

# EMILY FLYNN

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## EDUCATION

**Stanford University**, Stanford, CA June 2014 – August 2021 **GPA 3.98**  
Ph.D. Program in Biomedical Informatics Advisor: Dr. Russ B. Altman  
Thesis: Leveraging bioinformatics methods to examine sex-related variability in genetic and transcriptomic data  
NSF Graduate Research Fellow, NIH (F31) Graduate Research Fellow

**Smith College**, Northampton, MA September 2010 – May 2014 **GPA 3.99**  
B.A., Highest Honors, Computer Science and Biochemistry Majors, Biomathematical Sciences Concentration  
Clare Boothe Luce Computer Science Scholar, Goldwater Scholar

## RESEARCH AND TECHNICAL EXPERIENCE

**Graduate Researcher - Dr. Russ Altman's Lab, Stanford University** (March 2015 – present)

- Developed a Bayesian Mixture Model to identify sex-specific effects in GWAS summary statistics and applied the method to UK Biobank biomarker data from >300,000 individuals (R package [here](#))
- Inferred missing sex labels and assessed sex-related effects in a large publicly available gene expression database (>400,000 samples)
- Examined sex bias and sex-differential effects in drug and smoking-related expression data

**Technical Mentor - Stanford Data Science for Social Good Program** (Summer 2019)

- Member of leadership team for developing and coordinating summer program
- Mentored teams of student fellows on projects for the Stanford Blood Center on forecasting platelet use and for the Veteran's Health Administration on opiate adverse events in minority populations
- Developed course materials and led trainings on git, R programming, and reproducible analysis

**Undergraduate Researcher - Dr. Ileana Streinu's Lab, Smith College** (May 2012 – May 2014)

- Extended KINARI-Web, a server for protein rigidity analysis, to analyze nucleic acids and nucleic acid-protein complexes, and developed a method to compare and visualize rigidity results.

## PUBLICATIONS

Flynn, E., A. Chang, and R.B. Altman. Large-Scale Labeling and Assessment of Sex Bias in Publicly Available Expression Data. *BMC Bioinformatics*. 2021. [10.1186/s12859-021-04070-2](https://doi.org/10.1186/s12859-021-04070-2)

Flynn, E., Y. Tanigawa, F. Rodriguez, R.B. Altman, N. Sinott-Armstrong, and M.A. Rivas. Sex-specific genetic effects across biomarkers. *European Journal of Human Genetics*. 2020. [10.1038/s41431-020-00712-w](https://doi.org/10.1038/s41431-020-00712-w)

Wang, S., E. Flynn, and R.B. Altman. Gaussian embedding for large-scale gene set analysis. *Nature Machine Intelligence*. 2020, 2: 387-395. [10.1038/s42256-020-0193-2](https://doi.org/10.1038/s42256-020-0193-2)

Flynn, E. and I. Streinu. Matching multiple rigid domain decompositions of proteins. *IEEE Trans Nanobioscience*. 2017; 16(2):81-90.

Flynn, E. and I. Streinu. Consistent visualization of multiple rigid domain decompositions of proteins. *Proc. Bioinformatics Research and Applications (ISBRA)*, Lecture Notes in Computer Science. 2016; 9683, 151-162.

## GRANTS

FDA UCSF-Stanford Center of Excellence in Regulatory and Science Innovation grant. *Comprehensive Assessment of Sex-Differential Smoking-related Effects in Publicly Available Gene Expression Data*. Awarded Spring 2019. Collaboration with the FDA Office of Women's Health and Center for Tobacco Products.

Stanford Women's Health and Sex Differences in Medicine (WHSDM) Center Seed Grant.  
*Developing a robust baseline gene expression dataset for menstrual cycle variability in peripheral blood*.  
Awarded Fall 2017. \$21,000. Collaboration with Dr. Ruth Lathi and Dr. Russ Altman, Stanford University.

