Fan Zhang, PhD

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**Employment**

**Harvard Medical School (HMS) / Brigham and Women's Hospital** Boston, MA

Research Scientist (Immunogenomics Lab, Dr. Soumya Raychaudhuri) 2017 – Present

**Broad Institute of MIT and Harvard** Boston, MA

Associate Scientist 2017 – Present

**Chinese Academy of Sciences** Shenzhen, China

Research Associate 2012 – 2013

**Education** 

**Ph.D.** **Biomedical Engineering**, Worcester Polytechnic Institute (WPI), MA, US 2013 – 2017

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** (Full Fellowship), Jilin University, China 2009 – 2012

**B.S.** **Computer Science** (Ranking Top 1%), Jilin University, China 2005 – 2009

**Publications**

**Selected Peer Reviewed Articles**

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., the Accelerating Medicines Partnership Rheumatoid Arthritis and Systemic Lupus Erythematosus (AMP RA/SLE), 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. Defining inflammatory cell states in rheumatoid arthritis joint synovial tissues by integrating single-cell transcriptomics and mass cytometry. ***Nature immunology***, *20*(7), pp.928-942, 2019
2. **Zhang, F.**, Wang, C., Trapp, A., and Flaherty, P. A Global Optimization Algorithm for Sparse Mixed Membership Matrix Factorization. In ***Contemporary Biostatistics with Biopharmaceutical Applications*** (pp. 129-156), ICSA Book Series in Statistics. Springer, Cham, 2019
3. **Zhang, F.**, and Flaherty, P. Variational inference for rare variant detection in deep, heterogeneous next-generation sequencing data. ***BMC bioinformatics****, 18*(1), 45**,** 2017
4. **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

**Peer Reviewed Articles**

1. Fan, J.\*, Slowikowski, K, **Zhang, F**. Single-cell transcriptomics in cancer: computational challenges and opportunities. ***Nature Experimental & Molecular Medicine***, In press, 2020
2. Orange, D., Yao, V., Sawicka, K., Jak, J., Frank, M.O., Parveen, S., Blachere, N.E., Hale, C., **Zhang, F.**, Raychaudhuri, S., Troyanskya, O.G., Darnell, R.B. RNA Identification of PRIME Cells Predicting Rheumatoid Arthritis Flares. ***New England Journal of Medicine (NEJM)***, *383*(3), pp.218-228, 2020
3. Korsunsky, I., Millard, N., Fan, J., Slowikowski, K., **Zhang, F.**, Wei, K., Baglaenko, Y., Brenner, M., Loh, P., Raychaudhuri, S. Fast, sensitive and accurate integration of single-cell data with Harmony. ***Nature methods***, pp.1-8, 2019
4. Kuo, D.\*, Ding J.\*, Cohn, I., **Zhang, F.**, Wei, K., Rao, D., Rozo. C., Sokhi U.K., the AMP RA/SLE Consortium, DiCarlo, E.F., Brenner, M.B., Bykerk, V.P., Goodman, S.M., Raychaudhuri, S., Batsch, G., Ivashkiv, L.B., Donlin, L.T. HBEGF+ macrophages in rheumatoid arthritis induce fibroblast invasiveness. ***Science translational medicine****, 11*(491), 2019
5. 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., **Zhang, F**., Slowikovski K, 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., Pendergraft WF 3rd, Mclnnis E.A., Buyon, J.P., Petri, M.A., Putterman, C., Kalunian, L.C., Woodle, E.S., Lederer, J.A., Hildeman, D.A., Nusbaum, C., Raychaudhuri S., Kretzler, M., Anolik, J.H., Brenner, M.B., Wofsy D., Hacohen, N., Diamond, B., the AMP RA/SLE Consortium. The immune cell landscape in kidneys of patients with lupus nephritis. ***Nature immunology***, *20*(7), pp.902-914, 2019
6. 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
7. 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), 2012
8. 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
9. 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

**Preprint / In Review**

1. **Zhang, F.**, Mears, J.R., Shakib, L., Beynor, J.I., Shanaj, S., Korsunsky, I., Nathan, A., the Accelerating Medicines Partnership RA/SLE, Donlin, L.T., Raychaudhuri, S. IFN-γ and TNF-α drive a CXCL10+ CCL2+ macrophage phenotype expanded in severe COVID-19 and other diseases with tissue inflammation. *bioRxiv*, 2020
2. Mysore, V., Cullere, X., Mears, J., Rosetti, F., Okubo, K., Liew, P., **Zhang, F.**, Madera-Salcedo, I., Stone, R., Dr. Aster, J., Andrian, U.V., Raychaudhuri, S., Lichtman, A., Rosenbauer, F., and Mayadas, T. FcγR engagement reprograms neutrophils into antigen cross-presenting cells that elicit acquired immunity, 2020

**Invited Talks**

1. **Invited Talk. Research Methods Workshop,** Center for Skeletal Research at **Massachusetts General Hospital**, Boston, MA,May, 2020

Integration of single-cell transcriptomic and proteomic data to study autoimmune diseases

1. **Invited Talk.** ***American College of Rheumatology (ACR)****,* Atlanta, GA, Nov. 2019

System-level multi-modality data integration for single-cell transcriptomics

1. **Oral Talk.** ***American College of Rheumatology (ACR)****,* Atlanta, GA, Nov. 2019

Integration of single cells from inflammatory disease tissues reveals common and unique pathogenic cell states

1. **Oral Talk. The AMP RA/SLE face to face,** Washington DC, Sep. 2019

Integration of single cells from inflammatory disease tissues reveals common and unique pathogenic cell states”

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**.**

1. **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

1. **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

1. **Invited Talk**. ***American College of Rheumatology (ACR)****,* San Diego, CA. Nov. 2017.

