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DATE UPDATED: August 15, 2018

MAJOR PROFESSIONAL INTERESTS

Evolutionary genetics; quantitative genetics

EDUCATION

- 1996-2000 B.S. in Biological Sciences with departmental honors
Stanford University, Stanford, CA
Advisor: Dr. Matthew P. Scott
Dissertation: *in vivo* analysis of *Drosophila* heart-tube formation
- 2000-2008 Ph.D. in Biology
Massachusetts Institute of Technology (MIT), Cambridge, MA
Advisor: Dr. H. Robert Horvitz
Dissertation: The synthetic Multivulva genes and their suppressors regulate opposing cell fates through chromatin remodeling
- 2008-2013 Post-doctoral fellowship
Princeton University
Advisor: Dr. Leonid Kruglyak

PRE-DOCTORAL AWARDS, HONORS, AND FELLOWSHIPS

- 2005 - 2006 Anna Fuller Cancer Graduate Research Fellowship
2000 Firestone Medal for Excellence in Undergrad. Research (top Biological Sciences researcher)
1999, 1998 Howard Hughes Medical Institute Summer Research Fellowship
1998 Stanford University Undergraduate research small grant recipient
1996-1998 Robert C. Byrd Honors Scholarship recipient

POST-DOCTORAL RECOGNITIONS

- 2012 - 2013 Howard Hughes Medical Institute Post-doctoral Fellow
2011 - 2012 National Cancer Institute Post-doctoral Fellow, training grant T32-CA009528
2009 - 2011 Ruth L. Kirschstein National Research Service Award Recipient
2018 - 2023 National Science Foundation CAREER Award Recipient
2017 - Associate Editor for *BMC Genomics*
2015 - Editorial Board Member of *Trends in Genetics*
2015 - 2019 American Cancer Society Research Scholar
2015 - 2017 March of Dimes Basil O'Connor Research Scholar
2014 - 2018 Pew Scholar in the Biomedical Sciences

EMPLOYMENT

- 2013 - Assistant Professor of Molecular Biosciences, Northwestern University
 Preceptor for the Interdisciplinary Biological Sciences Graduate Program (IBiS)
 Full Member of the Robert H. Lurie Comprehensive Cancer Center
 Member of the Chemistry of Life Processes Institute (CLP)
 Member of Northwestern Institute on Complex Systems (NICO)
- 2008 - 2013 Post-doctoral fellow, Princeton University, Princeton, NJ, Advisor: Dr. Leonid Kruglyak
- 2000 - 2008 Graduate student, Biology Department at Massachusetts Institute of Technology (MIT),
 Cambridge, MA, Advisor: Dr. H. Robert Horvitz

RESEARCH SUPPORT**PRESENT**

- 2018 - 2023 National Science Foundation
 CAREER Award (1751035)
Discovery of the molecular mechanisms underlying microevolution of phenotypic plasticity in a developmental trait
 PI - Andersen
 Total costs \$530,812 (Andersen)
- 2018 - 2022 National Institutes of Health (U2C OD026506) - NIEHS
Genetics and quantum chemistry as tools for unknown metabolite identification
 Lead PI: Dr. Art Edison (UGA), co-PIs Andersen, Fernandez (Georgia Tech),
 McIntyre (U of Florida), Merz (Missouri State), Schroeder (Cornell)
 Total direct costs \$2,500,000, Andersen direct costs: \$235,000
- 2018 Google, Inc.
 Google Cloud Platform Research credit award
Optimization of computational pipelines to support the C. elegans Natural Diversity Resource
 PI - Andersen
 Total direct costs: \$5,000 (Andersen)
- 2018 - 2023 National Science Foundation (1764421) and Simons Foundation (597491)
 Research Center for Mathematics of Complex Biological Systems
Understanding organismal growth and development through quantitative approaches
 Lead PIs Dr. Rich Carthew and Dr. Bill Kath, co-PIs Andersen, Mangan, Bagheri, Braun, Wang
 Total direct costs: \$7,443,790, Andersen direct costs: \$65,000 (first year)
- 2018 - 2022 National Institutes of Health (R01 GM127433) - NIGMS
100k spontaneous mutations: the foundation for an evolutionary systems biology of C. elegans
 PI Dr. Charlie Baer (Univ. of Florida), PI Dr. Vaishali Katju (Texas A+M) with sub to Andersen
 Total direct costs \$1,600,000, Andersen direct costs \$550,000
- 2017 - 2021 National Institutes of Health (R01 DK115690) - NIDDK
Large scale nutrigenetics and genomics in a tractable metazoan model
 Multi-investigator Grant with EC Andersen, AJ Marian Walhout (UMass Medical School), Frank
 Schroeder (Cornell)
 Total direct costs \$2,000,000, Andersen direct costs \$800,000

- 2017 - 2019 National Institutes of Health (R21 AG053638) - NIA
High-throughput multi-modal analysis of natural variation in C. elegans healthspan
 Multi-investigator Grant with Chris Fang-Yen (Univ. of Pennsylvania) and Andersen
 Total direct costs \$275,000, Andersen direct costs \$137,500
- 2016 - 2019 National Institutes of Health (R21 AI121836) - NIAID
Discovery and validation of avermectin resistance loci in free-living and parasitic nematodes
 PI - Andersen with subcontract to Dr. Michael Kimber (Iowa State University)
 Total direct costs \$275,000, Andersen direct costs \$200,000
- 2015 - 2019 American Cancer Society Research Scholar Grant
Elucidating the genetic causes of variation in chemotherapy-based toxicity
 PI - Andersen
 Total direct costs \$787,658 (Andersen)
- 2014 - 2019 Pew Charitable Trusts, Scholars Program in the Biomedical Sciences
Elucidating the genetics of anthelmintic resistance in nematode-borne neglected tropical diseases
 PI - Andersen
 Total direct costs \$255,000 (Andersen)
- 2014 - 2019 National Institutes of Health (R01 GM107227) - NIGMS
Direct determination of the distribution of fitness effects of spontaneous mutations
 PI Dr. Charlie Baer (University of Florida) with subcontract to Andersen
 Total direct costs \$800,000, Andersen direct costs \$360,000
- PAST**
- 2016 - 2017 Amazon Web Services
Optimization of computational pipelines to support the C. elegans Natural Diversity Resource
 PI - Andersen
 Total direct costs \$3,000 (Andersen)
- 2016-2017 IDP/Sherman Fairchild Research Innovation Challenge Award, Robert H. Lurie Comprehensive Cancer Center
Validating individual differences in cytotoxicity to improve personalized chemotherapy treatment regimens
 Multi-investigator Grant with Andersen and Dr. Paul Burrige (Northwestern University)
 Total direct costs \$75,000, Andersen direct costs \$37,500
- 2015 - 2017 March of Dimes Basil O'Connor Starter Research Grant
Identification of hookworm anthelmintic resistance genes to ameliorate maternal and infant anemia
 PI - Andersen
 Total direct costs \$150,000 (Andersen)
- 2016 Weinberg College Research Innovation Grant, Northwestern University
The Caenorhabditis elegans Natural Diversity Resource - a powerful tool to facilitate biomedical discovery
 PI - Andersen
 Total direct costs \$40,000 (Andersen)

