Aug 15;8(1):255.
18. [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*, 27(3):362-373.
19. 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*, 11(8):1455-1476.
20. [Choate LA](#), [Danko CG](#) (2016). Poised for development. *Nature genetics*, 48(8):822-823. **Invited by the editor**
21. [Wang Z](#), [Martins AL](#), [Danko CG](#) (2016). RTFBSDB: an integrated framework for transcription factor binding site analysis. *Bioinformatics*, 32(19):3024-3026.
22. 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*, 62(1):63-78. Mar 24.
23. 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*, 13(2): 337-349. **Cover article**
24. 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.
25. Andersson R, Sandelin A, [Danko CG](#) (2015). A unified architecture of transcriptional regulatory elements. *Trends in genetics*, Aug;31(8):426-33.
26. Fuda NJ, Guertin MJ, Sharma S, [Danko CG](#), [Martins AL](#), Siepel A, 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.

27. **Danko CG**, Hyland SL, Core LJ, Martins AL, Waters CT, Lee HW, Cheung VG, Kraus WL, Lis JT, Siepel A (2015). Accurate identification of active transcriptional regulatory elements from global run-on and sequencing data. *Nature Methods*. P.011353.
28. Core LJ*, Martins AL*, **Danko CG**, Waters C, Siepel A, 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**
29. Luo X, Chae M, Krishnakumar R, **Danko CG**, Kraus WL (2014). Dynamic reorganization of the AC16 cardiomyocyte transcriptome in response to TNF α signaling revealed by integrated genomic analyses. *BMC genomics*, 15(1):155.
30. 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. *Journal of veterinary internal medicine*, 28(1):92-101.
31. Hah N, Murakami S, Nagari A, **Danko CG**, Kraus WL (2013). Enhancer Transcription Marks Active Estrogen Receptor Binding Sites. *Genome research*.
32. **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*, 50(2):212-222. **Cover article; Featured in a perspective piece; Recommended by Faculty of 1000**
33. 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.
34. Gronau I, Hubisz MJ, Gulko B, **Danko CG**, Siepel A. (2011). Bayesian inference of ancient human demography from individual genome sequences. *Nature genetics*, 43(10):1031-1034.
35. 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. *Journal of veterinary cardiology*, 13(2):101-113. **Cover article**
36. 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**
37. Schuster SC et al. (2010). Complete Khoisan and Bantu genomes from southern Africa. *Nature*, 463(7283):943-947. **Cover article**
38. **Danko CG**, Pertsov AM (2009). Identification of gene co-regulatory modules and associated cis-elements involved in degenerative heart disease. *BMC medical genomics*, 2(1):31.
39. **Danko CG**, McIlvain VA, Qin M, Knox BE, Pertsov AM (2007). Bioinformatic identification of novel putative photoreceptor specific cis-elements. *BMC bioinformatics*, 8(1):407.
40. 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.

Refereed Conference Papers

41. Wang Z, Christie M, Abeysinghe E, Chu T, Marru S, Pierce M, **Danko CG** (2018). Building a Science Gateway for processing and modeling sequencing data via Apache Airavata. Proceedings of the Practice and Experience on Advanced Research Computing (PEARC '18). ISBN #: 978-1-4503-6446-1. doi: 10.1145/3219104.3219141.

Seminars & Talks

Invited Seminars

- 2019 “Gene Regulatory Control through the Lens of ChRO-seq”, Skirball Institute of Biomolecular Medicine, NYU Langone Health Center, New York, NY.
- 2018 “Positive Selection Drives Changes in the Primate Immune System”, Cornell Center for Vertebrate Genomics, Cornell University, Ithaca, NY.
- 2018 “Glioblastoma multiforme through the lens of ChRO-seq”, Institute for Computational Biology, Weill Cornell Medical Center, New York, NY.
- 2018 “Glioblastoma multiforme through the lens of ChRO-seq”, Baker Advisory Council, New York, NY.
- 2017 “Chromatin Run-on Reveals Nascent RNAs That Differentiate Normal and Malignant Brain Tissue”, RNA Symposium, Cornell University, Ithaca, NY.
- 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, 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

Active

R01 HG010346 (Danko, Siepel) 05/01/19-04/30/23

Evolution of Chromatin Architecture and Transcriptional Regulation in Mammals

National Human Genome Research Institute (NHGRI)

The primary goal of this proposal is to understand how distinct layers of gene regulation evolve in concert to maintain, and sometimes change, organism phenotypes.

