

## Charles G. Danko, Ph.D.

Assistant Professor of Epigenetics  
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## Education

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

## Research & Work Experience

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<b>Assistant Professor, Genomics of Gene Regulation</b>		2014-
Baker Institute of Animal Health, College of Veterinary Medicine, Cornell University, Ithaca NY		
<b>Postdoctoral Fellow</b>		2009-2014
Biological Statistics & Computational Biology, Cornell University, Ithaca NY		
<b>Software Developer</b>		2007-2008
SUNY Microarray Core Facility, Syracuse, NY		

## Distinctions & Awards

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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

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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

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\* equal contribution, † corresponding author, Danko lab members

### Preprints Submitted for Peer-Review

1. Blumberg A, **Danko CG**, Kundaje A, Mishmar D (2017). A common pattern of DNase-I footprinting throughout the human mtDNA unveils clues for a chromatin-like organization. *bioRxiv*: <https://doi.org/10.1101/193037>
2. Chu T, Rice EJ, Booth GT, Salamanca HH, Wang Z, Core LJ, Longo SL, Corona RJ, Chin LS, Lis JT, Kwak H†, **Danko CG**† (2017). Chromatin run-on reveals nascent RNAs that differentiate normal and malignant brain tissue. *bioRxiv*: <https://doi.org/10.1101/185991>

### Journal Articles

3. Horibata S, Rice EJ, Zheng H, Mukai C, Chu T, Marks BA, Coonrod S†, **Danko CG**† (2018). A bi-stable feedback loop between GDNF, EGR1, and ER $\alpha$  contributes to endocrine resistant breast cancer. *PLoS One*. Apr 3;13(4):e0194522.
4. Horibata S, Rice EJ, Mukai C, Marks BA, Sams LK, Zheng H, Anguish LJ, Coonrod S†, **Danko CG**† (2018). ER-positive breast cancer cells are poised for RET-mediated endocrine resistance. *PLoS One*. Apr 2;13(4):e0194023.
5. 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.
6. **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*. doi: 10.1038/s41559-017-0447-5. **Featured in a perspective piece**
7. 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.
8. 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.
9. 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.
10. Wang Z, Chu T, Choate LA, **Danko CG**† (2017). Rgtsvm: Support Vector Machines on a GPU in R. arXiv preprint *arXiv*: <https://arxiv.org/abs/1706.05544>
11. 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.
12. 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.

13. Choate LA, **Danko CG** (2016). Poised for development. *Nature genetics*, 48(8):822-823. **Invited by the editor**
14. Wang Z, Martins AL, **Danko CG** (2016). RTFBSDB: an integrated framework for transcription factor binding site analysis. *Bioinformatics*, 32(19):3024-3026.
15. 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.
16. 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**
17. 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.
18. Andersson R, Sandelin A, **Danko CG** (2015). A unified architecture of transcriptional regulatory elements. *Trends in genetics*, 31(8):426-433.
19. 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.
20. **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.
21. 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**

#### Publications Prior to Tenure Track Appointment

22. Luo X, Chae M, Krishnakumar R, **Danko CG**, Kraus WL (2014). Dynamic reorganization of the AC16 cardiomyocyte transcriptome in response to TNF $\alpha$  signaling revealed by integrated genomic analyses. *BMC genomics*, 15(1):155.
23. Oxford EM, **Danko CG**, Fox P, Kornreich B, Moise NS (2014). Change in  $\beta$ -catenin localization suggests involvement of the canonical Wnt pathway in Boxer dogs with arrhythmogenic cardiomyopathy. *Journal of veterinary internal medicine*, 28(1):92-101.
24. Hah N, Murakami S, Nagari A, **Danko CG**, Kraus WL (2013). Enhancer Transcription Marks Active Estrogen Receptor Binding Sites. *Genome research*.
25. **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**
26. 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.
27. 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.
28. 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

29. 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**
30. Schuster SC et al. (2010). Complete Khoisan and Bantu genomes from southern Africa. *Nature*, 463(7283):943-947. **Cover article**
31. **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.
32. **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.
33. 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

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### Invited Seminars

- 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. **3<sup>rd</sup> 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

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### Active

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) 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).

- 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
- 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
- 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).
- 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
- 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, 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 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 determents of longevity in the *C. elegans* model.  
Role: Co-I

### Completed

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

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#### 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

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. Reproductive Genomics T32	2016-

### Graduate Students

Adriana Alexander, Comparative Biomedical Sciences (joint with Paula Cohen) NSF predoctoral fellowship, SUNY McNair Diversity Fellowship	2017-
Shao-Pei Chou, Genetics, Genomics & Development	2016-
Paul Munn, Computational Biology	2016-
Lauren Choate, Genetics, Genomics & Development Center for Vertebrate Genomics fellowship	2015-
Tin Yi Chu, Computational Biology Croucher Foundation Fellowship	2014-

### Rotation Students

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

Samantha Lin, Leadership student	2018
Zilu Wang, Ithaca High school student	2017
Connor Musick, Undergraduate	2017-
Vianne Gao, Undergraduate summer intern from Carleton College	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

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 (Marcos Simoes-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-
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

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

### Graduate Curriculum

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

## Administrative Experience

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### Intramural Service

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-  
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-  
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 (2) Nature Protocols (2)  
Molecular Biology & Evolution (3) Nature Genetics  
Molecular Systems Biology PLoS One

PCI Evolutionary Biology  
Nature Communications  
Nucleic Acids Research (2)  
PLoS Computational Biology  
Genome Biology & Evolution

Nature Methods  
Trends in Genetics  
Mol. Cancer Research  
Science  
G3