# *Software Engineer – Weissman Lab*
## *10/7/22*

Whitehead Institute for Biomedical Research is a leading, nonprofit research and educational institution that has defined the cutting edge of biomedical science, creating a legacy of research excellence and academic eminence since 1982. Wholly independent in its governance, finances and research programs, Whitehead shares a teaching affiliation with Massachusetts Institute of Technology (MIT), offering the intellectual, collegial and scientific benefits of a leading research university. Whitehead's Faculty Members and Fellows run pioneering programs in cancer research, immunology, developmental biology, stem cell research, regenerative medicine, genetics and genomics—programs with a record of success.

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Whitehead Institute is an Equal Opportunity Employer.

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| **Title:** | **Software Engineer** |
| **Department:** | **Weissman Lab** |
| **FLSA Classification:** | **Exempt** |
| **Reports to:** | **PI or other Supervisory Lab Personnel** |

## OVERALL RESPONSIBILITY

The Weissman lab (https://weissman.wi.mit.edu/) at Whitehead Institute is looking for one or more talented Software Engineers (primarily undergraduates/masters but also open to senior computational scientists) 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 students seeking 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), **dynamo** (aris-toteleo/ dynamo-release) and **spateo** (aristoteleo/spateo-release), that have functionalities ranging 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. Papers reporting the packages and methods will be published to promote the ecosystem and the candidate's career.

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.

## CHARACTERISTIC DUTIES

- Develop, optimize and maintain next generation predictive tools for the emergent single cell genomics applications.
- Contribute to two major aspects: software engineering and community outreach.
- Apply state-of-the-art software engineering practices to improve the modularity, organization, and quality of the existing code base.
- Contribute to the development of novel algorithms and the analysis of new single cell genomics datasets.
- Organize and participate in symposiums and workshops to teach and train users of dynamo, dynast and spateo to foster wider adoption of the Aristotle ecosystem.
- Manage issue tracker and discussion forum on each respective GitHub repository, and personal communications via email and or social media.
- Other duties, as assigned.

## QUALIFICATIONS

- The ideal candidate will need to be highly self-motivated, ambitious and passionate about open source software development and the ultimate goal of building a software ecosystem of foundational tools in single cell and spatial transcriptomics.
- Senior undergraduate or masters student majoring in computer science. Senior computational scientists will also be strongly considered.
- Excellent Python programming skills
- Software engineering experience developing large-scale computational toolkits
- Excellent written and oral communication skills, strong organizational skills.
- The ideal candidate will need to be adept in learning new skills and knowledge, especially related to single cell and spatial transcriptomics.
- No biology background required but can be helpful. Various mentorship will be provided by members in the lab.

**Interested candidates should apply online at wi.mit.edu/careers or submit a resume to resumes@wi.mit.edu**