- 2014 - 2016 Chicago Biomedical Consortium, Catalyst Grant
Uncovering "missing heritability" in an experimentally tractable model organism
 Multi-investigator Grant with Andersen and Ilya Ruvinsky (University of Chicago)
 Total direct costs \$240,000, Andersen direct costs \$120,000
- 2016 Data Scientist Initiative, Northwestern University
A novel statistical model to predict the removal of mobile genetic elements
 Multi-investigator Grant with Andersen and Jiping Wang (Northwestern University)
 Total direct costs \$20,000 (Andersen)
- 2013 - 2014 American Cancer Society, Institutional Research Grant [93-037-18]
Elucidating the genetic causes of variation in chemotherapy-based toxicity
 PI - Andersen
 Total direct costs \$30,000 (Andersen)
- 2013 - 2014 Chemistry of Life Processes, Chairman's Innovation Award
Using perturbations of heavy metal homeostasis to treat nematode-borne neglected tropical diseases
 Multi-investigator Grant with Andersen and Thomas O'Halloran (Northwestern University)
 Total direct costs \$28,000 (Andersen)
- PENDING**
- 2018 - 2023 National Institutes of Health (R01 ES029930) - NIEHS
Discovery of conserved molecular mechanisms underlying population-wide variation in toxin responses
 Lead PI: Erik Andersen, co-PIs: Baugh (Duke), Rockman (NYU)
 Priority score 25 (top in panel ZES1 LWJ-S (R2), expected start date Dec.1, 2018)
 Total direct costs \$2,500,000
- 2018 - 2020 National Science Foundation (1756495)
 Collections in Support of Biological Research: Living Stocks
Enhancing the efficiency of the C. elegans Natural Diversity Resource
 PI - Andersen
 Total direct costs \$463,664 (Andersen)
- 2018 - 2023 National Institutes of Health (R01 GM132599) - NIGMS
High-throughput genomic approaches to understand the evolution of metazoan developmental plasticity
 PI - Andersen
 Total direct costs \$1,250,000 (Andersen)
- 2018 - 2023 National Institutes of Health (R01 AA027539) - NIAAA
Species-wide and genus-wide approaches to identify natural variants in alcohol responses
 Lead PI Dr. Jon Pierce (Univ. of Texas - Austin), co-PI Andersen
 Total costs \$2,500,000, Andersen costs \$1,000,000
- 2019 - 2022 Human Frontiers Science Program (LIP000827/2019)
 Successful Letter of Intent (top 11%), 38% of applications in the next stage will be funded
The repeatability of genetic mechanisms underlying behavioral evolution
 Lead PI Andersen, co-PIs Dr. Andre Brown (Imperial Coll. London), Kathryn Hodgins (Monash)
 Total costs \$1,350,000, Andersen costs \$450,000
- 2019 - 2024 Chan Zuckerberg Initiative Ben Barres Early Career Acceleration Award
Identification of conserved genetic modifiers affecting neurodegeneration
 PI - Andersen
 Total direct costs \$2,500,000 (Andersen)

PUBLICATIONS

corresponding authors in bold, *undergraduate co-authors in italics*, graduate students and post-docs in underline

h-index=19, i10-index=23, link to Google Scholar page ([here](#))

1. Zdraljevic S, Fox BW, Strand C, Panda O, Tenjo-Castano FJ, Brady SC, Crombie TA, Doench JG, Schroeder FC, and **Andersen EC** (2018)
Natural variation in arsenic toxicity is explained by differences in branched chain amino acid catabolism
bioRxiv 373787; DOI: <https://doi.org/10.1101/373787>
Under review at *eLife*
2. Hahnel SR, Zdraljevic S, Rodriguez BC, Zhao Y, McGrath PT, and **Andersen EC** (2018)
Extreme allelic heterogeneity at a *Caenorhabditis elegans* beta-tubulin locus explains natural resistance to benzimidazoles
bioRxiv 372623; DOI: <https://doi.org/10.1101/372623>
Under review at *PLoS Pathogens*
3. Brady SC, Evans KS, Bloom JS, Tanny RE, Cook DE, Giuliani SE, *Hippleheuser SW*, Zamanian M, and **Andersen EC**.
Common genomic intervals underlie natural variation in diverse toxin responses
bioRxiv 325399; DOI: <https://doi.org/10.1101/325399>
Under revision at *Genetics*
4. Zamanian M, Cook DE, Zdraljevic S, Brady SC, Lee D, Lee J, and **Andersen EC** (2018)
Discovery of genomic intervals that underlie nematode responses to benzimidazoles
PLoS Neglected Tropical Diseases Mar 5; 12(3):e0006368
Citations: 2, Journal Impact Factor (2015): 3.948
5. Zdraljevic S and **Andersen EC** (2017)
Natural diversity facilitates the discovery of conserved chemotherapeutic response mechanisms
Current Opinions in Genetics and Development Dec;47:41-47
Citations: 1, Journal Impact Factor (2016): 5.825
6. Zdraljevic S, Strand C, Seidel HS, Cook DE, Doench JG, and **Andersen EC** (2017)
Natural variation in a single amino acid substitution underlies physiological responses to topoisomerase II poisons
PLoS Genetics Jul 12; 13(7):e1006891
Citations: 7, Journal Impact Factor (2016): 6.100
7. Lee D, Yang H, Kim J, Brady SC, Zdraljevic S, Zamanian M, Kim H, Paik Y, Kruglyak L, **Andersen EC** and **Lee J** (2017)
The genetic basis of natural variation in a phoretic behavior
Nature Communications Aug 17; 8(1):273
Citations: 7, Journal Impact Factor (2016): 12.124
8. Laricchia KM, Zdraljevic S, Cook DE, and **Andersen EC** (2017)
The causes and consequences of natural variation in the distribution and abundance of transposable elements across the *Caenorhabditis elegans* species.
Molecular Biology and Evolution Sept 1; 34(9):2187-2202
Citations: 3, Journal Impact Factor (2016): 13.649

9. Garcia-Gonzalez AP, Ritter AD, Shrestha S, Andersen EC, Yilmaz LS, **Walhout AJM** (2017)
Bacterial metabolism affects the *C. elegans* response to cancer chemotherapeutics.
Cell Apr 20; 169(3):431-441
Citations: 27, Journal Impact Factor (2016): 28.710
10. Cook DE and **Andersen EC** (2017)
VCF-kit: Assorted utilities for the variant call format
Bioinformatics May 15; 33(10):1581-1582
Citations: 5, Journal Impact Factor (2016): 7.307
11. Mashock MJ, Zanon T, Kappell AD, Petrella LN, Andersen EC, **Hristova KR** (2016)
Copper oxide nanoparticles impact several toxicological endpoints and cause neurodegeneration in *Caenorhabditis elegans*
PLoS ONE Dec 2; 11(12):e0167613
Citations: 5, Journal Impact Factor (2016): 2.806
12. Evans KS, Zhao Y, Brady SC, Long L, McGrath PT, **Andersen EC** (2016)
Correlations of genotype with climate parameters suggest *Caenorhabditis elegans* niche adaptations
G3 Nov 18; [10.1534/g3.116.035162]
Citations: 5, Journal Impact Factor (2016): 3.198
13. Cook DE, Zdraljevic S, Roberts JP, **Andersen EC** (2016)
CeNDR, the *Caenorhabditis elegans* Natural Diversity Resource.
Nucleic Acids Research Jan 4; 45(D1):D650-D657
Citations: 28, Journal Impact Factor (2016): 10.162
14. Cook DE, Zdraljevic S, Tanny RE, Seo B, Riccardi DD, Noble LM, Rockman MV, Alkema MJ, Braendle C, Kammenga JE, Wang J, Kruglyak L, Felix MA, Lee J, **Andersen EC** (2016)
The genetic basis of natural variation in *C. elegans* telomere length
Genetics Sept; 204(1):371-83
Citations: 28, Journal Impact Factor (2016): 5.963
15. Large EE, Xu W, Zhao Y, Brady SC, Long L, Butcher RA, Andersen EC, **McGrath PT** (2016)
Selection on a Subunit of the NURF Chromatin Remodeler Modifies Life History Traits in a Domesticated Strain of *Caenorhabditis elegans*
PLoS Genetics July 28; 12(7):e1006219
Citations: 8, Journal Impact Factor (2016): 6.100
16. Zamanian M and **Andersen EC**. (2016)
Prospects and challenges of CRISPR/Cas genome editing for the study and control of neglected vector-borne nematode diseases
FEBS Sep; 283(17):3204-21 **Commissioned review**
Citations: 18, Journal Impact Factor (2016): 4.237
17. Farhadifar R, Ponciano JM, Andersen EC, Needleman DJ, **Baer CF**. (2016)
Mutation Is a Sufficient and Robust Predictor of Genetic Variation for Mitotic Spindle Traits in *Caenorhabditis elegans*
Genetics Aug; 203(4):1859-1870
Citations: 8, Journal Impact Factor (2016): 5.963

