RESEARCH
FOUNDATION CUNY

Careers at RFCUNY
Job Openings

Job Title	Bioinformatics Engineer
PVN ID	HC-1607-001282
Category	Information Technology
Location	HUNTER COLLEGE
Department	Bioinformatics
Status	Full Time
Annual Salary	$90,000.00 - $110,000.00
Hour(s) a Week	35
Closing Date	Sep 25, 2016 (Or Until Filled)

General Description

The Center for Translational and Basic Research (CTBR), a scientific research center located on the Upper Eastside of Manhattan is seeking a highly motivated full-time Bioinformatics Engineer with diverse skill sets. Applications involve setting up and maintaining next-generation sequencing data pipelines, provide bioinformatics analysis services to faculty across departments, and participate in various research projects involving large-scale genomic datasets. The position also provides the opportunity to work on cutting-edge bioinformatics and cloud computing software development projects, and use of a private high-performance cluster as part of the research performed in the Bioinformatics Core.

CTBR is 'An AA/EO/ADA Employer' (Affirmative Action/Equal Opportunity Employer/Americans with Disabilities Act). We encourage minority applicants to apply.

Other Duties

Process, quantify and assess quality of biological samples and prepare the samples for sequencing. Retrieve and organize results following sequencing experiment completion, and perform data analysis using bioinformatics data analysis workflows currently available in the lab, in addition to developing new data workflows. As part of the duties for the position, the candidate will prepare posters and manuscripts for scientific conferences or peer-reviewed journals, in addition to mentoring more junior members of the lab on the use of sequencing and bioinformatics technologies.

Work closely with the other Bioinformatics Core members in maintaining the genomic data analysis resources, including keeping the software, databases, genome indexes and operating systems up to date. Help in preparing posters and presentations for scientific meetings.

Qualifications

- Applicants with background in molecular biology, genetics or similar field, strong laboratory experience and bioinformatics expertise are encouraged to apply.

- Masters or Bachelors with at least 2 years’ experience, in Bioinformatics, Computer Science, Computational Biology or related field.
- Strong computer skills on the analysis of genomic data using bioinformatics, in addition to working knowledge of sequencing technologies is required. The applicant must have clearly demonstrated skill for scientific research in the field through scientific publications, conference presentations and similar scholarly achievements.
- Programming experience with two scripting languages, either Python, Perl or Ruby, and standard algorithms - data structures.
- Familiarity with relational database systems and writing SQL queries for data management / storage / retrieval.
- Knowledge of next-generation sequencing technologies (primary Illumina, but also IonTorrent, Sanger, 454) data analysis protocols, software and data formats (read quality checks, read mapping and assembly, RNA seq, re-sequencing and SNP discovery).
- Parsing of next-gen datasets using programming libraries (BioPerl, BioPython)

Preferred Qualifications:

- Experience with the Galaxy Project platform for Bioinformatics Analysis
- Cloud Computing, including AWS
- Cloud API programming through scripting languages
- Proficient with the UNIX command line
- Familiar with Ubuntu and Centos Distros