Alyssa C. Frazee

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Education

Ph.D. (*expected*), Biostatistics, Johns Hopkins Bloomberg School of Public Health, 2015.
Advisor: Jeffrey Leek

B.A. *summa cum laude*, Mathematics, with distinction in Statistics, St. Olaf College, 2010

Honors, Awards, Scholarships

Hopkins Sommer Scholar, 2012-2015

Delta Omega Poster Competition, First Prize (Applied Research), 2014

Helen Abbey Award for Excellence in Teaching, 2012

Gertrude M. Cox Scholarship Winner, 2010

Phi Beta Kappa, 2010

Barry M. Goldwater Scholarship, Honorable Mention, 2009

NSF Undergraduate Research Fellowship, 2007-2010

Buntrock Academic Scholarship, St. Olaf College, 2006-2010

National Merit Scholar, 2006

Publications

Published

Frazee AC, Sabunciyan S, Hansen KD, Irizarry RA, Leek JT (2014). "Differential expression analysis of RNA-seq data at single-base resolution." *Biostatistics*. doi: 10.1093/biostatistics/kxt053. **[most-read article in *Biostatistics*, January 2014; 2nd-most read in February 2014]**

Frazee AC, Langmead B, Leek JT (2011). "ReCount: A multi-experiment resource of analysis-ready RNA-seq gene count datasets." *BMC Bioinformatics* 12:449. **[highly accessed]**

Frazee AC, Collado Torres L, Jaffe AE, Langmead B, Leek JT (2014). "Measurement, Summary, and Methodological Variation in RNA-sequencing" in S. Datta and D. Nettleton (Eds.), *Statistical Analysis of Next Generation Sequencing Data* (pp. 115-128): Springer.

Submitted

Frazee AC, Pertea G, Jaffe AE, Langmead B, Salzberg SL, Leek JT (2014). "Flexible isoform-level differential expression analysis with Ballgown." Submitted. Preprint available on bioRxiv.

Frazee AC, Jaffe AE, Langmead B, Leek JT (2014). "Polyester: simulating RNA-seq datasets with differential transcript expression." Submitted. Preprint available on bioRxiv.

Teaching

Johns Hopkins Bloomberg School of Public Health, Department of Biostatistics:

Statistical Methods in Public Health I-II (*Lab Instructor and Lead TA*), Fall 2013

Masters' in Public Health Capstone Projects (*Statistical Consultant*), Spring 2013 and Spring 2012

Data Analysis Workshop I-II (*Lead TA*), January 2013

Statistical Reasoning in Public Health I-II (*Lead TA*), Fall 2012 and Fall 2011

Coursera:

Statistical Reasoning for Public Health: Estimation, Inference, and Interpretation (*TA and forum moderator*), Spring 2014

St. Olaf College, Department of Mathematics, Statistics, and Computer Science:

Advanced Statistical Modeling (*TA*), Spring 2010

Peer Review Activities

Peer Reviewer for *Nucleic Acids Research* and *BMC Genomics*; assisted with peer reviews for *Genome Biology* and *Nature Protocols*

Presentations

[upcoming] Invited talk, RADIANT Workshop at the European Conference on Computational Biology, Strasbourg, France, September 2014: "Engineering annotation-agnostic tools for differential expression analysis"

[upcoming] Topic-Contributed research talk, Joint Statistical Meetings, Boston MA, August 2014: "Flexible isoform-level differential expression analysis with *Ballgown*"

[upcoming] Invited "short talk", Bioconductor Conference, Boston MA, July 2014: "Flexible analysis of RNA-seq data with *Ballgown*"

Invited talk, high school outreach program (MBGR), Johns Hopkins Biology Department, July 2014: "Adventures in Computational Biology"

Invited talk, James Madison University, Harrisonburg VA, June 2014: "Using statistics to untangle the mysteries of gene expression"

Contributed paper/talk, ENAR Spring Meeting, Baltimore MD, March 2014: "*Ballgown*: a general statistical framework for transcript assemblies"

Contributed poster, Statistical and Quantitative Genetics Conference, Seattle WA, November 2013: "*Ballgown*: A general statistical framework for transcript assemblies"

Invited talk, St. Olaf College, Northfield MN, November 2013: "Statistical methods for untangling the mysteries of gene expression"

Invited talk, Johns Hopkins University Young Investigators Symposium on Genomics and Bioinformatics, October 2013. "Downstream analysis of transcript expression with *Ballgown*"

Contributed paper/talk, ENAR Spring Meeting, Orlando FL, March 2013: "Differential expression analysis of RNA-seq data at single-base resolution."

Contributed poster, Statistical Methods for Very Large Datasets Conference, Baltimore MD, June 2011: "Cloud-scale differential gene expression from RNA-seq."

Other Research Activities

Research Assistant, Johns Hopkins Department of Biostatistics, 2011 - present. (Trainee; NIH predoctoral training program for genetics/genomics, 2010-2011)

NSF Undergraduate Researcher, Center for Interdisciplinary Research, St. Olaf College, 2007-2010

NSF-REU Summer Researcher, James Madison University, 2009

St. Olaf Mathematics Practicum student, January 2009

Service

Session Chair, Joint Statistical Meetings, 2012

Mentor to Baltimore City high school student through Incentive Mentoring Program, 2012 - 2014.

Coordinator, Johns Hopkins Biostatistics Tea Time (Thursday afternoon social hour/weekly seminar discussion), 2012 - 2013

Coordinator, Johns Hopkins Biostatistics Student Computing Club, 2011-2012

Employment

Technical Aide at 3M Company, Corporate Research Materials Laboratory, 2007-2008

Computing

Proficient: R, Python (including some experience with the Flask web framework), Git, Bash, LaTeX

Familiar: Stata, SQLite, Sun Grid Engine, HTML, CSS, D3.js

Cursory Knowledge: SAS, C++, Scheme

Additionally: Student in Summer 2013 batch of Hacker School, a three-month, immersive school for becoming a better programmer

Code for academic and side projects available on GitHub

Last updated: July 16, 2014