Technology in precision medicine: data analysis and integration of high dimensional data from rheumatoid arthritis joint tissue

1. **Oral Talk**. ***Immunogenomics***, HudsonAlpha Institute for Biotechnology, Huntsville, AL. Oct. 2017.

A novel computational method to resolve cellular heterogeneity in disease tissues

1. **Oral Talk**. Accelerating Medicines Partnership (AMP) RA/SLE Face-to-Face, Houston, TX, Feb. 2017.

Disease relevant signatures identification in rheumatoid arthritis (RA)

1. **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

**Posters** 

1. Wei, K.\*, Jonsson, A.H.\*, **Zhang, F.**\*, Nathan, A., Mears, J., Watts, G., Zhu, Z., Korsunsky, I., Donlin, L.T., Rao, D., Filer, A., Boyce, B., Gravallese, E., Holers, V.M., Moreland, L., Gregersen, P., Bykerk, V., Anolik, J., Raychaudhuri, S., Brenner, M. Towards a Single Cell Portrait of Rheumatoid Arthritis-Development of a Single Cell Multiomics Pipeline for Phase 2 of the Accelerating Medicine Partnership (AMP)-RA Network. ***American College of Rheumatology (ACR)****.* Atlanta, GA, 2019
2. Jonsson, A.H., **Zhang, F.**, Watts, G., Wei, K., Rao, D., Raychaudhuri, S., Brenner, M. An Expanded Granzyme K+ CD8 T Cell Population Induces Inflammatory Responses in Rheumatoid Arthritis Synovium. ***American College of Rheumatology (ACR)****.* Atlanta, GA, 2019
3. **Zhang, F.**, Mears, J., ..., Raychaudhuri, S. Integration of single cells from inflamed tissue in RA and SLE reveals shared immune and stromal cell population. ***Federation of Clinical Immunology Societies (FOCIS).*** Boston, MA, 2019
4. **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, Boston, MA, 2016
5. Saddiki, H., **Zhang, F.**, Trapp, A.C., Flaherty, P. A Deterministic Global Optimization Method for Variational Inference. ***Workshop at Neural Information Processing Systems (NIPS)***, Barcelona, Spain, 2016
6. **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
7. **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
8. **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 Skill**

**Computation/Statistics**: Bayesian statistics, mixture modeling, convex and global optimization, deep learning

**Genomic data analysis**:

* Multi-omics: single-cell RNA-seq, single-cell ATAC-seq, and single-cell CITE-seq data integration
* Rare variant detection: time-series next-generation sequencing (NGS) DNA-seq data

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

**Developed Software**

* RVD and RVD2 (Python): Identify rare variants in heterogeneous NGS clinical samples (Zhang, *et al*. 2017)
* GOP (Python): Identify global optimum for a parse mixed membership matrix factorization for heterogeneous gene expression samples (Zhang, *et al*. 2019)

**Grant Applications** 

* Integrating single-cell genomics and proteomics to define pathogenic cell states shared between RA and RA-ILD Grant K99 (NIH NIAMS, In submission) PI: Dr. Fan Zhang (2020)
* Differentiation of immune cells and fibroblasts in inflamed tissue in RA and SLE – Computational systems immunology core (NIH NIAID, In submission) PI: Dr. Soumya Raychaudhuri (2019)
* A genome-wide survey of point mutations modulating methotrexate

PhRMA Foundation Informatics Grant 2013080079 PI: Dr. Patrick Flaherty (2015)

**Teaching Experience** 

Teaching Assistant, Biomedical Data Analysis, WPI Jan. 2016 – May 2016

Teaching Assistant, Biomedical Engineering Design, WPI Aug. 2015 – Oct. 2015

Teaching Assistant, Biomedical Data Analysis, WPI Jan. 2014 – May 2014

**Student Supervision** 

Kathryn Weinand, Single-cell chromatin accessibility epigenetics, Harvard PhD student Aug 2019 – Present

Joseph Mears, Bioinformatics Analyst in single-cell 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, UMass Amherst student Summer 2016

Yifan Zhao and Tete Zhang, NGS data analysis, WPI Master student Summer 2015

**Awards & Honor****s**

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, *Cell Reports, iScience* 2020

Ad Hoc Reviewer, *Nature, Nature Communication, Genomics, Proteomics & Bioinformatics* 2019

Ad Hoc Reviewer, *Cancer Letters, Arthritis Research & Therapy, Journal of Computational Statistics* 2018

Ad Hoc Reviewer, *NESS (New England Statistics Symposium)* 2018

Ad HocReviewer, *Scientific Reports* 2016