18. Sterken MG, Snoek LB, **Kammenga JE, Andersen EC.** (2015)
The laboratory domestication of *C. elegans*
Trends in Genetics Mar; 31(5) 224-231
Citations: 47, Journal Impact Factor (2016): 11.45
19. Thompson OA, Snoek LB, Nijveen H, Sterken MG, Volkers RJM, Brenchley R, van't Hof A, Bevers RPJ, Cossins AR, Yanai I, Hajnal A, Schmid T, Perkins JD, Spencer D, Kruglyak L, Andersen EC, Moerman DG, Hillier LW, Kammenga JE, **Waterston RH.** (2015)
Remarkably divergent regions punctuate the genome assembly of the *Caenorhabditis elegans* Hawaiian strain CB4856
Genetics May 19; 200(3) 975-989
Citations: 43, Journal Impact Factor (2016): 5.963
20. **Andersen EC, Shimko TC,** Crissman JR, Ghosh R, Gerke JP, Seidel HS, **Kruglyak L.** (2015)
A powerful new quantitative genetics platform combining *Caenorhabditis elegans* high-throughput fitness assays with a large collection of recombinant strains
G3 Mar 13; 5(5) 911-920
Citations: 31, Journal Impact Factor (2016): 3.198
21. Farhadifar R, Baer CF, Valfort AC, Andersen EC, Muller-Reichert T, Delattre M, **Needleman DJ.** (2015)
Scaling, Selection, and Evolutionary Dynamics of the Mitotic Spindle
Current Biology Mar 16; 25(6) 732-740
Citations: 30, Journal Impact Factor (2016): 8.851
22. Balla K, Andersen EC, Kruglyak L, **Troemel E.** (2015)
A wild *C. elegans* strain has enhanced epithelial immunity to a natural microsporidian parasite
PLoS Pathogens Feb 13; 11(2)e1004583
Citations: 20, Journal Impact Factor (2016): 7.000
23. Etienne V*, Andersen EC*, Ponciano JM, Blanton D, Cadavid A, Joyner-Matos J, Matsuba C, Tabman B, **Baer CF.** (2015)
The Red Death Meets the Abdominal Bristle: Polygenic Mutation for Susceptibility to a Bacterial Pathogen in *Caenorhabditis elegans*
Evolution Feb; 69(2) 508-519 *equal contribution
Citations: 5, Journal Impact Factor (2016): 4.612
24. **Shimko TC, Andersen EC.** (2014)
COPASutils: an R package for reading, processing, and visualizing data from COPAS large-particle flow cytometers
PLoS One Oct 20; 9(10):e111090
Citations: 15, Journal Impact Factor (2016): 2.806
25. **Andersen EC,** Bloom JS, Gerke JP, **Kruglyak L.** (2014)
A variant in the neuropeptide receptor *npr-1* is a major determinant of *Caenorhabditis elegans* growth and physiology
PLoS Genetics Feb; 10(2):e1004156
Citations: 53, Journal Impact Factor (2016): 6.100

Publications from before Northwestern University:

undergraduate co-authors in italics, corresponding authors underlined

Felix MA, Jovelin R, Ferrari C, Han S, Cho YR, Andersen EC, Cutter AD, Braendle C. (2013)
Species richness, distribution and genetic diversity of *Caenorhabditis* nematodes in a remote tropical rainforest
BMC Evolutionary Biology 13(1), 10

Ghosh R, Andersen EC, Shapiro JA, Gerke JP, Kruglyak L. (2012)
Natural variation in a chloride channel subunit confers avermectin resistance in *C. elegans*
Science 335(6068): 574-578.

Andersen EC*, Gerke JP*, Shapiro JA*, Crissman JR, Ghosh R, Bloom JS, Felix MA, Kruglyak L. (2012)
Chromosome-scale selective sweeps shape *Caenorhabditis elegans* genomic diversity
Nature Genetics 44(3): 285-290. *equal contribution

Andersen EC. (2011)
PCR-directed *in vivo* plasmid construction using homologous recombination in baker's yeast
Molecular Methods for Evolutionary Genetics, 772; 409-421. *Invited book chapter

Raj A, Rifkin SA, Andersen EC, van Oudenaarden A. (2010)
Variability in gene expression underlies incomplete penetrance
Nature 463(7283): 913-918.

Bessler JB, Andersen EC, Villeneuve AB. (2010)
Differential localization and independent acquisition of the H3K9me2 and H3K9me3 chromatin modifications in the *Caenorhabditis elegans* adult germ line
PLoS Genetics 6(1): e1000830.

Reddy KC*, Andersen EC*, Kruglyak L., and Kim DH. (2009)
A polymorphism in *npr-1* is a behavioral determinant of pathogen susceptibility in *C. elegans*
Science 323(5912): 382-384. *equal contribution

Andersen EC, Saffer AM, and Horvitz HR. (2008)
Multiple levels of redundant processes inhibit *Caenorhabditis elegans* vulval cell fates
Genetics 179(4): 2001-2012.

Andersen EC and Horvitz HR. (2007)
Two *C. elegans* histone methyltransferases repress *lin-3* EGF transcription to inhibit vulval development
Development 134(16): 2991-2999.

Reddien PW, Andersen EC, Huang M., and Horvitz HR. (2007)
DPL-1 DP, LIN-35 Rb, and EFL-1 E2F act with the MCD-1 Zinc-finger protein to promote programmed cell death in *C. elegans*
Genetics 175(4): 1719-1733.

Andersen EC, Lu X, and Horvitz HR. (2006)
C. elegans ISWI and NURF301 antagonize an Rb-like pathway in the determination of multiple cell fates
Development 133(14): 2695-2704.

Furlong EE, Andersen EC, Null B, White KP, and Scott MP. (2001)
Patterns of gene expression during *Drosophila* mesoderm development
Science 293(5535): 1629-1633.

WORK NOW IN PROGRESS

corresponding authors in bold, *undergraduate co-authors in italics*, graduate students and post-docs in underline

The following five items are under preparation. Except for the collaborative book chapter, all of these manuscripts will be submitted to BioRxiv and to a traditional journal in fall 2018.

