Fan Zhang, PhD

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Employment

Harvard Medical School (HMS) — Boston, MA
Research Scientist (Dr. Soumya Raychaudhuri) — Jan. 2017 – Present

Broad Institute of Harvard and MIT/Brigham and Women's Hospital — Boston, MA
Associate Scientist — Jan. 2019 - Present
Research Associate — Jan. 2017 – Jan. 2019

Worcester Polytechnic Institute (WPI) — Worcester, MA
Teaching Assistant — Aug. 2013 – Dec. 2016

Chinese Academy of Sciences — Shenzhen, China
Research Associate — May 2012 – June 2013

Education

Ph.D. Bioinformatics, Worcester Polytechnic Institute (WPI), MA — Dec. 2016
Dissertation: Statistical Methods for Characterizing Genomic Heterogeneity in Mixed Samples
Advisor: Dr. Patrick Flaherty (Genomics Lab, now in Statistics Dep. in UMass Amherst)

M.S. Bioinformatics (with Full Fellowship), Jilin University, China — June 2012
Dissertation: Prediction of Drought-Resistant Genes in Arabidopsis thaliana using Microarray Data
Advisor: Dr. Yanchun Liang

B.S. Computer Science (with Honors), Jilin University, China — July 2009
Ranking: Top 1%

Publication

1. **Zhang, F.***, Wei, K.*, Slowikowski, K.*, Fonseka, C.Y.*, Rao, D.A.*, Kelly, S., Goodman, S.M., Tabechian, D., Hughes, L.B., Salomon-Escoto, K., Watts, G.F.M., Jonsson, A.H., Rangel-Moreno, J., Pellett, N.M., Rozo, C., Aprezzese, W., Eisenhaure, T.M., Lieb, D., Boyle, D.L., Mandelin A.M.,, Boyce, B.F., DiCarlo, E., Gravallese, E.M., Gregersen, P.K., Moreland, L., Firestein, G.S., Hacohen, N., Nusbaum, C., Lederer, J.A., Perlman, H., Pitzalis, C., Filer, A., Holers, M.V., Bykerk, V.P., Donlin, L.T., Anolik, J.H., Brenner, M.B., Raychaudhuri, S, the Accelerating Medicines Partnership RA/SLE. Defining Inflammatory Cell States in Rheumatoid Arthritis Joint Synovial Tissues by Integrating Single-cell Transcriptomics and Mass Cytometry. *Nature Immunology,* 2019. In Press.

2. Korsunsky, I., Fan, J., Slowikowski, K., **Zhang, F.**, Wei, K., Baglaenko, Y., Brenner, M., Loh, P., Raychaudhuri, S. Fast, sensitive, and flexible integration of single cell data with Harmony. 2019. **In review.**

3. Kuo, D.*, Ding J.*, Cohn, I., **Zhang, F.**, Wei, K., Rao, D., Rozo. C., Sokhi U.K., Accelerating Medicines Partnership RA/SLE Network, DiCarlo, E.F., Brenner, M.B., Bykerk, V.P., Goodman, S.M., Raychaudhuri, S., Batsch, G., Ivashkiv, L.B., Donlin, L.T. HBEGF$^+$ macrophages identified in rheumatoid arthritis promote joint tissue invasiveness and are reshaped differentially by medications. *Science Translational Medicine,* 2019. In press.

4. Arazi, A.*, Rao, D.A.*, Berthier, C.C.*, Davidson, A., Liu, Y., Hoover, P.J., Chicoine, A., Eisenhaure, T.M., Jonsson, A.H., Li, S., Lieb, D.J., Browne, E.P., Noma, A., Sutherby, D., Steelman, S., Smilek, D.E., Tosta, P., Apruzzese, W., Massarotti, E., Dall'Era, M., Park, M., Kamen, D.L., Furie, R.A., Payan-Schober, F., Buyon, J.P., Petri, M.A., Putterman, C., Kalunian, L.C., Woodle, E.S., Lederer, J.A., **Zhang, F.**, Hildeman, D.A., Nusbaum, C., Wofsy, D., Kretzler, M., Anolik, J.H., Brenner, M.B., The Accelerating Medicines Partnership in RA/SLE network, Hacohen, N., Diamond, B. The immune cell landscape in kidneys of lupus nephritis patients. *Nature Immunology*, 2019. In Press.

