

Bioinformatics Position: Waksman Institute, Rutgers University

Waksman Genomics Core Facility Job Posting April 20, 2012

General Features:

Waksman Genomics Core Facility is seeking a highly motivated and talented Bioinformatics scientist to our group at the Waksman Institute of Microbiology, Rutgers University, New Jersey, USA. At Waksman, we conduct research in plant/animal/microbial molecular genetics as well as on structural biology. The Core facility also maintains strong working relationships with University of Medicine and Dentistry of New Jersey. The candidate will be responsible for managing data analysis pipeline from the high-throughput sequencer SOLiD 5500xl. Initial appointment will be for one year with an opportunity to extend/upgrade further based on the performance. Rutgers University also offers a great range of benefits including retirement benefits.

Background:

Reporting to the Genomics Laboratory Supervisor at the Waksman Institute, this position is responsible for analyzing high throughput sequencing data on next generation genome sequencers. The analysis entails assessing the quality of the data, processing of the data through appropriate analysis pipelines, determining the quality of the analysis and whether further analysis should be done, and assembling results for researchers. Consults with researchers on experimental design related to data analysis, develops new pipeline analysis techniques and communicates project updates and results to researchers.

Requires a Ph.D degree or an equivalent combination of education and / or experience plus two years practical experience in bioinformatics, biology or computer science with experience in data analysis from the Next-Gen sequencing machines. Must be proficient in at least one script language (Ruby/python/Perl) and have experience with one statistical language (S/R/SPSS/MATLAB/Octav). Good communication and organizational skills while working with minimal supervision is required.

Main Responsibilities:

- * The successful candidate will join Waksman genomics core facility to develop and implement computational algorithms and statistical analysis pipelines using next-generation sequencing data.
- * Evaluate published bioinformatics tools and resources for analysis and interpretation of genomic data
- * Present results through clear and concise representation of ideas and concepts to other team members and the management
- * Manage multiple independent projects under tight deadlines
- * Work independently with minimal supervision as well as with other team members to tackle complex problems

Essential Requirements:

- * MS/Ph.D. in Bioinformatics, Computational Biology, or related discipline.
- * Strong programming and scripting skills (Perl, Python, Ruby, Java, C++, XML, using MySQL Server; and efficiency in Linux/Unix operating systems).
- * Knowledge in statistical language and machine learning concepts.
- * Independent problem solving skills.
- * Have good communication skills, strong team-work spirit with self-learning abilities.
- * 2+ years of experience in Bioinformatics data analysis tools and databases.

Desirable:

- * Knowledge about gene regulatory networks and graphical models.
- * Experience in analysis of genome, transcriptome, epigenome and other genomic datasets.

To Apply:

Submit a cover letter stating research interests, curriculum vitae, experience and contact details of three referees in a single pdf file to hr@waksman.rutgers.edu. Please, indicate "WGCF Bioinformatics" in the subject line. Deadline for application is 10 May 2012. For more information about this position please contact: Dr. Dibyendu Kumar 732 445 4737 or email (dk@waksman.rutgers.edu).

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