Deiparine S, Lee D, and **Andersen EC**

Chemotaxis assays reveal an opportunistic relationship between the model organism
Caenorhabditis elegans and the non-host terrestrial isopod *Porcellio scaber*

Organisms that live “boom-and-bust” lifestyles must move to food-rich environments once local environments are depleted of nutrients. Oftentimes, this movement from one niche to another is mediated by other more mobile organisms, called phoresy. Phoretic interactions are often mediated by chemical cues allowing the organisms to find each other. The nematode roundworm *Caenorhabditis elegans* rapidly proliferates in bacteria-rich environments and then upon food depletion must move to more favorable niches. *C. elegans* is hypothesized to have phoretic interactions with snails, millipedes, and terrestrial isopods because these nematodes are often found in close association in the natural environment. These interactions could be phoresy in which *C. elegans* hitches a ride with a more mobile second species to move to more favorable environments. We investigated the chemical cues that could promote interactions between *C. elegans* and the terrestrial isopod species *Porcellio scaber*, which is sometimes found with *C. elegans*. Using standard chemotaxis assays, we assayed if *C. elegans* is attracted to washes, extracts, or gas secretions from *P. scaber*. We found, that across two developmental stages and two diverse genetic backgrounds, *C. elegans* is not attracted to *P. scaber*. Our results suggest that any interactions in nature are likely stochastic but nevertheless beneficial to *C. elegans*. Additionally, this work sets the framework for future experiments to determine if *C. elegans* is attracted to snails or millipedes.

Zdraljevic S, Wang Y, Cook DE, Tanny RE, Frezal L, Felix MA, Rockman MV, Braendle C, Ailion M,
Sterken MG, Kammenga JE, Wang J, Bokman E, Topper A, Pritz C, and **Andersen EC**
Genome evolution across a large collection of *Caenorhabditis elegans* wild isolates

Using a collection of 746 whole-genome sequenced *Caenorhabditis elegans* wild strains, we investigated strain relationships, genome-wide relatedness, spatial population genetic clustering, and signatures of selection across the species. As we found previously, species-wide diversity is largely influenced by four selective sweeps that occurred in recent history. However, high levels of genomic diversity are found in strains isolated from Pacific Rim countries. We find at least 12 *C. elegans* subtypes by admixture analysis and evidence of at least two migration events. These data refine the haplotype structure of the species and give us the ability to better define regions of selection throughout the genome. Background selection caused by large central chromosomal regions of low recombination and arm chromosomal regions of high recombination drive diversity. Additionally, we find evidence weak spatial structure across genetic diversity worldwide. These data suggest that *C. elegans* likely originated from a Pacific Rim region where we find high levels of genetic diversity.

Crombie TA, Zdraljevic S, Cook DE, Brady SC, Tanny RE, Evans KS, Hahnel SR, Lee D, Rodriguez BC,
van der Zwaag J, and **Andersen EC**
The Hawaiian Islands harbor high levels of *Caenorhabditis elegans* species-wide natural diversity

Caenorhabditis is a diverse genus of nematodes that includes the well studied model organism *C. elegans*. Until recently, the ecology and niche preferences for nematodes in this genus were largely understudied. Consequently, many of the existing wild isolates originate from opportunistic samplings of human-associated habitats. Could this small, biased sampling effort play a role in the low genetic diversity associated with some *Caenorhabditis* taxa such as *C. elegans*? To address this question and elucidate niche preferences within the genus, we extensively sampled nematodes from the Hawaiian Islands, because many of the most genetically divergent *C. elegans* wild strains come from this location. We sampled nematodes at 2,263 collection sites across five islands, recording GPS coordinates and various niche parameters, including temperature, moisture, elevation, and substrate type. Because of the large scale of this sampling effort, data collection was streamlined using a customized data-collection application for mobile devices (Fulcrum®). In total, we isolated 2,531 distinct wild isolate strains to be genotyped in the lab. Wild isolates were genotyped by PCR to identify nematodes in the Rhabditida family, then Rhabditida-positive PCR products were sequenced to distinguish *Caenorhabditis* nematodes at the species level. Of 2,263 total collection sites, 233 (10%) contained Rhabditida nematodes. Of these isolates, 157 collections contained *Caenorhabditis* nematodes, including five separate species; *C. elegans*, *C. briggsae*, *C. tropicalis*, *C. kamaaina*, and a new species, named *C. oiwi*. This new species was typically found on flower substrates (10 of 12 collections) indicating a possible substrate preference. *C. elegans* was commonly found on fruits, nuts, and leaf litter, which challenges the hypothesis that it is infrequently isolated from leaf litter. At three collection sites, we found two *Caenorhabditis* species on the same substrate, illustrating some niche overlap within the genus. Analysis of niche parameters suggests that *C. tropicalis* and *C. oiwi* are restricted to warmer substrates, while *C. elegans* prefers higher elevation and cooler environments than other members of the genus. These findings begin to clarify niche preferences among *Caenorhabditis* species. Furthermore, whole-genome sequencing of the 95 *C. elegans* wild isolates collected in this study revealed additional genetic diversity and facilitated improved population genomic analyses of this species.

Evans KS, Sterken MG, Snoek B, Kammenga JE, and **Andersen EC**

Correlations of soil and climate attributes with genomic regions across the *Caenorhabditis elegans* species

Species inhabit a variety of environmental niches, and the adaptation to a particular niche is often controlled by genetic factors, including gene-by-environment interactions. The genetic variation that underlies the ability to colonize a niche is often difficult to identify, especially in the context of complex ecological systems and in experimentally uncontrolled natural environments. Quantitative genetic approaches provide an opportunity to investigate correlations between genetic factors and environmental parameters that might define a niche. Previously, we described correlations of climate variables with natural variation in a collection of 152 whole-genome sequenced wild *Caenorhabditis elegans* to identify 11 quantitative trait loci (QTL) for three climatic variables: elevation, relative humidity, and average temperature. In this study, we expanded our analyses to include isolation data from a total of 330 wild *C. elegans* strains and then collated updated climate parameters and a large collection of soil data sampled from SoilGrids. We used these data to perform genome-wide association studies and identify genomic intervals that underlie variation in climate and soil parameters. We find additional climate QTL and novel connections between soil parameters and *C. elegans* diverged haplotypes. These results suggest more about the niche where *C. elegans* might prefer to inhabit in nature.

Brady SC, Zdraljevic S, Cook DE, and **Andersen EC**

Variation in a histone demethylase underlies natural differences in *Caenorhabditis elegans* bleomycin sensitivity

Many chemotherapeutic drugs are differentially effective from one patient to the next. Understanding the causes of this variability is a critical step towards the development of personalized treatments and improvements to existing medications. Here, we investigate sensitivity to the naturally produced chemotherapeutic drug bleomycin using the model organism *Caenorhabditis elegans*. We show that two strains of *C. elegans* vary in their sensitivity to this drug, and we use an unbiased quantitative genetic approach to map and identify a histone demethylase gene (*jmjd-5*) underlying this differential sensitivity. Because bleomycin causes double-stranded DNA breaks (DSB), and this histone demethylase has been implicated in DSB repair, we believe that histone demethylation regulates bleomycin-induced DSBs.

Collaborative work in preparation for submission in summer 2018:

Daul A, Andersen EC, and Rougvie A

The *Caenorhabditis* Genetics Center and CeNDR

Commissioned book chapter for a forthcoming book entitled *Genetic Resources of Model Organisms - Strategies for Conservation* by Taylor and Francis Group, LLC

This chapter covers the available resources for the *Caenorhabditis* genus from tens of thousands of mutant *C. elegans* strains to wild strains isolated from nature. I contributed a description of the *C. elegans* Natural Diversity Resource, its composition, and future plans. CeNDR is the worldwide repository for all wild *C. elegans* strains, sequence data, and an association mapping portal (www.elegansvariation.org.)