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## **CONFERENCE PRESENTATIONS**

Flynn, E., A. Chang, and R. B. Altman. Sex Labeling and Bias in Publicly Available Expression Data. *Organization on the Study of Sex Difference Conference*. Marina del Rey, CA. May 2020. (accepted talk, cancelled due to COVID)

Flynn, E., A. Chang, and R. B. Altman. Sex Labeling and Assessment of Bias in Publicly Available Expression Data: A Focus on Smoking-Related Studies. *UCSF-Stanford Center for Excellence in Regulatory Sciences (CERSI) Summit*. San Francisco, CA. January 12, 2020. (poster)

Wang, S., E. Flynn, and R.B. Altman. Gene Set Representation via Gaussian Embedding. *RECOMB*, Washington, D.C., May 8<sup>th</sup>, 2019. (talk)

Flynn, E., R.B. Altman, and M.A. Rivas. Examining Sex-Differential Genetic Effects using Bayesian Mixture Models. *NLM Conference*, Nashville, TN, June 4<sup>th</sup>, 2018. (talk)

Flynn, E. and R.B. Altman. Meta-analysis of Sex-differential Expression in Human Liver. *Biocomputation at Stanford (BCATS)*, Stanford, CA, April 19<sup>th</sup>, 2018. (talk and poster)

Flynn, E. and R. B. Altman. Using ICA to Identify Functional Components of Drug Response in CMAP. *Big Data in Biomedicine Conference*, Stanford University, Stanford, CA. May 2016. (poster)

## **TEACHING AND MENTORING EXPERIENCE**

### **Introduction to R for Incoming Biosciences Students, Stanford** (Summers 2020, 2021)

- Teaching Assistant for twice weekly introduction to programming course in R (tidyverse)
- Led small group hands-on programming exercises (3-5 students)
- Performed a major update of course material to include biologically relevant examples and exercises
- Wrote and presented lectures on data visualization with ggplot and GWAS analysis

### **Introduction to Biomedical Informatics Algorithms, Stanford** (Fall 2016-2018)

- Teaching Assistant for core bioinformatics algorithms course (Python)
- Held weekly office hours, wrote and graded homework and exams, coordinated course activities, responded to student emails and concerns (Fall 2016, 2017)
- Designed and presented a lecture on gene set enrichment analysis
- Performed a major revision and update course projects (Fall 2018)

### **Altman Lab, Mentor to Undergraduate Students** (Winter 2018 - present)

- Mentored a senior undergraduate in Computer Science for an academic year
- Mentored a sophomore/junior undergraduate in Human Biology for a summer and two academic years

### **Stanford Biosciences, Mentor to Graduate Students** (Fall 2015– present)

- Mentored 1-2 first year graduate students per year as part of the Stanford Biosciences Student Association mentoring program
- Met with students 3-5 times each to help with multiple revisions of NSF graduate fellowship proposals, also helped mentor students through transition to graduate school and selecting rotations
- Mentored second- and third- year Biomedical Informatics students on writing NIH style proposals
- Led trainings on fellowship proposal writing for first year students in Biomedical Informatics and Bioengineering (2015-2018)

### **Volunteer Tutor and Instructor - East Palo Alto Tennis and Tutoring** (Fall 2018 – present)

- Extended day learning program for students from East Palo Alto
- Met with 1-2 high school students weekly to help with homework assignments and study skills
- Created and led an eight-week math SAT prep course for six high school students

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## **AWARDS AND HONORS**

- Organization of the Study of Sex Differences Elizabeth Young New Investigator Award (2020)
- Stanford Data Science Fellow (awarded 2020)
- NIH F31 Graduate Research Fellowship (awarded 2019)
- NSF Graduate Research Fellowship (awarded 2014)
- Goldwater Scholar (2013)
- Cold Spring Harbor Laboratory Undergraduate Research Fellow (URP) NSF REU in Computational Biology and Bioinformatics (2013)
- NSF UBM 'Four College Biomath Consortium' Fellow (2012-2014)
- Clare Boothe Luce Computer Science Scholar (2012-2014) (full tuition scholarship)

## **RELEVANT GRADUATE COURSEWORK**

**Technical:** Theory of Probability, Statistical Inference, Machine Learning, Probabilistic Graphical Models, Readings in Applied Data Science, Meta-Research, Modern Applied Statistics: Data Mining

**Biomedical applications:** Biomedical Informatics Research Methodology, Bioinformatics Algorithms, Translational Bioinformatics, Modeling Biomedical Systems, Data Driven Medicine, Smart Health Through Digital Medicine, Clinical Shadowing Seminar for Students in Biomedical Informatics

## **SKILLS:**

*Fluent* – R, python, Linux/Unix, SQL, git; *Proficient* – C++