Role: contact PI

17-EXO-17-2-0112 (Danko) 05/01/18-04/30/21

POL II Pausing as a Milestone on the Road to Complex Animals

National Aeronautics and Space Administration (NASA)

The primary goal of this proposal is to determine when and how paused RNA polymerase evolved.

Role: PI

R01 AI130379-01A1 (Tait Wojno) 09/25/17-08/31/22

Role of the Prostaglandin D2 Receptor CRTH2 in Helminth-Induced Type2 Inflammation in the Intestine

National Institutes of Allergy and Infectious Disease (NIH/NIAID)

The goal of this project is to study how the PGD2-CRTH2 pathway regulates IECs and integrates with cytokine networks during helminth infection, expanding our understanding of intestinal type 2 inflammation and informing the development and use of therapies that target CRTH2 to treat type 2 inflammatory diseases.

Role: Co-I

- TG-BIO160048 (Danko) 04/01/19-03/31/20
dREG Science Gateway
Extreme Science and Engineering Discovery Environment (XSEDE)
This project is a grant for time on the XSEDE high performance computing resources which provides the community with a web-based interface for our dREG software package.
Role: PI
Computer time. Resources: 6,560 GPU hours.
- R01 HG009309-01 (Danko) 02/01/17-01/31/22
Mapping RNA polymerase in tissue samples with ChRO-seq
National Human Genome Research Institute (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
- TG-MCB160061 (Danko) 04/01/19-03/31/20
Discovery of genomic control elements using machine learning
Extreme Science and Engineering Discovery Environment (XSEDE)
This project is a grant for time on the XSEDE high performance computing resources. The goal of this project is to use machine learning tools to identify the genomic location of active functional elements in mammalian genomes.
Role: PI
Computer time. Resources: 5,872 GPU hours.
- 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
- U01HL129958 (Lis, Henning, Zipfel) 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 mis-regulated to produce disease conditions and how effective therapies could be developed.
Role: Co-I
- 2R01AG024425-11 (Lee, Danko) 09/01/15-08/31/20
Genetic and Epigenetic Determinants of Longevity
National Institutes of Health
The goal of this project is to understand the genetic and epigenetic determinants of longevity in the *C. elegans* model.

Role: Co-I

Completed

TG-BIO160048 (Danko) 02/14/17-03/31/19

dREG Science Gateway

Extreme Science and Engineering Discovery Environment (XSEDE)

This project is a grant for time on the XSEDE high performance computing resources which provides the community with a web-based interface for our dREG software package.

Role: PI

Computer time. Resources: 50,000 service units (SUs).

TG-MCB160061 (Danko) 07/20/16-03/31/19

Discovery of genomic control elements using machine learning

Extreme Science and Engineering Discovery Environment (XSEDE)

This project is a grant for time on the XSEDE high performance computing resources. The goal of this project is to use machine learning tools to identify the genomic location of active functional elements in mammalian genomes.

Role: PI

Computer time. Resources: 419,968 service units (SUs).

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

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

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

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

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

Teaching & Mentoring

Cornell Graduate Field Memberships

Ecology & Evolutionary Biology (EEB)	2018-
Tri-Institutional Program for Computational Biology & Medicine (Tri-I CBM)	2016-
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

Gilad Barshad, Ph.D.	2019-
Mridusmita Saikia, Ph.D. (joint with Elia Tait-Wojno & Iwijn De Vlaminck)	2016-
James Lewis, Ph.D.	2016-
Reproductive Genomics T32	

Graduate Students

Alexandra Chivu, Genetics, Genomics & Development (joint with John Lis)	2019-
Jonathan Villanueva, Biological and Biomedical Sciences (joint with Praveen Sethupathy)	2018-
SUNY McNair Diversity Fellowship	
Adriana Alexander, Comparative Biomedical Sciences (joint with Paula Cohen)	2017-
NSF predoctoral fellowship, SUNY McNair Diversity Fellowship	
Shao-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 Croucher Foundation Fellowship	2014-
---	-------

Rotation Students

Iskander Said, Genetics, Genomics & Development	2019
Lauren Walter, Genetics, Genomics & Development	2019
Alexandra Chivu, Genetics, Genomics & Development	2018
Jonathan Villanueva, Biological and Biomedical Sciences	2018
Minsoo Kim, Tri-Institutional Program for Computational Biology & Medicine	2017
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

