



## **JOB DESCRIPTION**

**Job Title:** Bioinformatics Analyst

**Job Code:** 3115372

**Lab:** Yu

**Employing Hospital and Department:** MGH/Ragon Institute of MGH, MIT, and Harvard

**Minimum degree and field of knowledge:** BS in computational biology, bioinformatics, computer science, or a related field. M.S. in those fields preferred.

### **Summary:**

The Yu Laboratory at the Ragon Institute of MGH, MIT and Harvard at the Massachusetts General Hospital in Boston has an opening for a highly motivated Bioinformatician to join our team.

### **Job Duties:**

Under the direction of the principal investigator, the associated responsibilities will include:

- The successful candidate will use a variety of computational tools to analyze viral sequences, discover new therapeutic targets and develop new treatment strategies to find a cure for HIV infection
- Applicant will interact with physicians, scientists, and technologists to provide statistical and bio-computational support for experimental design, data processing, and data analysis procedures. The applicant is expected to deliver reports in written or oral formats in a concise way with vivid visualization
- The applicant will lead efforts in maintaining proper data management protocols for storage and sharing of genomic and clinical data. The candidate will provide training and technical support to all lab members for accurate and efficient electronic note taking, record keeping and data collection.
- This position will be supervised by a senior bioinformatician in the lab. Opportunities will be offered to a motivated individual to develop a strong ability to conduct independent research, participate in NIH-funded programs and contribute to future manuscripts intellectually.

### **Qualifications:**

- Essential skills:
  - Familiar with fundamental concepts in statistics and molecular biology, especially with next-generation sequencing technology
  - Experience with Linux operating system, R, Python and database management (SQL)

- Familiar with common bioinformatic file formats including but not limited to FASTA/FASTQ, SAM/BAM and BED.
- Proper record keeping, exceptional attention to detail is a must
- Desirable skills:
  - Experience with any of the following bioinformatic analyses: DNA-seq, RNA-seq and ATAC-seq
  - Demonstrated statistical and analytical ability with programming in R and Python
  - Software development skills, such as version control, and unit testing
  - Working experience with cluster and/or cloud computing is a plus
  - Experience with website development (HTML, JavaScript, and CSS) is also a plus