## UT Southwestern Medical Center

## **Bioinformatics and Computational Biology Postdoctoral Researcher**

A postdoctoral training position is available in the laboratory of <u>Tao Wang, Ph.D</u>., in the O'Donnell School of Public Health at UT Southwestern Medical Center to study projects that includes (1) developing novel methods for analysis and integration of genomics, proteomics, spatial/imaging and other forms of high-dimensional -omics data, and developing prediction models for patients' clinical outcomes, (2) assembling and statistical analyses of big biomedical data to reveal significant and novel biological insights, (3) creating databases and websites for management of big biological data. (4) Application for independent funding under the support of the PI. We welcome post-doctoral fellows with interest in 100% "dry" research or research that is half "dry" and half "wet". We welcome post-doctoral fellows who switch from 100% "wet" research background, as long as he/she has demonstrated a keen interest in, has a decent exposure to, and has a clear potential for "dry" research.

<u>The Tao Wang Lab</u> is a top and well-established bioinformatics research group at UTSW. Statistics, informatics, medicine, and biology are the four integral pillars of Tao Wang Lab's interdisciplinary research program. Dr. Wang's group has been working on mining public and in-house high throughput data to achieve a deeper understanding of the immunology of various human diseases, with a heavy emphasis on cancers, and its implications for diagnosis, prognosis, and treatment. The core research interest of Wang Lab is in development of methodologies for analyses of immunogenomics, computational immunology, scRNA-seq data, and spatial transcriptomics data. The ultimate goal is to impact the prognosis and treatment of patients suffering from cancers and other diseases, through modeling of high dimensional data, especially immunogenomics data. Tao Wang Lab has published 89 papers in top journals, such as Nature Methods (2024, Zhu, Chang, and Wang et al), Genome Biology (2023, Yang et al), Nature Machine Intelligence (2021, Lu et al), Nature Methods (2021, Zhang et al), Science Immunology (2020, Lu et al), Cancer Discovery (2018, Wang et al), SMMR (2020, Park et al), Cell (2019, Zhu et al), since its establishment in 2016. Wang Lab holds two patents.

The University of Texas Southwestern Medical Center (UTSW) is an elite research institution, with ongoing support from the National Institutes of Health and other federal agencies, foundations, individuals, and corporations.

At UTSW, there are great opportunities for scientists to collaborate with outstanding biomedical investigators and work on exciting research projects. UT Southwestern and the Tao Wang Lab provide a friendly, dynamic, collaborative, and integrative research and training environment with state-of-the-art facilities.

Candidates must hold a recent Ph.D. and/or M.D. degree in either one of the following fields, including genetics/genomics, bioinformatics, computational biology, computer science, biostatistics, or a related field.

Information on our postdoctoral training program, benefits, and a virtual tour can be found at <u>http://www.utsouthwestern.edu/postdocs</u>.

More information on Wang lab and our research environment can be found at

Tao Wang Lab | Quantitative Biomedical Research Center | UT SouthwesternTao Wang, Ph.D. - Faculty Profile - UT SouthwesternO'Donnell School of Public Health | Public Health Programs - UT Southwestern, Dallas, TexasQuantitative Biomedical Research Center | UT Southwestern

Interested individuals should send a CV and a statement of interest to:

Tao Wang, Ph.D.Email: <u>Tao.wang@utsouthwestern.edu</u> (please avoid attaching compressed .zip files, which will be blocked by UTSW firewall)

## **Recent publications**

- (1) Mapping cellular interactions from spatially resolved transcriptomics data. Nature Methods. 2024
- (2) Cytomulate: accurate and efficient simulation of CyTOF data. Genome Biology. 2023
- (3) Sprod for De-noising Spatial Transcriptomics Data Based on Position and Image Information. *Nature Methods*. 2022.
- (4) Benisse for Interpreting the B Cell Receptor Repertoire with Single Cell Gene Expression. *Nature Machine Intelligence*. 2022.
- (5) Deep learning-based prediction of the T cell receptor-antigen binding specificity. *Nature Machine Intelligence*. 2021.
- (6) Mapping the Functional Landscape of T Cell Receptor Repertoire by Single T Cell Transcriptomics. *Nature Methods*. 2020.
- (7) Tumor Neoantigenicity Assessment with CSiN Score Incorporates Clonality and Immunogenicity to Predict Immunotherapy Outcomes. *Science Immunology*. 2020.
- (8) Somatic Mutations Increase Hepatic Clonal Fitness and Regeneration in Chronic Liver Disease. Cell. 2019.

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