Pierce McMahon, Undergraduate	2018-
Jay Chia, Undergraduate	2018
Samantha Lin, Leadership student	2018
Hedda Somsen, Exchange student	2018
Zilu Wang, Ithaca High school student	2017-2018
Connor Musick, Undergraduate	2017-2018
Vianne Gao, Undergraduate summer intern from Carleton College	2017
Marlena Holter, VIP Student	2017
Gavisha Waidyaratne, Postbac	2017
Maria Dalby, Exchange student	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

Yingying Zhang, Biophysics (Yu)	2019-
Alexa Bracci, Genetics Genomics & Development (Koren)	2018-
Tommy Carter, Genetics Genomics & Development (Feschotte)	2017-
Michael DeBerardine, Genetics Genomics & Development (Lis)	2017-
Yeonui Kwak, Genetics Genomics & Development (Kwak)	2017-

Debadrita Bhattacharya, Biochemistry, Molecular & Cell Biology (Simoese-Costa)	2017-
Dashiell Massey, Genetics Genomics & Development (Koren)	2017-
Ellie Larson, Biological & Biomedical Sciences (Wagner)	2017-
Simon Frueh, Biological & Biomedical Sciences (Tait Wojno)	2017-
Alex Cheng, Biomedical Engineering (De Vlaminck)	2017-
Andrea Slavney, Genetics Genomics & Development (Clark)	2016-2017
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)	2015-2018
Digbijay Mahat, Biochemistry, Molecular & Cell Biology (Lis)	2014-2017
Joo Hyun Im, Genetics Genomics & Development (Lazzaro)	2014-2018
Wenke Wang, Biochemistry, Molecular & Cell Biology (Lee)	2014-2017

A-exam Committee Membership

Simon Frueh, Biological & Biomedical Sciences (Tait Wojno)	2018
Ellie Larson, Biological & Biomedical Sciences (Wagner)	2018
Yeonui Kwak, Genetics Genomics & Development (Kwak)	2018
Sylvia Chang, Genetics Genomics & Development (Feschotte)	2018
Debadrita Bhattacharya, Biochemistry, Molecular & Cell Biology (Simoese-Costa)	2018
Dashiell Massey, Genetics Genomics & Development (Koren)	2018
Brooke Marks, Biological & Biomedical Sciences (Coonrod)	2017
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-

Cellular Physiology (BioAP3160, White, Yen) 2018-

Veterinary Curriculum

Block 2, guest lecture on new tools in genomics and epigenetics 2018

Graduate Curriculum

Development and Evolution (BioMG4610) – guest lecture 2019

Critical Thinking in Genetics & Development (BioMG7810) – genomics workshop 2018

Precision and Genomic Medicine (BME6120, De Vlaminck) – guest lecture 2016, 2018

Problems in Genetics & Development (BioMG7810) 2015-2017

Computational Genetics & Genomics (BTRY4840/6840, Williams) – guest lecture 2015

Administrative Experience

Intramural Service

Undergraduate Thesis Review, Bio Honors Michael Zelko (Kwak) 2019

Undergraduate Thesis Review, Bio Honors Alex Friefeld (Cohen) 2019

Center for Comparative and Population Genomics (3CPG), Executive Committee 2018-

Genetics Genomics & Development graduate program, Steering Committee 2018-

Institute of Biotechnology, Core facilities @ Cornell, Advisory Board Member 2017-

Bio-IT Core Facility, Chair of the Advisory Board 2017

Graduate field of Computational Biology, Membership Committee 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 2016-2018

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

Perspectives in Comparative Genomics & Evolution, Workshop Session Organizer	2019
4DN Consortium Annual Meeting, Abstract Reviewer	2017
4DN Consortium Annual Meeting, Organizing Committee	2017-
4DN Consortium, Data Analysis Working Group	2016-
Canine Longevity Consortium, phenotype working group	2015
Canine Longevity Consortium, advisory committee meeting	2014-2015

Ad Hoc Journal Reviews

Bioinformatics (2)	BMC Bioinformatics
BMC Genomics	Cell (2)
Genome Research (4)	Nature Protocols (3)
Molecular Biology & Evolution (3)	Nature Genetics (2)
Molecular Systems Biology	Nature Methods
Nature Communications	PLoS One
PCI Evolutionary Biology	Trends in Genetics
Nucleic Acids Research (3)	Mol. Cancer Research
PLoS Computational Biology	Science
Genome Biology & Evolution (2)	G3 (2)
Human Molecular Genetics	eLife
The EMBO Journal	Nature (2)