

# Evan M. Cofer

## Computational Biology & Computer Science

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### Education

- September 2017 – Present **Ph.D. in Quantitative and Computational Biology**, *Princeton University*, Princeton, NJ.
- 2017 – 2019 **M.A. in Quantitative and Computational Biology**, *Princeton University*, Princeton, NJ.
- 2012 – 2017 **Bachelor of Science in Computer Science**, *Trinity University*, San Antonio, TX.  
*Computer Science GPA: 3.93/4.0*  
Trinity University Mach Research Fellow  
Trinity University Trustee's Scholarship

### Awards, Honors, and Scholarships

- March 2017 **Graduate Research Fellowship Program: Honorable Mention**, *National Science Foundation (NSF)*.  
“The program supports outstanding graduate students who are pursuing research-based master’s and doctoral degrees in science, technology, engineering, and mathematics (STEM) or in STEM education. The NSF accords Honorable Mention to meritorious applicants who do not receive Fellowship awards. This is considered a significant national academic achievement.”
- February 2017 **Trinity Computer Science Department Outstanding Senior Research Award**, *Trinity University*.  
“Not awarded every year, this honor is given to recognize that senior who has a particularly distinguished record of Computer Science research.”
- April 2016 **Mach Research Fellowship**, *Trinity University*.  
Yearly, each academic department recommends a rising senior for the Mach, which recognizes outstanding undergraduate research achievement. From these nominees, the Faculty Research Committee selects five recipients. I was nominated by the computer science department, and subsequently chosen as a recipient.
- April 2016 & December 2015 **No-Boundary Thinking Contest: First Place**, *Trinity University*.  
“Entrants should propose a computational solution to an interdisciplinary problem. In addition to an essay, submissions should include a presentation at the department colloquium.” I competed twice, winning both times. My first submission considered the use of authorship/topic networks for improving gene name disambiguation. For the second entry, I described a means of constructing lightweight ontologies to aid in the exploration of large datasets of leaked documents.
- December 2015 – May 2017 **Dean’s List**, *Trinity University*.  
Achieved a grade point average of 3.65 or higher while taking 15 or more hours.
- August 2012 – May 2017 **Trustee’s Scholarship**, *Trinity University*.  
Scholarship for academic merit.

## Research Experience

March 2018 – **Troyanskaya Lab**, *Princeton University*.

Present Researching deep learning methods for analyzing biological big data.  
<http://function.princeton.edu/>

May 2017 – **Kostic Lab**, *Joslin Diabetes Center and Harvard Medical School*.

September 2017 Conducted research in metagenomics and type 1 diabetes. Developed scalable and cost-efficient tools for bioinformatics in the cloud. Assisted with interviews for computational research staff.  
<http://www.kosticlab.org/>

January 2016 **Hibbs Lab**, *Trinity University*.

– June 2017 Quantified the rate at which somatic mutations accumulate in healthy, aging mammals. Developed a deep learning model to distinguish somatic mutations from noise in high volume DNA sequencing data (>13 trillion paired-end reads).  
<http://www.cs.trinity.edu/mhibbs/HibbsHome/Research.html>

April 2015 – **Jiang Lab**, *Trinity University*.

July 2015 Modelled the popular vote of battleground states in the 2012 United States presidential election. Predicted outcomes both nationally and state-by-state, using bootstrapping to counter poll sparsity.  
<http://www.cs.trinity.edu/xjiang/>

May 2013 – **Glawe Lab**, *Trinity University*.

July 2013 Analyzed the use and accuracy of rotating disc mechanical flow meters for recycling water condensation from air conditioning systems. In addition to research, managed all equipment and developed graphical user interfaces for lab instruments.  
<https://new.trinity.edu/faculty/diana-glawe>

## Relevant Work Experience

January 2017 **Teaching Assistant**, *Trinity University*.

– May 2017 Worked as a grader, tutor, and teaching assistant for CSCI-1323 Discrete Structures.

## Software

2018 **Selene**, <https://github.com/FunctionLab/selene>.