Bernstein MR, Zdraljevic S, Andersen EC, and **Rockman MV**

Near-isogenic lines reveal tightly linked antagonistic-effect loci underlying polygenic demographic variation in *C. elegans*

Recent work has provided strong empirical support for the classic polygenic model for trait variation. These findings suggest that an arbitrary region of genome is likely to harbor variation affecting an arbitrary trait. This view is hard to reconcile with the experience of researchers who define gene functions using mutagenesis, in which many mutants are identified, examined, and compared one-at-a-time to the wild type. Here, we use the approach of experimental genetics to show that, indeed, arbitrary regions of genome have detectable effects on complex traits. We used high-throughput phenotyping to characterize demography as a multivariate trait in growing populations of *Caenorhabditis elegans* recombinant inbred lines sensitized by nickel stress to show that demography under these conditions is genetically complex. We then focused on an arbitrary 1.4-Mb region of the X chromosome using Near Isogenic Lines that differ across this whole region. These lines were phenotypically indistinguishable, but when we subdivided the region into fifteen intervals, each encompassing ~0.001 of the genome, we found that eleven of intervals have significant effects. These effects are often similar in magnitude to those of genome-wide significant QTL mapped in the recombinant inbred lines but antagonized by the effects of variants in adjacent intervals. Contrary to the expectation of small additive effects, our findings point to large-effect variants whose effects are masked under normal conditions by epistasis or linkage disequilibrium.

PROFESSIONAL TALKS

Departmental seminars and invited conference presentations (not including trainees):

- 2019 Dept. of Infectious Diseases, Univ. of Georgia, Athens, GA
Dept. of Biology, Georgia Institute of Technology, Atlanta, GA
- 2018 Max Planck Institute for Developmental Biology, Tübingen, Germany
Dept. of Evolutionary Ecology and Genetics, Christian-Albrechts-Universität, Kiel, Germany
Berlin Seminar for Resistance Research, Freie Universität Berlin, Berlin, Germany
RH Lurie Cancer Center, Northwestern University, Chicago, IL
Dept. of Genetics, Washington University School of Medicine, St. Louis, MO
Dept. of Genetics, University of Pennsylvania, Philadelphia, PA
Dept. of Pathobiology, University of Pennsylvania, Philadelphia, PA
Dept. of Microbiology, Seoul National University, Seoul, Korea
Dept. of Biology, University of Oregon, Eugene, OR
Dept. of Biological Sciences, University of Southern California, Los Angeles, CA
Dept. of Cell Biology and Anatomy, Rosalind Franklin University, Chicago, IL
New York Univ. Center for Genomics and Sys. Bio. Parasite Workshop, Abu Dhabi, UAE
- 2017 Department of Biology, Univ. of California - San Diego, San Diego, CA
Department of Biology, Duke University, Durham, NC
Donnelly Centre for Cellular And Biomolecular Research, University of Toronto, Toronto, ON
Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY
Medical Research Council, London Institute of Medical Sciences, London, UK
Department of Biology, Carnegie Mellon University, Pittsburgh, PA
Host-Parasite Interactions, University of Calgary, Banff, Canada
Florida Area Worm Meeting (keynote), Florida Institute of Technology, Melbourne, FL
Department of Biology, Skirball Institute, New York University Medical School, New York, NY
Department of Biology, University of Minnesota, Minneapolis, MN
Department of Biology, Indiana University, Bloomington, IN
New York University Center for Genomics and Systems Biology Symposium in Abu Dhabi, UAE
- 2016 Midwest Quantitative Biology at Purdue University, West Lafayette, IN
Molecular and Cellular Biology of Helminth Parasites X, Hydra, Greece
Computational Research Day, Northwestern University, Evanston, IL
Evolutionary Biology of *Caenorhabditis* and other nematodes (keynote), CSHL, Cold Spring Harbor, NY
Department of Genetics, University of Utah, Salt Lake City, UT
Department of Biology, University of Iowa, Iowa City, IA
Department of Biomedical Sciences, Iowa State University, Ames, IA
Anthelmintics: Discovery to Resistance II, San Diego, CA
- 2015 Program in Systems Biology, University of Massachusetts Medical School, Worcester, MA
Evolution seminar series, University of Wisconsin, Madison, WI
Biotechnology Training Program, Northwestern University, Evanston, IL
Department of Biology, Johns Hopkins University, Baltimore, MD
Department of Biology, University of Maryland, College Park, MD
Department of Pharmacology, Feinberg School of Medicine, Northwestern University, Chicago, IL
Midwest Neglected Infectious Disease Meeting, Notre Dame University, South Bend, IN
Quantitative genetics workshop, 20th International *C. elegans* meeting, UCLA, Los Angeles, CA
Michigan Area Worm Meeting, van Andel Institute, Grand Rapids, MI
- 2014 Northwestern Institute on Complex systems, Northwestern University, Evanston, IL
Fondation de Treilles: Revisiting the roles of phenotypic plasticity in evolution, Provence, France
Biology Department, Marquette University, Milwaukee, WI
Pharmacogenomics group, University of Chicago, Chicago, IL

Seminars before starting at Northwestern:

- 2013 Quantitative genetics workshop, 19th International *C. elegans* meeting, UCLA, Los Angeles, CA
Molecular Bioscience Department, Northwestern University, Evanston, IL
Program in Systems Biology, University of Massachusetts Medical School, Worcester, MA
- 2012 Biology Department, Dartmouth University, Hanover, NH
Human Genetics Department and Life Sciences Institute, University of Michigan, Ann Arbor, MI
Genetics Department, University of Georgia, Athens, GA
Biology Department, Case Western Reserve University, Cleveland, OH
Biology Department and BioDesign Institute, Arizona State University, Phoenix, AZ
Center for Computational and Integrated Biology, Rutgers University, Camden, NJ
Biology Department, University of Florida, Gainesville, FL
- 2011 Evolution workshop, 18th International *C. elegans* meeting, UCLA, Los Angeles, CA
Laboratory of Toxicology, NIEHS, Research Triangle Park, NC
- 2010 Institute for Evolutionary Biology Department, University of Edinburgh, Edinburgh, UK
- 2008 Featured talk at *C. elegans* Aging, Stress, and Pathogenesis meeting, Madison, WI
- 2000 Undergraduate research symposium, Stanford University, Stanford, CA

Seminars chosen from abstracts (not including trainees): (*selected for oral presentation)

