

# Daniel E. Cook

☎ 773-382-0440 • ✉ danielecook@gmail.com • 🌐 danielecook.com

## Experience

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| <b>Swanton Lab, Crick Institute</b><br><i>Principal Research Fellow (Senior Bioinformatician)</i>   | <b>London, UK</b><br><i>2018-Present</i> |
| ◦ Development of bioinformatic pipelines as part of the TRACERx study. The project uses high-depth, whole-exome sequence data from multiple tumor regions to study many aspects of lung cancer. |  |
| <b>Vectorbase</b><br><i>Scientific Developer</i>  | <b>Remote</b><br><i>2018</i>             |
| <b>Tempus, Inc.</b><br><i>Bioinformatics Intern</i>   | <b>Chicago, IL</b><br><i>2017</i>        |
| <b>Andersen Lab, Northwestern University</b><br><i>Graduate Student</i>   | <b>Evanston, IL</b><br><i>2014-2018</i>  |
| ◦ Assembled, organized, and processed the largest collection of <i>C. elegans</i> wild isolate sequence data in existence.  |  |
| ◦ Identified a gene and variant underlying natural variation in telomere length across the <i>C. elegans</i> species.   |  |
| ◦ Created a web-based platform for performing studies of natural diversity in <i>C. elegans</i> (elegansvariation.org).   |  |
| ◦ Co-discovered a new species: <i>C. oiwi</i> .   |  |
| <b>Ober Lab, University of Chicago</b><br><i>Research Assistant</i>   | <b>Chicago, IL</b><br><i>2012-2013</i>   |
| ◦ Assisted with development of databases for phenotypic and genotypic data.   |  |
| ◦ Helped disclose carrier status to individuals.  |  |
| <b>Murray Lab, University of Iowa</b><br><i>Research Assistant</i>  | <b>Iowa City, IL</b><br><i>2009-2012</i> |
| ◦ Conducted geographic analysis of Iowa newborn screen data.  |  |
| ◦ Collected human placental tissue for genetic, epigenetic, and expression studies.   |  |

## Computational Skills

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<b>Projects:</b> <a href="https://github.com/danielecook">GitHub.com/danielecook</a>	<b>Development:</b> git, Jenkins, Travis-CI
<b>Programming:</b> Python, nim, Go, R, Bash, Javascript, Stata, L <sup>A</sup> T <sub>E</sub> X	<b>Database:</b> SQL, BigQuery, Google Datastore
<b>Machine Learning:</b> scikit-learn, scikit-image, pandas	<b>Pipelines:</b> Nextflow, Snakemake
<b>Cloud:</b> AWS, Google Cloud Platform	<b>Misc:</b> Web development, Django/Flask

## Education

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<b>Northwestern University</b> <i>Ph.D. Biological Sciences (Emphasis on Bioinformatics and Genomics)</i>	<b>Evanston, IL</b> <i>2013-2018</i>
<b>University of Iowa</b> <i>B.S. Biology with Honors</i>	<b>Iowa City, IA</b> <i>May 2010</i>

## Honors and Awards

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- **2014 - NSF-GRFP:** National Science Foundation Graduate Research Fellowship (Approx. \$130,000)

## Software

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Additional work can be seen on my GitHub profile: [GitHub.com/danielecook](https://github.com/danielecook)

### *Python Packages*

- VCF-kit - Command line utility for analyzing genetic variation.
- CeNDR ([elegansvariation.org](http://elegansvariation.org)) - Flask website that provides tools for working with wild isolates of the *C. elegans* species including a genome browser and a genome-wide association mapping pipeline.
- IEX-API-python - Python library for accessing data from the Investors Exchange (IEX) stock/financial data API.

### *R Packages*

- rdatastore - provides an R-based interface for Google Datastore.

### *Open Source Contributions*

- mosdepth - Added coverage summary for depth of coverage calculations of sequencing data.
- memoise - developed functionality for caching function results (memoisation) using cloud-based environments such as Amazon S3.

### *Side projects*

- hntrending.com - A website that queries HackerNews stories and comments in unique ways, and sorts the most popular stories by week/month/year.
- upvote.pub [source] - A reddit-style clone specifically geared towards scientific publications. This website was experimental and is no longer active.

### *Stata Programs*

- manhattan - Generation of Manhattan plots.
- ccmatch - Utility for case/control studies.