A PyTorch-based software library to enable and enhance the development of deep learning models of genomic sequences and other biological sequencing data

2016 **Reddigest**, <https://github.com/evancofer/reddigest-scalafied>.

Collaborated with two other developers to create Reddigest, a web application based around Reddit. Reddigest filters out links on Reddit that a user has already viewed. Initially built with PHP/javascript/Apache HTTP, but rewritten in Scala/Scala.js/Play to improve maintainability, scalability, and overall quality.

2015 **Polling Data Retrieval Program**.

A Java program to fetch and parse XML polling data from the Huffington Post. Retrieved data is processed with MATLAB. Source code available upon request.

Many **Miscellaneous Code and Projects**, <https://github.com/evancofer>.

Source code available upon request.

## Relevant Coursework

**Completed at Princeton University, (\* denotes courses in progress).**

Foundations of Applied Statistics and Data Science with Applications in Biology\*, Fundamentals of Machine Learning, Introduction to Genomics and Computational Molecular Biology, Method and Logic in Quantitative Biology

**Completed at Trinity University.**

Computer Science Thesis I & II, Artificial Intelligence, Compilers, Software Engineering, Principles of Functional Languages, Theoretical Computer Science, Database Systems, UNIX Power Tools, Web Application Development, Advanced Algorithms, Principles of Computer Design, Computer Science Thesis Reading, Data Abstraction, Computational Game Theory and Multi-agent Systems, Discrete Data Structures, Principles of Computer Science I & II, Probability & Statistics for Scientists & Engineers, Differential Equations & Linear Algebra, Calculus I, II, & III, Directed Studies in Computer Science, Competitive Programming, Electronic Circuits & Lab, Physics I & II, Thermodynamics I, Mass and Energy Balance

## Proficiencies

**Languages and Technologies.**

C++, Python, R, PyTorch, TensorFlow (Keras), Scala (Akka, Play, Scala.js), bash, git, Linux, C, SQL, JavaScript, Haskell, HPC (Torque, Slurm), MongoDB, L<sup>A</sup>T<sub>E</sub>X, CSS/HTML, MIPS Assembly

## Academic and Professional Affiliations

February 2017 **Member, Upsilon Pi Epsilon.**

– Present International honor society for computer scientists.  
<http://upe.acm.org/>

May 2016 – **Member, International Society for Computational Biology (ISCB).**

Present Scholarly society for researchers in computational biology and bioinformatics.  
<https://www.iscb.org>

August 2015 – **Member, Association for Computing Machinery (ACM).**

Present Professional society for computer scientists.  
<https://www.acm.org>

## Other Academic Experience

**Referee.**

*NeurIPS: Workshop on Machine Learning for Health (ML4H), Machine Learning for Healthcare (MLHC), Scientific Reports*

## Publications

Chen KM\*, **Cofer EM\***, Zhou J, and Troyanskaya OG. Selene: a PyTorch-based deep learning library for sequence-level data [accepted]. *Nature Methods*, 2019. (\*Equal contribution)

Ching T, Himmelstein DS, Beaulieu-Jones BK, Kalinin AA, Do BT, Way GP, Ferrero E, Agapow P, Zietz M, Hoffman MM, Xie W, Rosen GL, Lengerich BJ, Lanchantin J, Israeli J, Woloszynek S, Carpenter AE, Shrikumar A, Xu J, **Cofer EM**, Lavender CA, Turaga SC, Alexandari AM, Zhiyong L, Harris DJ, DeCaprio D, Qi Y, Kundaje A, Peng Y, Wiley LK, Segler MHS, Boca SM, Swamidass J, Huang A, Gitter A<sup>†</sup>, and Greene CS<sup>†</sup>. Opportunities and obstacles for deep learning in biology and medicine. *Journal*

of the *Royal Society Interface*, 16(141), April 2018. doi:[10.1098/rsif.2017.0387](https://doi.org/10.1098/rsif.2017.0387). (Random ordering where not marked by †)

JM Luber, BT Tierney, **Cofer EM**, CJ Patel, and AD Kostic. Aether: Leveraging linear programming for optimal cloud computing in genomics. *Bioinformatics*, December 2017. doi:[10.1093/bioinformatics/btx787](https://doi.org/10.1093/bioinformatics/btx787).

