Fei Wang

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Google scholar: https://scholar.google.com/citations?user=4ZN8M5gAAAAJ&hl=en

Spatial omics | Multi-omics integration | Statistics & ML Modeling | Reproducible Pipelines | R, Python & Bash

PROFESSIONAL SUMMARY

Bioinformatics and computational biologist with a Ph.D. in Neuroscience, academic wet-lab training, and more than two years of pharmaceutical R&D experience analyzing high-dimensional biological data. Experienced in bulk and single-cell transcriptomics, proteomics, spatial omics, and multi-omics integration. Strong R, Python, and Bash programming skills, with abundant experience developing reproducible pipelines, packages, interpretable statistical and machine-learning models, and interactive tools. Proven ability to translate complex molecular datasets into mechanistically informed, testable biological hypotheses through differential analysis, feature prioritization, cell-type inference, and pathway-level interpretation. Effective cross-functional collaborator with experimental, computational, statistical, and translational scientists.

TECHNICAL SKILLS

- **Programming & Reproducible Computing:** R, Python, and Bash; Git/GitHub; Docker; package and pipeline development; AWS EC2; Posit Workbench.
- **Transcriptomics & Multi-Omics:** Bulk and single-cell RNA-seq analysis (Seurat); spatial transcriptomics and proteomics; data QC, differential analysis (DESeq2, edgeR, limma), integration, and feature prioritization.
- **Statistics & Machine Learning:** Linear mixed models, regression and classification, random forest, multivariate analysis, PCA, clustering, feature selection, cross-validation, and interpretable modeling.
- **Spatial & Systems Biology:** Cell-type deconvolution and inference, spatial niche and cell-cell interaction analysis; pathway enrichment (GSEA/ORA), cross-species signature comparison, and ECM remodeling.
- **Visualization & Interactive Tools:** R Shiny applications, interactive data exploration; publication-quality scientific visualization (Adobe Illustrator, Adobe Premiere, Graphpad Prism).
- **Proteomics Methods:** Laser microdissection-based spatial proteomics; DIA/DDA workflows; insoluble ECM protein extraction; high-throughput workflow optimization.
- **Biological & Experimental Expertise:** Cell culture, histology, microscopy imaging (confocal, two-photon), molecular biology (CRISPR, cloning), genetic screening; collaboration across computational and bench teams.

INDUSTRY EXPERIENCE

AbbVie — Postdoctoral Fellow | Computational Biology, Data & Digital Science & Proteomics

- Led end-to-end analysis of **bulk, spatial, and single-cell transcriptomic and proteomic datasets** across rheumatoid arthritis, pulmonary fibrosis, breast cancer, and inflammatory bowel disease, from QC and statistical modeling through biological interpretation for early target and biomarker prioritization
- Integrated **spatial proteomics and transcriptomics with scRNA-seq references** to **infer cell populations, resolve spatial niches, and characterize cell interactions** in RA, IPF, and TNBC tissue microenvironments.
- Mapped **lung extracellular-matrix remodeling** across age, sex, and anatomic region by **multi-factor statistics analysis**, identifying region- and age-associated protein programs for mechanistic follow-up.
- Compared disease and treatment-response signatures across **anti-CD40 colitis, additional mouse IBD models, and human IBD** to assess cross-species translational alignment.
- Improved proteomics data generation by optimizing **Azo-based insoluble ECM extraction from a two-step to a single-step workflow** and refining a plasma **SWATH-DIA workflow** for reproducible protein measurement.
- Developed reproducible **R/Python pipelines and packages, interpretable statistical** and **machine-learning workflows,** and **R Shiny applications**; deployed interactive tools on **AWS EC2** and **Posit Workbench** that enable bench and domain scientists to independently explore and interpret complex omics datasets with minimal coding.

SELECT SOFTWARE & OPEN-SOURCE WORK

Cell type inference pipeline: https://github.com/outobi/query_and_overlap_method_pipeline
Cell type inference R package Cell2Spatial: https://github.com/outobi/cell2spatial
Representative interactive pipeline with AWS HPC deployment: https://omics.feiwangbio.com

SELECT PUBLICATIONS

Spatial and single-cell omics integration for disease associated cell type and signature identifications

- Wang, X.*, **Wang, F.*** et al. (2025). *Integrative spatial proteomics and single-cell RNA sequencing unveil molecular complexity in rheumatoid arthritis for novel therapeutic targeting.* **Proteomes**, 13(2), 17. (* Co-first author)
- **Wang, F.**, Jin, L., Wang, X. et al. (2025). *Novel integration of spatial and single-cell omics datasets enables deeper insights into IPF pathogenesis.* **Proteomes**, 13(1), 3.
- Hunt, A.L.*, **Wang, F.***, Abulez, T., et al. *Spatially resolved proteomic characterization of the triple-negative breast cancer tumor immune microenvironment.* (In press, **Clinical Proteomics**) (* Co-first author)

ECM remodeling with comprehensive multi-factor statistical analysis

- Towler, A.G.*, **Wang, F.***, et al. Systematic Quantitative Analysis of the Aging Rat Lung enabled by High-throughput Extracellular Matrix Proteomics (Under revision at Nature Communications) (* Co-first author)

High-throughput proteomics workflow development

- Towler, A.G., Perciaccante, J.A., Aballo, J.T., Zhu, Y., **Wang, F.** et al. (2025). *A single-step protein extraction for lung extracellular matrix proteomics enabled by photocleavable surfactant Azo and timsTOF Pro.* **Molecular & Cellular Proteomics**, 24(8), 100950.
- Jin, L., **Wang, F.**, Wang, X. et al. (2023). *Identification of plasma biomarkers from rheumatoid arthritis patients using an optimized SWATH proteomics workflow.* **Proteomes**, 11(4), 32.

Mechanistic biology in axon regeneration

- **Wang, F.***, Ruppell, K.T.*, Zhou, S.* et al. (2023). *Gliotransmission and adenosine signaling promote axon regeneration.* **Developmental Cell**, 58, 660-676. (* Co-first author)

WORK & EDUCATION

Postdoctoral fellow, Developmental Science, AbbVie Bioresearch Center, Worcester, MA	**2023/01-2025/08**
Ph. D., **Neuroscience**, Morningside Graduate of Biomedical Sciences, University of Massachusetts Chan Medical School, Worcester, MA	**2014/09-2022/08**
B. S., **Biological Science**, Peking University, Beijing, China	**2010/09-2014/07**

HONORS & AWARDS

- **Weibo Li Scholarship**, Umass Chan Medical School, 2018 (for 5 top graduate students each year)
- **President** of the Chinese Students and Scholars Association, Umass Chan Medical School, 2017
- **Leica Scholarship,** Peking University, 2013 (for top 10% outstanding undergraduates in School of Life Sciences)
- The first prize of the **National Biology Olympics** of China, 2009

SELECT PRESENTATIONS

2025 Next generation omics meeting, talk	2025/10, Boston, MA
2025 US HUPO annual meeting, lightning talk, poster	2025/02, Philadelphia, PA
2024 ASMS annual meeting, poster	2024/06, Anaheim, CA
2024 Next generation omics meeting, poster	2024/03, Boston, MA
2016 Society for Neuroscience meeting, poster	2016/11, San Diego, CA