- 2018 *Evolutionary biology of *Caenorhabditis* and other nematodes meeting, Hinxton, UK
Evolutionary biology of *Caenorhabditis* and other nematodes meeting (poster), Hinxton, UK
*Anthelmintics III, Indian Rocks Beach, FL
- 2017 *Molecular Helminthology: An Integrated Approach, Cape Cod, MA
- 2015 *Midwest Neglected Infectious Disease meeting, U. of Notre Dame, Notre Dame, IN
*Bridging the divide, 20th International *C. elegans* meeting, UCLA, Los Angeles, CA
- 2013 *19th International *C. elegans* meeting, UCLA, Los Angeles, CA
Society for Molecular Biology of Evolution, Chicago, IL
- 2012 *Evolutionary biology of *Caenorhabditis* and other nematodes meeting, CSHL, NY
- 2011 *18th International *C. elegans* meeting, UCLA, Los Angeles, CA
18th International *C. elegans* meeting (poster), UCLA, Los Angeles, CA
- 2010 *Evolutionary biology of *Caenorhabditis* and other nematodes meeting, Hinxton, UK
- 2010 Evolutionary biology of *Caenorhabditis* and other nematodes meeting (poster), Hinxton, UK
Cold Spring Harbor Labs Automated Imaging and High-throughput Phenotyping, CSHL, NY
- 2009 *17th International *C. elegans* meeting, UCLA, Los Angeles, CA
Gordon Research Conference on Quantitative Genetics and Genomics, Galveston, TX
- 2007 Department of Biology Annual Retreat, MIT, ** poster prize winner
- 2006 *C. elegans* Evolution and Development meeting, Univ. of Wisconsin, Madison, WI
- 2005 *15th International *C. elegans* meeting, UCLA, Los Angeles, CA
Chromatin Structure and Function meeting, Nassau, Bahamas
- 2004 East Coast *C. elegans* meeting, Yale, New Haven, CT
- 2003 *14th International *C. elegans* meeting, UCLA, Los Angeles, CA
- 2002 East Coast *C. elegans* meeting, University of New Hampshire, Durham, NH

PEER REVIEW AND RELATED ACTIVITIES**Editorial board:***Trends in Genetics***Associate editor:***BMC Genomics (Multicellular invertebrate genomics)*

Guest editor:*PLoS Genetics***Reviewing activity: Academic Journals**

American Naturalist, Biological Journal of the Linnean Society, BMC Evolutionary Biology, BMC Genetics, BMC Genomics, Cell, Development, eLife, EMBO, Environmental Microbiology, Genes and Development, G3, Genetics, Genome Research, Journal of Visualized Experiments, Heredity, Nature, Nature Scientific Reports, Nature Genetics, PLoS Genetics, PLoS Neglected Tropical Diseases, PLoS ONE, PLoS Pathogens, PNAS, Science, Scientific Reports, Trends in Genetics, Trends in Molecular Medicine, Trends in Parasitology

Reviewing activity: Grants and fellowships

2018 Scientific Advisory Board for P01AI127338 (PI Michael Ferdig, Notre Dame Univ.)
 2017 *Ad hoc* reviewer for Bill and Melinda Gates Foundation
 2014 *Ad hoc* reviewer for Human Frontiers Science Program
 2014 *Ad hoc* reviewer for National Science Foundation (IOS)

PROFESSIONAL AFFILIATIONS AND SERVICE**Membership in Professional Societies:**

Genetics Society of America, member

Society of Molecular Biology and Evolution, member

Professional service:

2019 Organizing committee for the 22nd International *C. elegans* meeting
 2018 Organizing committee for *C. elegans* dev., cell bio., and gene exp. meeting (Barcelona, Spain)
 Chair of the Natural Variation session, *C. elegans* dev., cell bio., and gene exp. meeting
 Co-organizer of the Chicago Area Worm Meeting (ChAWM, www.chawm.org)
 Scientific Advisory Board Member for P01AI127338 (PI Dr. Michael Ferdig, Notre Dame Univ.)
 Organizing committee for Parasitic Nematodes meeting, NYU Abu Dhabi
 External thesis committee member for Victoria Vu (Fraser lab, University of Toronto)
 Poster judge, Northwestern Undergraduate Research Symposium
 2017 Organizing committee for the 21st International *C. elegans* meeting
 Chair of the Evolution and Ecology parallel session, 21st International *C. elegans* meeting
 2015 Organizing committee for the 20th International *C. elegans* meeting
 Poster judge, 20th International *C. elegans* meeting - Evolution and Genomics section
 Genetics Soc. of America Mentor Lunch, *Postdoc search*, 20th International *C. elegans* meeting
 2014 Panelist, NUIN Post-doc Association, *Interviews and Start-up packages*
 Poster judge, Northwestern Undergraduate Research Symposium
 Panelist, Pathways to the Professoriate, *How to prepare for a job interview?*
 2013 Poster judge, Northwestern Undergraduate Research Symposium
 Panelist, Bioscientist Freshman seminar; *How to find a research lab?*
 Poster judge, 19th International *C. elegans* meeting - Evolution and Genomics section

***C. elegans* community service:**

2016 - Creator and director of the *C. elegans* Natural Diversity Resource (CeNDR, [link](#))
 This resource organizes and disseminates wild *C. elegans* strains, whole-genome sequence data, and enables genome-wide association mappings through a cloud-based service. Since 2016, over 1400 strains have been distributed to the community and over 2000 mappings have been performed.

TEACHING AND ADVISING

Undergraduate teaching:

- 2018 **Biological Sciences 393: *Genetic Analysis* (winter, 32 students)**
 Biological Sciences 398: *Tutorial in Biology* (Karol Bisaga)
 Biological Sciences 399: *Independent Research*
 (Karol Bisaga, Kimberly Collins, Selina Deiparine, Grace Park)
- 2017 **Biological Sciences 393: *Genetic Analysis* (spring, 27 students)**
 Biological Sciences 398: *Tutorial in Biology* (Kimberly Collins)
 Biological Sciences 399: *Independent Research*
 (Selina Deiparine, Samuel Hamilton, Grace Park)
- 2016 **Biological Sciences 393: *Genetic Analysis* (spring, 17 students)**
 Biological Sciences 398: *Tutorial in Biology*
 (Sarah Bier, Mattlyn Cordova, Selina Deiparine, Samuel Hamilton, Grace Park)
- 2015 *Guest Lecture: University of Wisconsin-Madison Biology 675 - Evolution seminar*
 (fall, 8 students)
New course: Biological Sciences 393: *Genetic Analysis* (spring, 12 students)
 Biological Sciences 398: *Tutorial in Biology* (Lautaro Cilenti)
 Biological Sciences 399: *Independent Research* (Kreena Patel, Hillary Tsang)
- 2014 Biological Sciences 398: *Tutorial in Biology* (Mazeed Aro-Lambo, Kreena Patel, Hillary Tsang)

Graduate teaching:

- 2018 Interdisciplinary Biological Sciences 421: *Rigor and Reproducibility*
 (summer, one guest lecture, 25 students)
 Interdisciplinary Biological Sciences/Chemistry 416: *Practical Training in Chemical Biology Methods and Experimental Design*
 (spring, five lectures, 17 students)
- 2017 Interdisciplinary Biological Sciences 421: *Rigor and Reproducibility*
 (summer, one guest lecture, 15 students)
 Interdisciplinary Biological Sciences/Chemistry 416: *Practical Training in Chemical Biology Methods and Experimental Design*
 (spring, five lectures, 19 students)
 Interdisciplinary Biological Sciences 421: *Rigor and Reproducibility*
 (spring, one guest lecture, 5 students)
- 2016 Interdisciplinary Biological Sciences: *Graduate Computational Biology Bootcamp*
 (fall, 3 days, eight hours per day, 19 students) - www.GitHub.com/AndersenLab/IBiS-Bootcamp
- 2015 Interdisciplinary Biological Sciences 402: *Eukaryotic Molecular Biology*
 (fall, one guest lecture, 22 students)
 Interdisciplinary Biological Sciences: *Graduate Computational Biology Bootcamp*
 (fall, 3 days, eight hours per day, 22 students) - www.GitHub.com/AndersenLab/IBiS-Bootcamp
 Interdisciplinary Biological Sciences 423: *Ethics of peer review*
 (spring, one guest lecture, 41 students)
- 2014 Interdisciplinary Biological Sciences 402: *Eukaryotic Molecular Biology*
 (fall, one guest lecture, 16 students)
New course: Interdisciplinary Biological Sciences: *Graduate Computational Biology Bootcamp*
 (fall, 3 days, eight hours per day, 16 students) - www.GitHub.com/AndersenLab/IBiS-Bootcamp
 Interdisciplinary Biological Sciences 423: *Ethics of peer review*
 (spring, one guest lecture, 42 students)
- 2013 Interdisciplinary Biological Sciences 402: *Eukaryotic Molecular Biology*
 (fall, one guest lecture, 24 students)