## Professional Activities

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- **2015, 2016** - NSF Data Science Workshop @ University of Washington

## Teaching

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- **Fall 2016** - *Biol. Sci. 390* - Advanced Molecular Biology
- **Spring 2015** - *Biol. Sci. 393* - Genetic Analysis
- **Summer 2014-2016** - IBiS Computational Biology Bootcamp

## Mentorship

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**Joshua Roberts, 2015-2016** - *Computer Science (CS) Undergraduate* - Improved software engineering practices, data handling ability, and developed web-application skillset. Joshua is now a software engineer at Lyft.

**Rohit Rastogi, 2016-2017** - *CS Undergraduate* - Fostered development of programming skills in R and Python. Rohit now works as a software engineer at Google.

## Publications

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**2019 Long-read sequencing reveals intra-species tolerance of substantial structural variations and new subtelomere formation in *C. elegans***

Kim, Chuna, Jun Kim, Sunghyun Kim, **Cook, Daniel E**, Kathryn S Evans, Erik C Andersen, and Junho Lee  
2019 *Genome research* 29.6. PMID: 31123081 DOI: 10.1101/gr.246082.118.

**A Novel Gene Underlies Bleomycin-Response Variation in *Caenorhabditis elegans***

Brady, Shannon C, Stefan Zdraljevic, Karol W Bisaga, Robyn E Tanny, **Cook, Daniel E**, Daehan Lee, Ye Wang, and Erik C Andersen  
2019 *Genetics*. PMID: 31171655 DOI: 10.1534/genetics.119.302286.

**[Preprint] Selection and gene flow shape niche-associated copy-number variation of pheromone receptor genes**

Lee, Daehan, Stefan Zdraljevic, **Cook, Daniel E**, Lise Frézal, Jung-Chen Hsu, Mark G Sterken, Joost AG Riksen, John Wang, Jan E Kammenga, Christian Braendle, et al.  
2019 *bioRxiv*. DOI: 10.1101/580803.

**[Preprint] Population selection and sequencing of *C. elegans* wild isolates identifies a region on chromosome III affecting starvation resistance**

Webster, Amy K, Anthony Hung, Brad T Moore, Ryan Guzman, James M Jordan, Rebecca EW Kaplan, Jonathan D Hibshman, Robyn E Tanny, **Cook, Daniel E**, Erik Andersen, et al.  
2019 *bioRxiv*. DOI: 10.1101/635417.

**[Preprint] Deep sampling of Hawaiian *Caenorhabditis elegans* reveals high genetic diversity and admixture with global populations**

Crombie, Timothy A, Stefan Zdraljevic, **Cook, Daniel E**, Robyn E Tanny, Shannon C Brady, Ye Wang, Kathryn S Evans, Steffen Hahnel, Daehan Lee, Briana C Rodriguez, et al.  
2019 *BioRxiv*. DOI: 10.1101/716928.

**2018 Discovery of genomic intervals that underlie nematode responses to benzimidazoles**

Zamanian, Mostafa, **Cook, Daniel E**, Stefan Zdraljevic, Shannon C Brady, Daehan Lee, Junho Lee, and Erik C Andersen  
2018 *PLoS neglected tropical diseases* 12.3. PMID: 29601575 DOI: 10.1371/journal.pntd.0006368.

**Shared genomic regions underlie natural variation in diverse toxin responses**

Evans, Kathryn S, Shannon C Brady, Joshua S Bloom, Robyn E Tanny, **Cook, Daniel E**, Sarah E Giuliani, Stephen W Hippleheuser, Mostafa Zamanian, and Erik C Andersen  
2018 *Genetics* 210.4. PMID: 30341085 DOI: 10.1534/genetics.118.301311.

**2017 Natural variation in the distribution and abundance of transposable elements across the *Caenorhabditis elegans* species**

Laricchia, KM, S Zdraljevic, **Cook, DE**, and EC Andersen  
May 2017 *Mol. Biol. Evol.* PMID: 28486636 DOI: 10.1093/molbev/msx155.

**Natural variation in a single amino acid substitution underlies physiological responses to topoisomerase II poisons**

Zdraljevic, Stefan, Christine Strand, Hannah S Seidel, **Cook, Daniel E**, John G Doench, and Erik C Andersen  
July 2017 *PLoS Genet.* 13.7. PMID: 28700616 DOI: 10.1371/journal.pgen.1006891.

**VCF-kit: Assorted utilities for the variant call format.**

**Cook, DE** and EC Andersen

Jan. 2017 *Bioinformatics (Oxford, England)*. PMID: 28093408 DOI: 10.1093/bioinformatics/btx011.

**2016 CeNDR, the *Caenorhabditis elegans* natural diversity resource**

**Cook, Daniel E**, Stefan Zdraljevic, Joshua P Roberts, and Erik C Andersen

Oct. 2016 *Nucleic Acids Research*. PMID: 27701074 DOI: 10.1093/nar/gkw893.

