Job Title:

Postdoctoral Fellow — Whole-Cell Model-Driven Gene Function Discovery

Workplace:

The Agmon Lab, part of the Center for Cell Analysis and Modeling at UConn Health, is advancing the field of computational biology by developing comprehensive computational models for understanding cellular behavior at multiple levels. Our projects range from the molecular basis of cellular processes to the intricate dynamics of microbial communities, supported by our open-source platform, Vivarium. For more information about our lab and projects, visit https://eagmon.github.io/. This role involves a collaboration with Basis, a leading applied AI research organization in NYC/Boston, and the Pacific Northwest National Lab (PNNL).

Project Description:

We are starting a project aimed at streamlining our approach to identifying missing or unknown gene functions using whole-cell models, particularly focused on extending an established whole-cell model of *E. coli*. By integrating whole-cell modeling with a modular simulation platform and a probabilistic inference workflow, we aim to automate the discovery and curation of gene functions. This project will enhance the predictive accuracy of the *E. coli* model under various conditions, leveraging extensive datasets and high-performance computing resources for simulation and analysis.

Job Description:

We seek a highly motivated Postdoctoral Researcher to lead this groundbreaking project. The ideal candidate will have a robust background in probabilistic modeling, simulation, and computational biology, with a passion for solving complex biological questions. This role involves generating and analyzing thousands of E. coli model variants, using advanced computational techniques to infer and curate new gene functions. This work will refine the model's predictive capability across numerous conditions.

Requirements:

- PhD in Computational Biology, Bioinformatics, Systems Biology, Applied Mathematics, or a related field.
- Proven experience with probabilistic modeling, simulation, and data analysis.
- Strong programming skills, preferably in Python.
- Familiarity with systems biology modeling, high-performance computing, and bioinformatics databases is a plus.
- Excellent communication and collaboration skills, including the ability to work effectively with external collaborators.

Responsibilities:

- Develop and implement the simulation-based inference workflow for gene function discovery.
- Conduct simulations of E. coli variants, analyze results, and integrate findings to enhance the model.

- Collaborate closely with the Basis team and research teams to intake experimental data and validate model predictions.
- Publish findings in high-impact journals and present at international conferences.

Benefits:

- Competitive salary with comprehensive medical and dental insurance.
- Access to state-of-the-art computational resources and collaboration with leading researchers in the field.
- Opportunity to contribute to groundbreaking research.
- Flexible work schedule and a supportive, inclusive lab environment.
- Collaboration with Basis
- Competitive salary, up to \$100,000/year

Availability:

- This position is available with a starting date in Summer/Fall 2024. For further details or to apply, please contact Dr. Eran Agmon at agmon@uchc.edu.