5. **Zhang, F.**, Wang C., Trapp, A., and Flaherty, P. A scalable deterministic global optimization algorithm for sparse mixed-membership matrix factorization. *arXiv* 1610.06145. New Advances in Statistics and Data Science, *ICSA Book Series in Statistics*, Springer, August, 2018. In Press.

6. **Zhang, F.**, and Flaherty, P. Variational inference for rare variant detection in deep, heterogeneous next-generation sequencing data. *BMC Bioinformatics*, *18*(45), 2017

7. He, Y., **Zhang, F.**, and Flaherty, P. RVD2: an ultra-sensitive variant detection model for low-depth heterogeneous next-generation sequencing data. ***Bioinformatics****, 31*(17), 2785-2793, 2015

8. **Zhang, F.**, Chen, S., Zhang, H., Zhang, X., and Li, G. Bioelectric signal detrending using smoothness prior approach. ***Medical engineering & physics****, 36*(8), 1007-1013, 2014

9. Geng, Y., **Zhang, F.**, Yang, L., Zhang, Y., and Li, G. Reduction of the effect of arm position variation on real-time performance of motion classification. In *Engineering in Medicine and Biology Society (**EMBC**), 2012 Annual International Conference of the IEEE* (pp. 2772-2775). IEEE, 2012

10. Liang, Y., **Zhang, F.**, Wang, J., Joshi, T., Wang, Y., and Xu, D. Prediction of drought-resistant genes in Arabidopsis thaliana using SVM-RFE. ***PloS one****, 6*(7), e21750, 2011

11. Wang, J., **Zhang, F.**, Wang, Y., Fu, Y., Xu, D., and Liang, Y. Identification of Salt Tolerance Genes in Rice from Microarray Data using SVM-RFE. *The 3rd International Conference on Bioinformatics and Computational Biology (**BICoB**)*, New Orleans, (pp. 30-35), 2011

Selected Talks

1. **Oral Talk. Single Cell Biology Keystone Symposia,** Breckenridge, CA, Jan. 2019
   Integrating single-cell transcriptomics and mass cytometry to define cell states in rheumatoid arthritis**.**

2. **Keynote Speak**. *IV European Conference "Genomics of Complex Diseases: New Challenges*". Pfizer-University of Granada-Junta de Andalucia Center for Genomics and Oncological Research (GEYNO), Granada, Spain. Oct. 2018
    Functional genetics and genomics to define rheumatoid arthritis.

3. **Invited Talk**. *Federation of Clinical Immunology Societies (FOCIS)*, San Francisco, CA. June 2018.
   Defining inflammatory cell states in rheumatoid arthritis joint synovia tissues by single-cell technology.

4. **Invited Talk**. *American College of Rheumatology (ACR),* San Diego, CA. Nov. 2017.
   Technology in precision medicine: data analysis and ontegration of high dimensional data from rheumatoid arthritis joint tissue**.**

5. **Oral Talk**. *Immunogenomics*, HudsonAlpha Institute for Biotechnology, Huntsville, AL. Oct. 2017.
   A novel computational method to resolve cellular heterogeneity in disease tissues.

6. **Oral Talk**. Accelerating Medicines Partnership (AMP) RA/SLE Face-to-Face, Houston, TX, Feb. 2017.
   Disease relevant signatures identification in rheumatoid arthritis (RA).

7. **Invited Talk**. Computational Biomedicine, **Boston University** and **Dana-Farber Cancer Institute**, 2016
   From data to the clinic: statistical methods for characterizing genomic heterogeneity in mixed samples.

8. **Oral Talk**. Bioinformatics & Computational Biology seminar at **WPI**, 2016
   Variational inference for rare variant detection in deep, heterogeneous next-generation sequencing data.

