Position: Research Associate - Bioinformatics Trainer and Analyst
Location: Harvard Chan Bioinformatics Core,
Harvard T.H. Chan School of Public Health, Department of Biostatistics

We are looking for a bioinformatician or computational biologist interested in working with our bioinformatics training team to provide education and training to the Harvard community. The ideal candidate will be interested in training biologists to analyze data, and in working with data from a wide variety of experimental platforms, particularly next-gen sequencing technologies. This role provides a unique and rewarding opportunity to train the next generation of world-class researchers making a profound impact on human health.

About us
The Harvard Chan Bioinformatics Core (HBC) is a center for bioinformatics research, services and training at the Harvard T.H. Chan School of Public Health. We work closely with biomedical scientists across Harvard to develop and execute innovative approaches to analyze, interpret, visualize and distribute scientific discoveries using omic information.

Our training team is tasked with the mission of educating the Harvard community on best practices in experimental design, analysis workflows, and data management. Workshops are designed to foster independence and confidence among the participants, who are predominantly wet-lab biologist taking their first steps at performing computational analysis. As a team, we embrace an open source approach to computing and training by teaching with open source tools and contributing to the development of open source tools/projects. Our training materials are freely accessible on GitHub (https://www.github.com/hbctraining/).

To facilitate the continued development of our bioinformatics skills and ensure up-to-date knowledge of current best practices, all of our trainers participate in analyses via consulting for the HBC. We work closely with investigators from the Harvard, MIT and the Broad communities across a broad range of disciplines, and with industry collaborators. Projects range from short-term projects (e.g. transcriptomics analyses that may take up to a month) to long term collaborations that involving large data sets or multiple omics data types. The HBC emphasizes teamwork and a supportive environment where we can learn from each other.

About you
You have a background in biomedical or quantitative science and a strong interest in helping medical and/or biological researchers. You thrive on scientific challenges, love sharing knowledge and enjoy working within a tightly integrated, interdisciplinary team. You can synthesize your knowledge of biology, genetics and cell biology with your computational knowledge to excel at communicating with programmers and wet-lab scientists alike. You are able to simplify complex concepts and explain them in written and spoken form. You are motivated to continually expand your skills and are keen to learn and apply new methods. You have good code and data management skills to enable reproducible research and are capable
of simultaneously working on different projects and deadlines. You are experienced with
next-generation sequencing analysis and have an interest in training.

Duties
As a Trainer/Analyst, you will be involved in both the training and support missions of the Core,
but will focus predominantly on training. The Core’s director and associate director oversee
consulting activities; the training director oversees training-related activities. You will work
closely with all Core staff, particularly with the training team.

In your role as a trainer, you will help to develop, organize and teach workshops to students,
postdocs and faculty from the greater Harvard community. Training topics include basic data
skills (Unix, version control, R, high-performance computing, Python), reproducible research and
next-generation sequencing analysis (eg. RNA-seq, ChIP-seq, variant calling). You will be
required to develop lessons based on best practices at the Core and help teach them at
workshops. You will assist in logistics associated with workshops, including scheduling,
screening applicants and reviewing exit surveys. You will be fully involved in determining the
future direction of the training program.

As an analyst, you will support selected research projects, working independently with
researchers at the Harvard Chan School, Harvard and the broader Boston biomedical
community. Tasks will focus on area(s) of expertise in one of the following bioinformatics
domains: sequencing (whole genome, exome, bulk RNA, small RNA, single cell RNA, ChIP,
methylation), data integration of multiple data types, functional analysis (enrichment studies,
GSEA, networks), or data management and visualization. You will analyze incoming data using
existing analytical approaches commonly used in the Core, assessing new methods where
appropriate. You will document all work thoroughly, providing manuscript-level reporting of
analyses and results. Other duties will include data management (coordinating with
collaborating Research Computing groups and Core developers to ensure consistent data
storage), participation in Core and lab meetings and other collaborator meetings around various
campuses, and liaising with collaborating researchers. Where appropriate, you may participate
in developing manuscripts for publication.

Qualifications
Basic
Master's or doctoral degree in biological sciences, statistics or related computational field (eg.
computational biology or bioinformatics) required.
Proven training experience (at or above undergraduate level).
Scripting abilities (Python, R proficiency, shell scripting) required.
Working knowledge of biology, genetics and cell biology required.
Experience in at least one of the following next-generation sequencing domains required:
   - Whole genome sequencing
   - Exome-seq
   - Bulk RNA-seq (preferred)
- Small RNA-seq
- Single cell RNA-seq (preferred)
- ChIP-seq
- Bisulfite-seq

**Additional**
Knowledge of functional analysis (enrichment studies, GSEA, networks), data management and visualization.
Proven ability to interpret and analyze large data sets and present results.
Excellent written English and a familiarity with presenting biological results.
Strong interpersonal skills.
Statistical background experience.
Github or other version control experience
Ability to produce reproducible code (R Markdown, Latex, Jupyter notebooks, etc)

Please submit your application online at:

Contact email: hbctraining@hsph.harvard.edu