

# Fan Zhang, PhD

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## Employment

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<b>Harvard Medical School (HMS)</b> Research Scientist (Dr. Soumya Raychaudhuri)	Boston, MA Jan. 2017 – Present
<b>Broad Institute of Harvard and MIT/Brigham and Women's Hospital</b> Associate Scientist Research Associate	Boston, MA Jan. 2019 - Present Jan. 2017 – Jan. 2019
<b>Worcester Polytechnic Institute (WPI)</b> Teaching Assistant	Worcester, MA Aug. 2013 – Dec. 2016
<b>Chinese Academy of Sciences</b> Research Associate	Shenzhen, China May 2012 – June 2013

## Education

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<b>Ph.D. Bioinformatics</b> , Worcester Polytechnic Institute (WPI), MA, US Dissertation: Statistical Methods for Characterizing Genomic Heterogeneity in Mixed Samples Advisor: Dr. Patrick Flaherty (Genomics Lab, now in Statistics Dep. in UMass Amherst)	Dec. 2016
<b>M.S. Bioinformatics</b> (with Full Fellowship), Jilin University, China Dissertation: Prediction of Drought-Resistant Genes in Arabidopsis thaliana using Microarray Data Advisor: Dr. Yanchun Liang	June 2012
<b>B.S. Computer Science</b> (with Honors), Jilin University, China Ranking: Top 1%	July 2009

## Selected Publications

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- 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 RA/SLE, Boyce, B.F., DiCarlo, E., Gravallesse, 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), p.928. (2019).
- Korsunsky, I., 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*, doi:10.1038/s41592-019-0619-0, 2019, (2019).
- 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 in rheumatoid arthritis induce fibroblast invasiveness. *Science Translational Medicine* 11.491, eaau8587, (2019).
- 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, McInnis 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 Accelerating Medicines Partnership in RA/SLE network. The immune cell landscape in kidneys of patients with lupus nephritis. *Nature Immunology* (2019)
- Zhang, F.**, Wang C., Trapp, A., and Flaherty, PA 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).

6. Der, E, Suryawanshi, H, Morozov, P, Kustagi, M, Goilav, B, Ranabathou, S, Izmirly, P, Clancy, R, Belmont, HM, Koenigsberg, M, Mokrzycki, M, Rominiaki, H, Graham, JA, Rocca, JP, Bornkamp, N, Jordan, N, Schulte, E, Wu, M, Pullman, J, Slowikowski, K, Raychaudhuri, S, Guthridge, J, James, J, Buyon, J, Tuschl, T, Putterman, C; Accelerating Medicines Partnership Rheumatoid Arthritis and Systemic Lupus Erythematosus (**AMP RA/SLE**) Consortium. Tubular cell and keratinocyte single-cell transcriptomics applied to lupus nephritis reveal type I IFN and fibrosis relevant pathways. *Nature immunology*, 20(7), p.915. (2019). AMP RA/SLE Consortium includes **Zhang, F**.
7. Donlin, LT, Rao, DA, Wei, K, Slowikowski, K, McGeachy, MJ, Turner, JD, Meednu, N, Mizoguchi, F, Gutierrez-Arcelus, M, Lieb, DJ, Keegan, J, Muskat, K, Hillman, J, Roza, C, Ricker, E, Eisenhaure, TM, Li, S, Browne, EP, Chicoine, A, Sutherby, D, Noma, A; Accelerating Medicines Partnership Rheumatoid Arthritis and Systemic Lupus Erythematosus (**AMP RA/SLE**) Consortium, Nusbaum, C, Kelly, S, Pernis, AB, Ivashkiv, LB, Goodman, SM, Robinson, WH, Utz, PJ, Lederer, JA, Gravallese, EM, Boyce, BF, Hacohen, N, Pitzalis, C, Gregersen, PK, Firestein, GS, Raychaudhuri, S, Moreland, LW, Holers, VM, Bykerk, VP, Filer, A, Boyle, DL, Brenner, MB, Anolik, JH. Methods for high-dimensional analysis of cells dissociated from cryopreserved synovial tissue. *Arthritis research & therapy*, 20(1), p.139. (2018). AMP RA/SLE Network includes **Zhang, F**.
8. **Zhang, F.**, and Flaherty, P. Variational inference for rare variant detection in deep, heterogeneous next-generation sequencing data. *BMC Bioinformatics*, 18(45), (2017)
9. 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)
10. **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)
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). IEEE, (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 3<sup>rd</sup> International Conference on Bioinformatics and Computational Biology (BICoB)*, New Orleans, (pp. 30-35), (2011)

## Invited Talks

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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”.
2. **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.
3. **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.
4. **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.
5. **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.
6. **Oral Talk. Immunogenomics**, HudsonAlpha Institute for Biotechnology, Huntsville, AL. Oct. 2017.  
A novel computational method to resolve cellular heterogeneity in disease tissues.
7. **Oral Talk. Accelerating Medicines Partnership (AMP) RA/SLE Face-to-Face**, Houston, TX, Feb. 2017.  
Disease relevant signatures identification in rheumatoid arthritis (RA).
8. **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.

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

## Posters

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1. 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
2. **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.
3. 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.
4. **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.
5. **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.
6. **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

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

### Genomics data analysis:

- Single-cell and bulk RNA-seq, Single-cell ATAC-seq, mass cytometry data analysis and integration
- Rare variant detection in time-series next-generation sequencing (NGS) DNA-seq data

### Genome analysis toolkits:

- RVD2, Harmony, GATK, Seurat, Monocle, SAMTools, Mutect, Strelka, TopHat, Cufflinks, etc.

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

## Grant Application

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- 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 (June, 2019)
- Accelerating Medicines Partnership (AMP) RA/Lupus co-leading Systems Biology Group NIAMS/NIAID 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

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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

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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

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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

**Professional Affiliations**

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

**Scientific Activities**

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Ad Hoc Reviewer, <i>Nature</i>	2019
Ad Hoc Reviewer, <i>Nature Communication</i>	2019
Ad Hoc Reviewer, <i>Genomics, Proteomics and Bioinformatics</i>	2019
Ad Hoc Reviewer, <i>Cancer Letters</i>	2019
Ad Hoc Reviewer, <i>Arthritis Research &amp; Therapy</i>	2018, 2019
Ad Hoc Reviewer, <i>Journal of Computational Statistics</i>	2018
Reviewer, <i>NESS (New England Statistics Symposium)</i>	2018
Ad Hoc Reviewer, <i>Scientific Reports</i>	2016