Posters

1. **Zhang, F.,** Wang, C., Trapp, A.C., Flaherty, P. A global optimization algorithm for sparse mixed membership matrix factorization. ***Conference of Reproducibility in Personalized Medicine Research***. Department of Biostatistics at the Harvard TH Chan School of Public Health, 2016.

2. Saddiki, H., **Zhang, F.**, Trapp, A.C., Flaherty, P. A Deterministic Global Optimization Method for Variational Inference. ***Workshop at Neural Information Processing Systems (NIPS)***, 2016.

3. **Zhang, F.,** and Flaherty, P. Variational inference for rare variant detection in deep, heterogeneous next-generation sequencing data. ***New England Statistics Symposium (NESS)***, Yale, CT, 2016.

4. **Zhang, F.,** and Flaherty, P. Variant detection model with improved robustness and accuracy for low-depth targeted next-generation sequencing data. The 22th Annual International Conference on ***Intelligent Systems for Molecular Biology (ISMB)***. Boston, MA, 2014.

5. **Zhang, F.,** and Flaherty, P. Variant detection model with improved robustness and accuracy for low-depth targeted next-generation sequencing data. The 18th Annual International Conference on ***Research in Computational Molecular Biology (RECOMB).*** Pittsburgh, PA, 2014.

Professional Skills

Computation/Statistics: Bayesian statistics, mixture modeling, convex and global optimization, and deep learning based canonical correlation analysis

Genomics data analysis:
- Single-cell RNA-seq, ATAC-seq, mass cytometry data analysis and integration, batch effect correction
- Time-series next-generation sequencing (NGS) data analysis and rare variant detection

Genome analysis toolkits:
- Harmony, Seurat, RVD2, Monocle, GATK, SAMTools, Mutect, Strelka, VarScan2, TopHat, Cufflinks etc.

Programming: Proficient in Python and R, and shell scripting in Linux.

Grant Writing Experience

Contribute to the proposal for NIH grants:
- Accelerating Medicines Partnership (AMP) co-leading Systems Biology Group
  NIAID/NIAMS Grant 1UH2AR067677-01   PI: Dr. Soumya Raychaudhuri

- A genome-wide survey of point mutations modulating methotrexate
  PhRMA Foundation Informatics Grant 2013080079   PI: Dr. Patrick Flaherty

Teaching Experience

Teaching Assistant, Biomedical Data Analysis, WPI	Mar. 2016 – May 2016
Teaching Assistant, Biomedical Engineering Design, WPI	Aug. 2015 – Oct. 2015
Teaching Assistant, Biomedical Data Analysis, WPI	Mar. 2014 – May 2014

Student Supervision

Joseph Mears, Bioinformatics Analyst in 10X genomics, Dartmouth College student	Aug. 2018 – Present
Gaurav Luthria, Text mining in single-cell RNA-seq annotation, Harvard PhD student	Aug. 2017 – Dec. 2017
Jeanie Lim, Workshop on RNA-Seq data analysis on Linux, UMass Amherst	Summer 2016
Yifan Zhao and Tete Zhang, NGS data analysis pipeline, WPI Master student	Summer 2015

Awards & Honor

Full Fellowship for Graduate Student, Jilin University	Sep. 2009 – Aug. 2012
Outstanding Graduate Student, Jilin University (Top 1%)	Sep. 2011
Graduate Student Entrance Scholarship, Jilin University	Sep. 2009
"Outstanding Star" of Software Engineering for Undergraduate, IBM	Mar. 2007

Professional Affiliations

Member, American College of Rheumatology (ACR)	Sep. 2017 – Present
Member, International Society for Computational Biology (ISCB)	April. 2014
Member, American Association for the Advancement of Science (AAAS)	Sep. 2013 – Present

Scientific Activities

Ad Hoc Reviewer, Cancer Letters	2019
Ad Hoc Reviewer, Arthritis Research & Therapy	2018
Ad Hoc Reviewer, Journal of Computational Statistics	2018
Reviewer, NESS (New England Statistics Symposium)	2018
Ad Hoc Reviewer, Scientific Reports	2016