

## Recruiting Python Programmers to Develop Predictive Single Cell Spatiotemporal Analysis Toolkit

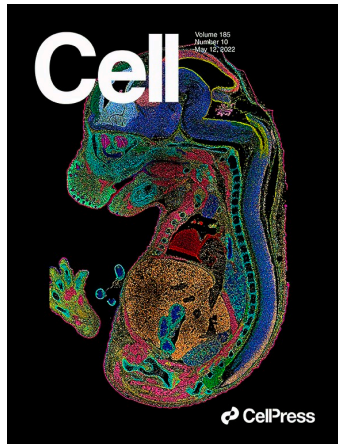
The Weissman lab (<https://weissman.wi.mit.edu/>) at Whitehead Institute & MIT is looking for one or more talented programmer (primarily undergraduates/masters but also open to senior computational scientist) with strong python programming and software engineering backgrounds to develop, optimize and maintain next generation predictive tools for the emergent single cell genomics applications. This position is particularly well suited for senior undergraduates or masters seeking for research experience before continuing their education or industrial career. The goal of the projects is to develop a foundational software ecosystem, Aristotle (<https://github.com/aristoteleo>), that marries machine learning, dynamical systems and other systems biology approaches with advanced single cell genomics to empower biologists to gain mechanistic and predictive insights of cell fate transitions in development and diseases. The representative publications related to this position include: **Genome-wide perturb-seq**: Replogle, Saunders, et. al, Cell, 2022; **Stereo-seq**: Chen, et. al, Cell, 2022; **Dynamo**: Qiu, Zhang, et. al, Cell, 2022.

The ideal candidate will join us to further develop and improve the Aristotle ecosystem, an end-to-end computational framework that provides advanced spatiotemporal modeling of single cell and spatial genomics datasets. The Aristotle ecosystem currently consists of a coherent set of three major python packages on Github: **dynast** ([aristoteleo/dynast-release](https://github.com/aristoteleo/dynast-release)), **dynamo** ([aristoteleo/dynamo-release](https://github.com/aristoteleo/dynamo-release)) and **spateo** ([aristoteleo/spateo-release](https://github.com/aristoteleo/spateo-release)), that have functionalities range from raw sequencing data processing to downstream predictive frameworks of biophysical modeling of RNA kinetics, machine learning of the RNA velocity vector field, and spatiotemporal modeling of single cell resolution spatial transcriptomics in 3D space, etc. The ideal candidate will contribute to two major aspects: software engineering and community outreach. The candidate will apply state-of-the-art software engineering practices to improve the modularity, organization, and quality of the existing code base. Additionally, the candidate will contribute to the development of novel algorithms and the analysis of new single cell genomics datasets. The candidate will be encouraged to participate in community activities to foster wider adoption of the Aristotle ecosystem. Papers reporting the packages and methods will be published to promote the ecosystem and the candidate's career.

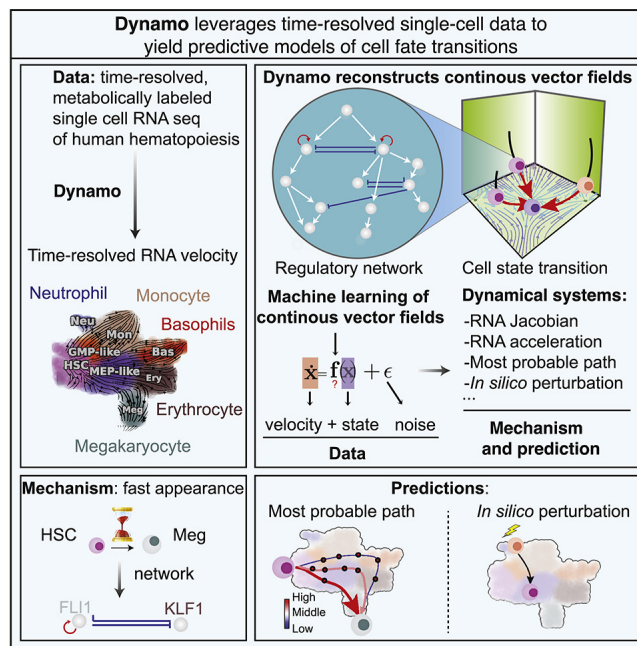
The Weissman lab at Whitehead Institute & MIT is a leader in functional genomics including the development of ribosome profiling, CRISPRi, CRISPRa, and CRISPRoff, Perturb-seq, lineage tracing and novel predictive computational tools. The lab is well-known for its highly stimulating and collaborative environment, as well as its strong track record for placing students into top graduate programs and as a training ground for leaders in academia and industry. A competitive salary will be offered, following Whitehead Institute standard based on training level. The candidate will need to primarily work in the lab, located in the vibrant Kendall Square area in Cambridge, which is a hub for science, engineering and biotechnology and is proximal to the MIT campus.

If you are interested in this position, please email your CV and github account ID to **BOTH** Dr. Jonathan Weissman ([weissman\\_admin@wi.mit.edu](mailto:weissman_admin@wi.mit.edu)) **AND** his post-doc Dr. Xiaojie Qiu ([xqiu@wi.mit.edu](mailto:xqiu@wi.mit.edu)) who will provide many hands-on supervision on the proposed projects.

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**Stereo-seq:** Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays. (Chen, Liao, Cheng, Mai, Wu, Lai, and Qiu, et al, Cell 2022)



**Dynamo:** Mapping Transcriptomic vector fields of single cells. (Qiu and Zhang et al, Cell 2022)