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## Preprints

Chen KM\*, **Cofer EM\***, Zhou J, and Troyanskaya OG. Selene: a PyTorch-based deep learning library for sequence-level data. *bioRxiv*, October 2018. doi:[10.1101/438291](https://doi.org/10.1101/438291). (\*Equal contribution)

Luber JM, Tierney BT, **Cofer EM**, Patel CJ, and Kostic AD. Aether: Leveraging linear programming for optimal cloud computing in genomics. *bioRxiv*, July 2017. doi:[10.1101/162883](https://doi.org/10.1101/162883).

Ching T, Himmelstein DS, Beaulieu-Jones BK, Kalinin AA, Do BT, Way GP, Ferrero E, Agapow P, Xie W, Rosen GL, Lengerich BJ, Israeli J, Lanchantin J, Woloszynek S, Carpenter AE, Shrikumar A, Xu J, **Cofer EM**, Harris DJ, DeCaprio D, Qi Y, Kundaje A, Peng Y, Wiley LK, Segler MHS, Gitter A†, and Greene CS†. Opportunities and obstacles for deep learning in biology and medicine. *bioRxiv*, May 2017. doi:[10.1101/142760](https://doi.org/10.1101/142760). (Random ordering where not marked by †)

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## Conference Presentations, Posters, and Talks

**Cofer EM** and Hibbs MA. Determining the age-associated somatic mutation rate in diverse mouse tissues [talk]. *The Computational Systems for Integrative Genomics (CSIG) Conference*, June 2017. Princeton University. Princeton, NJ.

**Cofer EM**. The rate of somatic mutations in aging mice [undergraduate thesis]. *Trinity University Computer Science Undergraduate Honors Thesis*, April 2017. Trinity University. San Antonio, TX.

**Cofer EM**. Accurately measuring the mammalian somatic mutation rate using deep learning [talk]. *Computer Science Colloquium*, March 2017. Trinity University. San Antonio, TX.

**Cofer EM** and Hibbs MA. Accurately measuring the mammalian somatic mutation rate using deep learning [platform talk & poster]. *Conference for Science at the Forefront of Basic and Translational Research*, October 2016. University of Texas at San Antonio. San Antonio, TX.

**Cofer EM**. Using deep learning to classify mutations [talk]. *Computer Science Colloquium*, September 2016. Trinity University. San Antonio, TX.

**Cofer EM**, Kennedy RM, and Hibbs MA. Accurately measuring the mammalian somatic mutation rate [poster]. *International Conference on Intelligent Systems for Molecular Biology*, July 2016. Orlando, FL.

**Cofer EM** and Hibbs MA. Using deep learning to classify mutations [talk]. *Trinity University Summer Undergraduate Research Conference*, July 2016. Trinity University. San Antonio, TX.

**Cofer EM\*** and Witecki I\*. Ontology construction: a means of improving data-driven journalism [talk]. *Computer Science Colloquium*, April 2016. Trinity University. San Antonio, TX. (\*Equal contribution)

**Cofer EM.** Gene name disambiguation: a novel approach [talk]. *Computer Science Colloquium*, December 2015. Trinity University. San Antonio, TX.

**Cofer EM,** Kwessi EA, Nguyen HV, Nishikawa KA, and Jiang AX. Modeling the 2012 presidential election's battleground states [talk]. *Trinity University Summer Undergraduate Research Conference*, July 2015. Trinity University. San Antonio, TX.

**Cofer EM\***, Ybarra T\*, and Glawe DD. Positive displacement meter performance [talk]. *Trinity University Summer Undergraduate Research Conference*, July 2013. Trinity University. San Antonio, TX. (\*Equal contribution)