Job Title	Bioinformatics Engineer
PVN ID	HC-1505-000510
Category	Research
Location	HUNTER COLLEGE
Department	Biological Sciences
Status	Full Time
Salary	Depends on qualifications
Hour(s) a Week	35
Closing Date	Jul 12, 2015 (Or Until Filled)

General Description

We are seeking skilled scientific programmers to develop next-gen sequencing data analytics applications on a workflow management platform currently under development. Successful candidates will be part of a software engineering team, following agile software development practices. A successful candidate will contribute to the development of standardized genomic data analysis workflows and APIs, within a scalable, portable platform ecosystem of software tools.

Other Duties

As part of the project, you will have the chance to participate in efforts at the forefront of the bioinformatics field research, aimed at establishing best practices and standards for genomic data representation and analysis. Specifically, responsibilities include development of custom analytics workflows using open source bioinformatics software applications, working on a platform that enables implementation of scalable, cloud-enabled workflows to disseminate analytical advances to the research community. Establish and maintain standards for structured software engineering, including design and testing, quality control, cloud platform configuration, software version release management and project management. Furthermore, provide documentation and user support allowing researchers inside and outside of our campus to access and the bioinformatics tools.

Qualifications

We welcome candidates with doctorate or master's degrees in computational biology, computer science, or related technical disciplines. Candidates with bachelor's degrees and significant accomplishments in real-world work experience will also be considered. Pay-scale will be based on education level and work experience. Advanced skills in a high level programming language - preferably Python and significant expertise working on the Linux command line is required. Knowledge of virtualization systems (VirtualBox, Docker) and cloud computing platforms such AWS is a must. Experience in analyzing next-generation sequencing data, both core data analysis pipelines (RNAseq, Exome, CHIPseq, Bi-sulfite) in addition to data formats and manipulation (BAM, SAM, VCF, BED, Wig etc) is a must have. Experience using software engineering methods for specifying, designing, and implementing systems. Ability to prioritize multiple tasks, excellent communication, analytical and organizational skills, both written and verbal. Comfortable to work independently and as part of a team while being collaborative in resolving problems. A desire to change the bioinformatics field by creating new technologies for large-scale analysis with genomic data.