Postdoctoral Researcher Position in Multimodal ML for protein and tissue dynamics

We invite outstanding candidates to apply for postdoctoral research positions in the Zhang lab at AITHYRA, the new Research Institute for Biomedical Artificial Intelligence of the Austrian Academy of Sciences (https://www.oeaw.ac.at/aithyra/research#c292352). Our group, in a highly interdisciplinary institute, offers exciting opportunities for innovations in machine learning methods to integrate multimodal and spatiotemporal data to achieve a holistic understanding of cell states, tissue microenvironments, and perturbation effects. The research program is flexible and we welcome machine learning researchers without prior biological research experience, who are excited to work on biomedical problems.

Core Themes

Our goal is to gain mechanistic insights into cellular and tissue regulation across scales—from protein localization and interaction in single cells to cell fate decisions in organoids and tissues. By modeling the cellular dynamics and interactions in the tissue context, we aim to enable virtual profiling of genetic and chemical perturbations to identify potential therapeutic targets for disease-associated changes in protein localization, cell states, and tissue architecture.

1. Tissue-specific protein localization and interaction.

Protein subcellular localization and protein-protein interactions (PPIs) are essential to many biological processes and are tightly regulated by cell and tissue states. We develop computational models that predict protein localization and interactions with single-cell and tissue specificity. These models enable predictions of how disease-associated genetic mutations or changes in cell state alter protein localization and interactions, ultimately supporting therapeutic discovery.

2. Modeling the dynamics and interactions in the tissue microenvironment to study cell fate.

We develop computational frameworks to model the tissue microenvironment and study how genetic and chemical perturbations influence cell states in tissue over time. By integrating perturbation modeling with temporal dynamics, feature learning, physical principles, and disentanglement of multimodal information, our goal is to understand the interplay between the molecular and mechanical signaling underlying cell fate decisions in tissue. This understanding could enable virtual profiling of gene expression, morphology, and molecular phenotypes under unseen conditions.

3. Clinical applications in metabolic disease, cancer, and neurodegeneration.

Our methods are designed to be broadly applicable to large-scale patient and drug-screening datasets. We aim to extend this to study the effect of patient-specific genetic variants on cell state using imaging, spatial omics, and histopathology data, which could enable functional interpretation of risk variants in metabolic disease, cancer, neurodegeneration. By developing robust, interpretable, and generalizable models, our goal is to link mechanistic insights of cellular regulation to therapeutic target discovery.

Qualifications: PhD (or near completion) in computer science, machine learning, statistics/biostatistics, computational biology, data science, or related field. Experience with modern deep learning frameworks (e.g., PyTorch, JAX, TensorFlow). Prior experience in biological research is not required.

Please send your application as a single PDF including:

- Curriculum vitae (including a full publication list)
- A short research statement explaining your interests and fit for the position
- Names and contact information for two references

to xzhang@aithyra.at.