**The Genetic Basis of Natural Variation in *Caenorhabditis elegans* Telomere Length**

**Cook, Daniel E**, Stefan Zdraljevic, Robyn E Tanny, Beomseok Seo, David D Riccardi, Luke M Noble, Matthew V Rockman, Mark J Alkema, Christian Braendle, Jan E Kammenga, John Wang, Leonid Kruglyak, Marie-Anne Félix, Junho Lee, and Erik C Andersen

Sept. 2016 *Genetics* (204(1):371-83). PMID: 27449056 DOI: 10.1534/genetics.116.191148.

**2015 DYRK1A controls the transition from proliferation to quiescence during lymphoid development by destabilizing Cyclin D3**

Thompson, Benjamin J, Rahul Bhansali, Lauren Diebold, **Daniel E Cook**, Lindsay Stolzenburg, Anne-Sophie Casagrande, Thierry Besson, Bertrand Leblond, Laurent Désiré, Sébastien Malinge, and John D Crispino

2015 *Journal of Experimental Medicine* 212.6. DOI: 10.1084/jem.20150002.

**2013 The influence of maternal disease on metabolites measured as part of newborn screening**

Ryckman, Kelli K, Oleg A Shchelochkov, **Daniel E Cook**, Stanton L Berberich, Sara Copeland, John M Dagle, and Jeffrey C Murray

Sept. 2013 *The J. of Maternal-Fetal & Neonatal Medicine* (26(14):1380-3). PMID: 23550828 DOI: 10.3109/14767058.2013.791267.

**The heritability of metabolic profiles in newborn twins.**

Alul, Farah Y, **Cook, Daniel E**, Oleg A Shchelochkov, Lauren G Fleener, Stanton L Berberich, Jeffrey C Murray, and Kelli K Ryckman

Mar. 2013 *Heredity* (110(3):253-8). PMID: 23149456 DOI: 10.1038/hdy.2012.75.

**Clinical and environmental influences on metabolic biomarkers collected for newborn screening**

Ryckman, Kelli K, Stanton L Berberich, Oleg A Shchelochkov, **Daniel E Cook**, and Jeffrey C Murray

Jan. 2013 *Clinical Biochemistry* (46(1-2):133-8). PMID: 23010448 DOI: 10.1016/j.clinbiochem.2012.09.013.

**Generating Manhattan plots in Stata**

**Cook, Daniel E**, Kelli R Ryckman, and Jeffrey C Murray

2013 *Stata Journal* (13(2):323-328).

**2012 Replication of clinical associations with 17-hydroxyprogesterone in preterm newborns**

Ryckman, Kelli K, **Daniel E Cook**, Stanton L Berberich, Oleg A Shchelochkov, Susan K Berends, Tamara Busch, John M Dagle, and Jeffrey C Murray

Jan. 2012 *J. of Ped. Endo. and Met.* (25(3-4):301-5). PMID: 22768660 DOI: 10.1515/jpem-2011-0456.

## Presentations

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**2016 The genetic basis of natural variation in *C. elegans* telomere length**

Selected Talk – International Conference on Quantitative Genetics, Madison WI.

**The *C. elegans* natural diversity resource**

Selected Talk – Midwest *C. elegans* meeting

Van Andel Research Institute, Grand Rapids, MI.

**2015 Genome-Wide and Species-Wide Variation in *C. elegans* Reveals Association of Telomere Length With Population Differences in *pot-2***

Selected Talk – International Worm Meeting 2015, UCLA.

**2012 Mapping Newborn Screening Data: A Geographic Exploration**

Poster – Pediatric Academic Societies Meeting, Boston, MA.

## Volunteer Activities

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**Americorps**

**Boston, MA**

*Volunteer*

*2010-2011*

- Worked for ten months on a team with 15 fellow volunteers at the Maurice J. Tobin K-8 school.
- Tutored and mentored a 6<sup>th</sup>-grade classroom.
- Helped run an after-school program in partnership with community organizations.

**Table-To-Table (2007-2010)** - Salvaged food every week from grocery stores and distributors in central Iowa for distribution at area food pantries.

**Appalachia Service Project** - Went on eight annual one-week trips during high-school and college to make homes safer, warmer, and drier for disadvantaged families in the Appalachian mountains of Kentucky and Tennessee.

**Alpha Phi Omega** - Member, 3.5 years; Engaged in a large variety of volunteer work, including performing environmental cleanups and teaching first-aid to boy scouts.