Hao (Harry) Feng

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Employment

- **Assistant Professor (tenure-track)**   2019-now
  Department of Population and Quantitative Health Sciences
  Case Western Reserve University

Education

- **Ph.D. in Biostatistics and Bioinformatics**   2014-2019
  Emory University, Laney Graduate School
  — Advisor: Hao Wu
  — Dissertation: *Statistical Methods for High-throughput Epigenomics Data.*
  [** **Michael Kutner Distinguished Doctoral Student Award** **]

- **MSPH in Biostatistics and Bioinformatics**   2011-2013
  Emory University, Rollins School of Public Health
  — Advisors: Hao Wu, Karen Conneely
  — Thesis: *A Hierarchical Bayesian Approach to Detect Differentially Methylated Loci from Bisulfite Sequencing Data*

- **B.S. in Biosciences**   2007-2011
  University of Science and Technology of China (USTC)

Work Experience

- **May 2017–August 2017, Statistician/Full-Time Summer Intern** Pfizer Inc, Global Research & Development, La Jolla, California
  — Developing Bayesian methods for tumor growth inhibition study

- **June 2013–April 2014, Data Analyst**, Department of Human Genetics, School of Medicine, Emory University, Atlanta, Georgia.
  — Statistical model development and analysis for high-throughput omics data

Research Interests

- <u>Statistical Methodology</u>: Bioinformatics, methods in high-throughput omics data, computational biology.

- <u>Applications</u>: Epigenetics, cell-free DNA, single-cell RNA/BS-seq, biomarker discovery, neurodegenerative diseases, PTSD, cancers.

Publications

Google Scholar citation statistics (as of August 2019): All citations: 488. h-index: 7. i10-index: 7.

Statistical Methodology

1. **Feng H**, Jin P, Wu H (2018) *Disease prediction by cell-free DNA methylation.* **Briefings in Bioinformatics** doi: 10.1093/bib/bby029

2. Zhang WW$^\$$, **Feng H**$^\$$, Wu H, Zheng XQ (2017) *Accounting for tumor purity improves cancer subtype classification from DNA methylation data.* **Bioinformatics** Volume 33, Issue 17, pages 2651-2657. doi: 10.1093/bioinformatics/btx303

3. Wu H, Xu T, **Feng H**, Chen L, Li B, Yao B, Qin ZS, Jin P, Conneely KN (2015) *Detection of differentially methylated regions from whole-genome bisulfite sequencing data without replicates.* **Nucleic Acids Research** Volume 43, Issue 21, pages e141. doi: 10.1093/nar/gkv715

4. **Feng H**, Conneely KN, Wu H (2014) *A Bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data.* **Nucleic Acids Research** Volume 42, Issue 8, pages e69. doi: 10.1093/nar/gku154

$^\$$ These authors contributed equally to this work.

Collaborative

5. Kennedy EM, Powell DR, Li Z, Bell JSK, Barwick BG, **Feng H**, McCrary MR, Dwivedi B, Kowalski J, Dynan WS, Conneely KN, Vertino PM (2018) *Galactic cosmic radiation induces persistent epigenome alterations relevant to human lung cancer.* **Scientific Reports** doi:10.1038/s41598-018-24755-8

6. Qin Y, **Feng H**, Chen M, Wu H and Zheng X (2018) *InfiniumPurify: An R package for estimating and accounting for tumor purity in cancer methylation research.* **Genes & Diseases** Volume 5, Issue 1, pages 43-45. doi: 10.1016/j.gendis.2018.02.003

7. Almli L, Lori A, Meyers J, Shin J, Fani N, Maihofer A, Nievergelt C, Smith A, Mercer K, Kerley K Leveille J, **Feng H**, ... , Conneely KN and Ressler K (2017) *Problematic alcohol use associates with sodium channel and clathrin linker 1 (SCLT1) in trauma-exposed populations.* **Addiction Biology** Volume 23, Issue 5, pages 1145-1159. doi: 10.1111/adb.12569

8. Zhang F, Hammack C, Ogden SC, Cheng Y, Lee EM, Wen Z, Qian X, Nguyen H, Li Y, Yao B, Xu M, Xu T, Chen L, Wang Z, **Feng H**, Huang W, Yoon K, Shan C, Huang L, Qin ZS, Christian KM, Shi PY, Xu M, Xia M, Zheng W, Wu H, Song H, Tang H, Ming G, Jin P (2016) *Molecular signatures associated with ZIKV exposure in human cortical neural progenitors.* **Nucleic Acids Research** Volume 44, Issue 18, pages 8610-8620. doi: 10.1093/nar/gkw765

9. Kennedy E, Powell DR, Li Z, Bell JSK, **Feng H**, Dynan W, Dwivedi B, Kowalski J, Conneely KN and Vertino PM (2016) *Space radiation exposure induces stable epigenome alterations relevant to human lung cancer.* [abstract nr B08] **Cancer Research** Volume 76, Issue 2, page B08. doi: 10.1158/1538-7445.CHROMEPI15-B08