K-12 advising:

Britney Sun, Glenbrook North High School (summer 2018)
 Ethan Schonfeld, Glenbrook North High School (summer 2018)
 Lillian Tushman, Oak Park and River Forest High School (2016-2017 academic year)
 Caitlin Westerfield, Evanston Township High School (2015-2016 academic year)
 Matteo di Bernardo, Evanston Township High School (2015-2016 academic year)
 Ainsley Tran, Oak Park and River Forest High School (2015-2016 academic year)
 Lauren Mann, Oak Park and River Forest High School (2014-2015 academic year)
 Jacob Cruger, Latin School of Chicago (summers 2013, 2014)
 Gina Liu, Illinois Math and Science Academy (2013-2014 academic year)

Undergraduate advising:

Katie Introcaso (2018 - , Class of 2022), Biological Sciences Major
 Ellen Chao (2018 - , Class of 2021), Biological Sciences Major
2018 Summer URG recipient
 Tim Sheng (2018 - , Class of 2019), Biological Sciences Major
2018 Summer URG recipient
 Yihong Hu (2018 - , Class of 2021), Biological Sciences Major
2018 Program in Biological Sciences Summer Grant recipient
 Grace Park (2016 - , Class of 2019), Biological Sciences Major
2016 Posner Fellowship recipient
2017 Program in Biological Sciences Summer Grant recipient
 Peter Finnegan (2017 - 2018, Class of 2020), Biological Sciences Major
2017 Program in Biological Sciences Summer Grant recipient
 Karol Bisaga (2017 - 2018, Class of 2020), Biological Sciences Major
2017 NU Bioscientist Summer Grant recipient
 Kimberly Collins (2016 - 2018, Class of 2020), Biological Sciences Major
2017 NU Bioscientist Summer Grant recipient
 Selina Deiparine (2016 - 2018, Class of 2018), Biological Sciences Major
2016 Summer URG recipient, 2016 Academic URG recipient
 Rohit Rastogi (2016 - 2017, Class of 2019), Computer Science and Statistics Majors
 Sarah Bier (2016 - 2017, Class of 2019), Biological Sciences Major
2016 Summer URG recipient
 Mattlyn Cordova (2016 - 2017, Class of 2019), Gender Studies Major
2016 Program in Biological Sciences Summer Grant recipient
 Joshua Roberts (2015-2016, Class of 2016), Computer Science Major
 Nicholas Irons (2015, Class of 2018), Physics Major
2015 Summer URG recipient
 Annika Zhang (2014-2015, Class of 2018), Biological Sciences Major
2015 Weinberg College Summer Grant recipient
 Tyler Shimko (summers 2012, 2013, 2014, 2015, University of Utah Class of 2015), Biology Major
Barry Goldwater Scholarship recipient
Myriad Academic Scholarship recipient
Thomas Verender Hanks Scholarship recipient
National Science Foundation Graduate Research Fellowship recipient
Department of Energy Computational Science Graduate Fellowship Honorable Mention
 Mazeed Aro-Lambo (2014, Class of 2017), Biological Sciences Major
2014 NU Bioscientist Summer Grant recipient
 Stevie Hippleheuser (2014 - , Class of 2017), Biological Sciences Major
2016 Program in Biological Sciences Summer Grant recipient
2015 Summer URG recipient
2014 Weinberg College Summer Grant recipient

Camille Calvin (2014, Class of 2017), Mechanical Engineering Major
2014 Posner fellowship recipient

Hillary Tsang (2013 - 2016, Class of 2016), Biological Sciences Major
2015 Weinberg Summer Grant recipient
2014 Summer URG recipient
2014 Academic URG recipient

Lautaro Clienti (2013 - 2015, Class of 2017), Mechanical Engineering Major
2014 Academic URG recipient

Kreena Patel (2013 - 2015, Class of 2015), Biological Sciences and Psychology Double Major
2015 Emmanuel Margoliash Prize for Basic Research recipient
Winfred Hill Award recipient
James Alton James Scholar
Ellen Taus Scholarship recipient
J.G. Nolan Scholarship recipient
2014 Academic URG recipient

Zifan Xiang (2014 - 2015, Class of 2015), Biomedical Engineering Major

Stephen Chan (2013 - 2014, Class of 2014), Computer Science Major
2013 Summer URG recipient

Masters student advising:

Ryan (Heechul) Chung (Quantitative and Systems Biology Masters), 2018 - 2019

Suma Aldakeel (advisor, Cindy Voisine - Northeastern Illinois Univ.) 2016 - 2017

Nick Timkovich (advisor, Luis Amaral) 2015

Kristen Larrichia (advisor, Nyree Zerega – Program in Plant Biology and Conservation), 2014 - 2015

Lucie Bastin-Heline (Master's exchange student, Ecole Normale Superior, Paris, France), 2014

Graduate student and post-doctoral advising:

Graduate PhD candidates:

Clayton Dilks (2018 -), Ph.D. student, Interdisciplinary Biological Sciences Program
Funded by the Biotechnology NIH Training grant cluster (2019)

Ye Wang (2017 - 2019), Visiting Ph.D. student, Sichuan Agricultural University, China
Funded by China Scholarship Council

Kathryn Evans (2016 -), Ph.D. student, Interdisciplinary Biological Sciences Program
Funded by the Cell and Molecular Basis of Disease NIH Training grant (2017-2019)
Recipient of travel awards from IBiS and the Northwestern Graduate School (2017)
Recipient of Biotechnology NIH Training grant cluster member, declined (2017)

Shannon Brady (2015 -), Ph.D. student, Interdisciplinary Biological Sciences Program
Recipient of the Dr. John N. Nicholson Fellowship (2018-2019)
Funded by the Biotechnology NIH Training grant (2015-2017)
National Science Foundation Graduate Research Fellowship Program (Honorable Mention)
Recipient of travel award from Union Biometrika (2016)
Recipient of travel awards from IBiS and the Northwestern Graduate School (2017)
Poster first prize winner Northwestern Computational Research Day (2017)
Poster prize winner 21st International C. elegans meeting
Best TA award IBiS Graduate Program (2017)

Daniel Cook (2014 - 2018), Ph.D. student, Driskill Graduate Program
 Current position: Senior Programmer at VectorBase, London, U.K.
Funded by a National Science Foundation Pre-doctoral Fellowship (2015-2018)
Recipient of travel awards from IBiS and the Northwestern Graduate School (2016)
Northwestern Presidential Fellowship Finalist (2017)

Stefan Zdraljevic (2014 -), Ph.D. student, Interdisciplinary Biological Sciences Program
Recipient of the IBiS Rappaport Award for Research Excellence (2018)
Funded by the Cell and Molecular Basis of Disease NIH Training grant (2015-2017)
Recipient of travel awards from Northwestern Center for Genetic Medicine (2016, 2017)
Recipient of travel awards from IBiS and the Northwestern Graduate School (2015, 2017)
Chemistry of Life Processes Drug Discovery Scholar (2017)

Post-doctoral researchers:

