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

5. Fan, J.*, Slowikowski, K, **Zhang, F**. Single-cell transcriptomics in cancer: computational challenges and opportunities. ***Nature Experimental & Molecular Medicine***, In press, 2020

6. 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

7. 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

8. 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

9. 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

10. 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

11. 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

12. 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

13. 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

14. **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

15. 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

2. **Invited Talk. *American College of Rheumatology (ACR),*** Atlanta, GA, Nov. 2019
   System-level multi-modality data integration for single-cell transcriptomics

3. **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

4. **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"

5. **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**.**

6. **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

7. **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

8. **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

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

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

11. **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 (National Institute of Arthritis and Musculoskeletal and Skin Diseases) AR077068-01 (In submission)   PI: Dr. Fan Zhang (2020)

- Differentiation of immune cells and fibroblasts in inflamed tissue in RA and SLE – Computational systems immunology core) PAI148102A (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 & Honors

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 Hoc Reviewer, *Scientific Reports*	2016