10. Almli LM, Duncan R, **Feng H**, Ghosh D, Binder EB, Bradley B, Ressler KJ, Conneely KN, Epstein MP (2014) *Correcting systematic inflation in genetic association tests that consider interaction effects: application to a genome-wide association study of posttraumatic stress disorder.* **JAMA Psychiatry** Volume 71, Issue 12, page 1392-1392. doi: 10.1001/jamapsychiatry.2014.1339

11. Almli LM, Srivastava A, Fani N, Kerley K, Mercer KB, **Feng H**, Bradley B, Ressler KJ (2014) *Correspondence.* **Biological Psychiatry** Volume 76, Issue 4, page e3-e4. doi: 10.1016/j.biopsych.2014.01.017

12. Almli LM, Mercer KB, Kerley K, **Feng H**, Bradley B, Conneely KN, Ressler KJ (2013) *ADCYAP1R1 genotype associates with post-traumatic stress symptoms in highly traumatized African-American females.* **American Journal of Medical Genetics Part B: Neuropsychiatric Genetics** Volume 162, Issue 3, pages 262-272. doi: 10.1002/ajmg.b.32145

Honors and Awards

- **Senior Ph.D. Student Presentation Award**, 2018
- **ENAR Distinguished Student Paper Award**, 2017
- **Michael Kutner Distinguished Doctoral Student Award**, 2017
- **SAMSI trave award** for epigenetics workshop, 2015
- Finalist for the **Charles C. Shepard Award**, 2013
  — The best master's thesis of the Rollins School of Public Health
- **Outstanding Student Scholarship** from USTC Overseas Alumni Foundation, 2007

Software Developed/Co-Developed

- **DSS**: Dispersion Shrinkage for Sequencing. An R/Bioconductor package for differential analysis from high-throughput sequencing data, including differential expression for RNA-seq and differential methylation for bisulfite-sequencing data. Available at `http://www.bioconductor.org/packages/release/bioc/html/DSS.html`.
  Total downloads over the past year (2018) : **11,618**.
  — Software partially based on publication Feng et al. 2014 **Nucleic Acids Research**

- **InfiniumPurify**: A comprehensive R package for estimating and accounting for tumor purity based on DNA methylation Infinium 450k array data. 'InfiniumPurify' provides functionalities for tumor purity estimation. In addition, it can perform differential methylation detection and tumor sample clustering with the consideration of tumor purities. Available at `https://cran.r-project.org/web/packages/InfiniumPurify/index.html`.
  — Software based on publication Zhang & Feng 2017 **Bioinformatics**

- **cfDNAMethy**: Reference-free and reference-based methods for disease prediction by cell-free DNA methylation. Available at `https://github.com/haoharryfeng/cfDNAmethy`.
  — Software based on publication Feng 2018 **Briefings in Bioinformatics**

Presentations

- Oral Presentation, Senior Ph.D. students presentation competition, Emory University, Atlanta, GA. September, 2018
  — Statistical methods for high-throughput epigenomics data.

- Oral Presentation, Pfizer Global Research and Development, La Jolla, CA. August, 2017
  — A Bayesian method in tumor growth inhibition study.

- Oral Presentation, JSM 2017, Chicago, IL. August, 2017
  — Accounting for tumor purity improves cancer subtype classification from DNA methylation data.

- Oral Presentation, ENAR 2017 Spring meeting, Washington, DC. March, 2017
  — Accounting for tumor purity improves cancer subtype classification from DNA methylation data.
  [** ENAR Distinguished Student Paper Award **]

- Poster, Statistical and Applied Mathematical Sciences Institute (SAMSI) workshop, Research Triangle Park, NC. March, 2015
  — A Bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data.

- Poster, American Society of Human Genetics (ASHG) 63rd annual meeting, Boston, MA. October, 2013
  — A Bayesian hierarchical model to detect differentially methylated loci from single nucleotide resolution sequencing data.

Teaching Experience

My role	Semester	Class	Class level	Class size
Assistant	Fall 2015	Statistical Methods I	Master's	75
Assistant	Fall 2015	Lab for Statistical Methods I	Master's	36
Assistant	Spring 2016	Sampling Applications	Master's	50
Associate	Fall 2016	High-throughput data analysis using R and Bioconductor	Master's	14
Associate	Spring 2017	Bayesian Models	Doctoral	24
Associate	Fall 2018	Advanced Statistical Computing	Doctoral	19

Editorial Activities

Journal Reviewer

- **Aging**
- **Biomedicine and Pharmacotherapy**
- **BMC Supplements**
- **Journal of Alzheimer's Disease**
- **Journal of Applied Statistics**
- **Meta Gene**

- **Neoplasma**
- **Oncotarget**
- **Statistical Methods in Medical Research**
- **Scientific Reports**
- **PLOS One**

Professional Membership

American Statistical Association (ASA)
The International Biometric Society — Eastern North American Region (ENAR)
International Chinese Statistical Association (ICSA)
American Society of Human Genetics (ASHG)

Computational Skills

- Programming Languages: *R, SAS, Perl, C*
- Operating Systems: *Windows, Unix*