EMILY FLYNN

erflynn@stanford.edu | 617-910-7975 | github.com/erflynn

EDUCATION

Stanford University, Stanford, CA June 2014 – August 2021 (Expected graduation) **GPA 3.98**
Ph.D. Program in Biomedical Informatics Advisor: Dr. Russ B. Altman
Thesis Focus: Leveraging bioinformatics methods to understand variability in gene expression and genome-wide association (GWAS) data related to drug response, sex, and hormonal status

Smith College, Northampton, MA September 2010 – May 2014 **GPA 3.99**
Bachelor of Arts, Computer Science and Biochemistry Majors, Biomathematical Sciences Concentration

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)

- 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

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

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

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

UCSF-Stanford Center of Excellence in Regulatory and Science Innovation (CERSI) project.
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 Research 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. Collaboration with Dr. Ruth Lathi and Dr. Russ Altman.

CONFERENCE PRESENTATIONS

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 8th, 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 4th, 2018. (talk)

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

AWARDS AND HONORS

- Stanford Data Science Fellow (awarded 2020)
- NIH F31 Graduate Research Fellowship (awarded 2019)
- NSF Graduate Research Fellowship (awarded 2014)
- Highest Honors in Computer Science, B.A. Smith College (2014)
- Goldwater Scholar (2013)
- National Science Foundation (NSF) UBM ‘Four College Biomath Consortium’ Fellow (2012-2014)

TEACHING EXPERIENCE

Introduction to R for Biosciences Students, Stanford (Summers 2020, 2021)
- Teaching Assistant for introduction to programming course in R (tidyverse)
- Wrote and presented lectures on data visualization with ggplot and GWAS analysis

Introduction to Biomedical Informatics Algorithms, Stanford (Fall 2016-2018)
- Teaching Assistant: 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

MENTORING EXPERIENCE

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 first year Biosciences graduate students, helped with NSF graduate fellowship proposals, advised on transitioning to graduate school and selecting coursework and rotations
- Led three trainings on fellowship proposal writing (2015-2018)

RELEVANT GRADUATE COURSEWORK

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

Health application focused: Biomedical Informatics Research Methodology, Data Driven Medicine, Translational Bioinformatics, Preparation and Practice: Science Policy, Smart Health Through Digital Medicine, Modeling Biomedical Systems, Clinical Shadowing Seminar for Students in Biomedical Informatics

SKILLS:

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