Gaotian Zhang (2018 -), Ph.D. from Ecole Normale Supérieure, Paris, advisor Dr. Marie-Anne Felix
 Timothy Crombie (2017 -), Ph.D. from University of Florida, advisor Dr. David Julian
 Steffen Hahnel (2017 - 2018), Ph.D. from Justus-Liebig University, advisor Dr. Christoph Grevelding
 Current position: Scientist at Bayer Animal Health, Germany
Recipient of DFG German Science Fellowship (2018-2020)
Recipient of Northwestern Post-doctoral Travel Award (2018)
Recipient of Burroughs-Wellcome Travel Award (2018)
 Daehan Lee (2017 -), Ph.D. from Seoul National University, advisor Dr. Junho Lee
 Mostafa Zamanian (2014 - 2016), Ph.D. from Iowa State University, advisor Dr. Timothy Day
 Current position: Assistant Professor of Pathobiological Sciences, University of Wisconsin - Madison
Recipient of NIH/NIAID K22 Career Transition Award (2016)
Recipient of Northwestern Post-doctoral Travel Award (2016)
Funded by the Bill and Melinda Gates Foundation (2014)
 Bryn Gaertner (2014), Ph.D. from University of Oregon, advisor Dr. Patrick Phillips

Additional rotation graduate students:

Julie Liang (Spring, 2018), Elan Ness-Cohn (DGP, Spring, 2018) Kyle Siegel (Spring, 2018), Clayton Dilks (Winter, 2018), Garth Fisher (Fall, 2017), Nicholas Sepulveda (Spring, 2017), Michael Schamber (Winter, 2017), Evan Buechel (Spring, 2016), Nic Daffern (Spring, 2016), Bryan Eder (Winter, 2016), Ryan Abdella (Winter, 2015), Erin Baker (Fall, 2014), Alex Karge (Spring, 2014), Saiorse McSharry (Winter, 2014), Amy Nilles (Fall, 2013), Ian Wolff (Summer, 2013)

Graduate thesis committee memberships:

Alex McFarland (advisor, Erica Hartman) 2018 -
 Sumach Aldakeel (advisor, Cindy Voisine - Northeastern Illinois Univ.), 2016 - 2017
 Adam Hockenberry (advisors, Luis Amaral and Michael Jewett) 2015 - 2017
 Rachel Bakker (advisor, Rich Carthew) 2015 -
 Joseph Muldoon (advisors, Neda Bagheri and Josh Leonard) 2015 -
 Sarah Stainbrook (advisor, Keith Tyo) 2015 -
 Timothy Toby (advisor, Neil Kelleher) 2015 - 2018
 Rose Njoroge (advisor, Sarki Abdulkadir – DGP, Feinberg School of Medicine), 2014 - 2018
 Keila Torre-Santiago (advisor, Sadie Wignall) 2014 - 2017
 Aaron Sue (advisor, Thomas O'Halloran), 2014 -
 Arianne Rodriguez (advisor, Yun Wang), 2014 (Transferred to DGP)
 Ritika Giri (advisor, Richard Carthew), 2013 -
 Lilien Voong (advisor, Alec Wang), 2013 - 2017

DEPARTMENT, COLLEGE, AND UNIVERSITY SERVICE

Departmental Service:

2017 Departmental Strategic Planning committee
 2016 Faculty search committee for quantitative biology
 Departmental Strategic Planning committee

2015 Faculty search committee
 2014 Departmental Program Review committee

Weinberg College of Arts and Sciences Service:

2016 Faculty search committee for the Neurobiology Department
 2014 NUIN Post-doc Association, *Interviews and Start-up packages*

University-level Service:

2018 IBiS Graduate Admissions committee
 Steering committee for NUSeq Facility in Northwestern Medicine
 Qualifying examination committee, Chair (Alex McFarland, Hartman lab)
 Masters Program in Quantitative and Systems Biology, Curriculum committee
 Poster judge, Northwestern Undergraduate Research Symposium
Ad hoc reviewer for Chemistry of Life Processes undergraduate grants and fellowships
Ad hoc reviewer for Data Science Initiative grants and fellowships
 2017 Discussion organizer, Northwestern Computational Research Day
 Steering committee for NUSeq Facility in Northwestern Medicine
Ad hoc reviewer for Chemistry of Life Processes undergraduate grants and fellowships
Ad hoc reviewer for Data Science Initiative grants and fellowships
 2016 IBiS Computational Bootcamp for incoming graduate students
 Lurie Cancer Center American Cancer Society IRG review panel
 Steering committee for NUSeq Facility in Northwestern Medicine
Ad hoc reviewer for Chemistry of Life Processes undergraduate grants and fellowships
Ad hoc reviewer for Data Science Initiative grants and fellowships
 2015 IBiS Graduate Admissions committee
 2015 IBiS Retreat committee, Co-chair
 IBiS Computational Bootcamp for incoming graduate students
 Qualifying examination committee (Rachel Bakker, Carthew lab)
 Qualifying examination committee, Chair (Joseph Muldoon, Bagheri and Leonard labs)
 Qualifying examination committee (Sarah Stainbrook, Tyo lab)
 Qualifying examination committee (Timothy Toby, Kelleher lab)
 2014 Creation of IBiS Computational Bootcamp for incoming graduate students
 IBiS Retreat committee, Co-chair
 Qualifying examination committee (Aaron Sue, Morimoto lab)
 Qualifying examination committee (Arianne Rodriguez, Wang lab)
 Qualifying examination committee (Rose Njoroge, Abdulkadir lab)
 Masters thesis examination committee (Kristen Larrichia, Zerega lab)
 Poster judge, Northwestern Undergraduate Research Symposium
 2013 IBiS Graduate Admissions committee
 Qualifying examination committee (Lilien Voong, Wang lab)
 Qualifying examination committee (Ritika Giri, Carthew lab)
 Poster judge, Northwestern Undergraduate Research Symposium

COMMUNITY WORK

2018 - Mentored Britney Sun from Glenbrook North High School on variation in zinc responses
 2018 Mentored Ethan Schonfeld from Glenbrook North High School on variation in stress responses
 2016 - 2017 Mentored Lillian Tushman from Oak Park and River Forest High School on glucose responses
Recipient of 3rd place All-Illinois Science Research Competition
 2016 - 2017 Mentored Lillian Kameny from Alameda Community Learning Center on etoposide variation
 2016 - Assistant Den Leader, Pack 922
 2016 - 2017 American Youth Soccer Organization (AYSO) U8 Head Coach, *The Storm*

- 2015 - Hosted 80 5th grade students from Lincolnwood Elementary School for a day of science
- 2015 - 2016 Mentored Caitlin Westerfield from Evanston Township High School on pathway evolution
- 2015 - 2016 Mentored Ainsley Tran from Oak Park and River Forest High School on iron sensitivity
- 2015 - 2016 American Youth Soccer Organization (AYSO) U8 Head Coach, *Golden Ninjas*
- 2015 - 2016 Mentored Matteo di Bernardo from Evanston Township High School on anthelmintic sensitivity,
Recipient of Columbia University Scientific Scholars Fellowship
- 2014 - Lecturer on *C. elegans* genetics to the Latin School of Chicago advanced biology class
- 2014 Mentored Lauren Mann from Oak Park and River Forest High School on iodine sensitivity
- 2014 Co-organized with Jacob Cruger nematode collections with the Punahou School, Hawaii
- 2013, 2014 Mentored Jacob Cruger from Latin School of Chicago
- 2009 Organized nematode collections with Vassalboro Community School, Maine