

NON-TENURE TRACK RESEARCH ASSOCIATE DATA SCIENTIST FACULTY  
POSITION AVAILABLE AT THE JOHNS HOPKINS CONVERGENCE INSTITUTE FOR  
CANCER RESEARCH

The Convergence Institute at the Sidney Kimmel Comprehensive Cancer Center at Johns Hopkins University School of Medicine, (SKCCC) seeks a Research Associate on the Data Science track to coordinate clinical genomics data and analysis pipelines. We are looking for a self-motivated and organized individual to lead the group's analysis pipelines, manage and organizing project data, and oversee cloud computing environments for high-throughput genomics, single-cell, and imaging data.

The Convergence Institute leads hybrid computational and experimental translational group advancing genomics and single-cell analysis of clinical trials to uncover the mechanisms of immunotherapy response and resistance. The overarching goal of the Convergence Institute is to bring together the brightest minds in clinical oncology, engineering, and computational biology to make new discoveries and to bring forward the next generation of cancer therapies. The Institute consists of a highly transdisciplinary team of faculty and co-mentored trainees across disciplines and career stages, with joint leadership in computational methods development overseen by co-Director Dr. Elana Fertig with direct clinical translation overseen by Dr. Elizabeth Jaffee. This collaborative, transdisciplinary research environment promoted by this Institute and the broader Johns Hopkins University fosters a diverse and inclusive community.

To further the mission of the Convergence Institute Gastrointestinal Cancer Research Group, we are seeking an experienced bioinformatician and programmer for a faculty level, non-tenure track Data Scientist track, Research Associate position. The successful applicant will maintain and organize all computational data in the Institute. Additionally, the successful applicant will work closely with the PIs, fellows, and students to facilitate interactions at all levels of project planning, analysis, and pipeline development, and maintain lab code. The Institute is committed to using free and open-source software programs and bioinformatics tools and to maintaining the highest standards of reproducible research. The successful candidate should have broad experience with these tools.

There will be additional opportunities to participate in the following activities:

- Developing and disseminating novel bioinformatics analysis pipelines
- Designing and analysis of diverse genomic projects and genomics databases
- Training PIs, fellows, and students in the selection and use of bioinformatics tools

**Required**

- Master's degree, in an area of computational biology, bioinformatics, computer science, math, or statistics.
- Experience managing data storage and analysis pipelines on high performance computing clusters and cloud computing environments.

- Knowledge of next generation sequencing pipelines and experience manipulating, analyzing, and annotating very large biological sequence data sets, both in exploratory and pipelined fashions.
- Experience running and disseminating pipelines, leveraging best practices for version control (e.g., Git) and container tools (e.g, Docker).
- Established commitment to industry standards of reproducible data analysis and management.
- Highly capable of being involved collaboratively with an interdisciplinary team, including laboratory scientists, clinicians, bioinformaticians, statisticians, and data analysts.
- Self-motivated and highly organized, be involved independently or in a team environment, and be able to multi-task.
- Fluency in scripting languages, such as python and R. Familiarity with command line manipulation and shell scripting.

### **Preferred**

- Experience in the development of novel methods for analysis of high throughput molecular data.
- Knowledge of bioinformatics package development, including Bioconductor and/or Bioconda standards. Experience in C++ and Julia, preferred.
- Experience with database structures and maintenance.
- Ph.D. in an area of computational biology, bioinformatics, computer science, math, or statistics.

### **To Apply**

A complete application should include

- Current CV
- Three letters of recommendation
- Examples of bioinformatics software development/implementation
- Cover Letter

Send application materials to [OncBioSearch@jhmi.edu](mailto:OncBioSearch@jhmi.edu)

The Johns Hopkins University is an Equal Opportunity/Affirmative Action employer. We strongly encourage qualified women and under-represented minorities to apply.