

Jack M. Fu

<https://jfbiostats.com>
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EDUCATION

- **08/2013 - 05/2018** **Johns Hopkins Bloomberg School of Public Health**
 - Ph.D. Biostatistics
 - *Doctoral Advisors:*
Ingo Ruczinski, Ph.D.
Jeff Leek, Ph.D.
- **08/2009 - 05/2013** **Duke University**
 - Major: Statistics with Distinction
 - Minor: Computational Biology
 - *Summa Cum Laude*
 - *Thesis Advisor:* Fan Li, Ph.D.

PROFESSIONAL EXPERIENCE

- **06/2018 - Current** **Massachusetts General Hospital**
 - Research Fellow
 - *Advisor:* Michael Talkowski, Ph.D.
- **06/2014 - 05/2018** **Johns Hopkins Bloomberg School of Public Health**
 - Ph.D. Researcher
 - *Advisors:*
Ingo Ruczinski, Ph.D.
Jeff Leek, Ph.D.
- **06/2015 - 08/2015** **Pacific Biosciences**
 - Bioinformatics Contractor
 - *Supervisor:* Elizabeth Tseng, Ph.D.
- **06/2012 - 05/2013** **Duke University**
 - Undergraduate Researcher
 - *Advisor:*
Fan Li, Ph.D.

HONORS AND AWARDS

- **Symposium on Advances in Genomics, Epidemiology, and Statistics (SAGES)** **2018**
Best poster presentation
- **Johns Hopkins Department of Biostatistics** **2018**
Helen Abbey Award for excellence in teaching
- **Johns Hopkins Department of Biostatistics** **2017**
Jane & Steve Dykacz Award for outstanding student paper in medical biostatistics
- **Summer Institute in Statistical Genetics at University of Washington** **2016**
Travel and tuition award
- **JHSPH and the Institute for Clinical and Translational Research** **2016**
1st place Genomic and Bioinformatics Symposium poster competition
- **The Maryland Genetics, Epidemiology, and Medicine Training Program** **2016**
2nd place poster competition

TEACHING EXPERIENCE

• Johns Hopkins Bloomberg School of Public Health

- **2016-17:** Lead Teaching Assistant - Biostatistics 620s
 - * Instructors: Marie Diener-West, Ph.D. and Karen Bandeen-Roche, Ph.D.
 - * Weekly lab instructor for Biostatistics 620s, a core curriculum for MPH students
 - * Substitute lecturer on occasions in front of 200+ students
- **2015-17:** Teaching Assistant - Design of Clinical Experiments
 - * Instructors: Elizabeth Sugar, Ph.D. and Jay Herson, Ph.D.
 - * Weekly office hours and grading
- **2015-16:** Teaching Assistant - Biostatistics for Undergraduates
 - * Instructors: Leah Jager, Ph.D. and Margaret Taub, Ph.D.
 - * Weekly lab instructor
- **2014-15:** Teaching Assistant - Biostatistics 720s
 - * Instructors: Brian Caffo, Ph.D. and Hongkai Ji, Ph.D.
 - * Weekly office hours and grading for Biostatistics 720s, the core Ph.D. curriculum

RESEARCH

• Manuscripts

1. Sherman, T., **Fu, J.**, Scharpf, R., Bureau, A., Ruczinski, I. (2018), Detection of rare disease variants in extended pedigrees using RVS. [Submitted *Bioinformatics*].
2. **Fu, J.**, Leslie, E. J., Scott, A. F., Murray, J. C., Marizita, M. L., Beaty, T. H., Scharpf, R. B., and Ruczinski, I. (2017), Detection of de novo copy number deletions from targeted sequencing trios. [In review *Bioinformatics*].
3. **Fu, J.**, Kammers, K., Nellore, A., Collado-Torres, L., Leek, J., and Taub, M. (2017), RNA-seq transcript quantification from reduced-representation data in recount2. [Submitted *Genome Biology*].
4. Ramachandran, K. V., **Fu, J.**, Schaffer, T. B., Na, C., and Margolis, S. S. (2017), Activity-dependent degradation of nascentome by the neuronal membrane proteasome. [In review *Mol. Cell*].

• Peer-reviewed Publications

1. **Fu, J.**, Beaty, T. H., Scott, A. F., Hetmanski, J., Parker, M. M., Wilson, J. E. B., Marazita, M. L., Mangold, E., Albacha-Hejazi, H., Murray, J. C., Bureau, A., Carey, J., Cristiano, S., Ruczinski, I. and Scharpf, R. B. (2017), Whole exome association of rare deletions in multiplex oral cleft families. *Genet. Epidemiol.*, 41: 6169. doi:10.1002/gepi.22010

SOFTWARE

• Author

1. *MDTS*: A R package to facilitate the calling of de novo deletions in targeted sequencing trios with high sensitivity and positive predictive value. [Bioconductor]
2. *recountNNLS*: A R package to apply a non-negative linear model that only requires summary coverage statistics for transcript abundance estimation. [Github]

• Maintainer

1. *ballgown*: A R package designed to facilitate flexible differential expression analysis of RNA-Seq data. It also provides functions to organize, visualize, and analyze the expression measurements for your transcriptome assembly. [Bioconductor]
2. *polyester*: A R package designed to simulate RNA sequencing experiments with differential transcript expression. [Bioconductor]

LANGUAGES

- **Programming:** R, java, perl, python, latex, bash, MATLAB
- **Languages:** English (fluent), Mandarin Chinese (fluent), Cantonese (fluent), French (conversational)

PROFESSIONAL SOCIETIES

- American Statistical Association
- The American Society of Human Genetics