

## **Job description; Junior Bioinformatician – BiNGS Core**

We are seeking a junior bioinformatician for the Tisch Cancer Institute Bioinformatics for Next Generation Sequencing (BiNGS) core, to lead transcriptomics and epigenetics data analysis projects related to cancer biology, skin biology, developmental biology, diabetes, and neuron biology.

The mission of BiNGS is to enhance scholarship and facilitate research related to various biological systems by providing access to state-of-the-art bioinformatics analysis, and training. The BiNGS staff supports a broad range of bioinformatics analyses for multiple applications spanning genomics, transcriptomics and epigenomics research, through standard and custom analysis, data management, bioinformatics tools development, access to biocomputing resources, and advanced computational training in data analysis. We are focused on delivering a comprehensive, rapid and user-friendly service.

More specifically, we are working on multiple projects together with PIs in the Tisch Cancer institute and the broader Mount Sinai community to analyze NGS related datasets. For example, we are working to understand the role of the histone variant H2Az in the regulation of chromatin organization in melanoma utilizing enhancers analysis, transcriptomic analysis, open chromatin analysis and transcription factor network analysis; in another project, we are working to understand transcription factor networks and their role in regulating aberrant transcriptional programs in colorectal cancer utilizing ChIP-seq, RNA-seq, ATAC-seq, scRNA-seq and scMultiome analysis. Finally, we are utilizing FIBER-seq (third generation PacBio long read sequencing), to understand the chromatin landscape in postmortem human brain samples.

We are seeking highly motivated Bioinformatic Scientists who wants the opportunity to significantly impact the growth and success of our research programs, the bioinformatics core and the services we provide. The candidate will work closely with TCI investigators to facilitate and enhance the processing of their projects. Commitment to accuracy, high attention-to-detail, and ability to work independently are critical competencies for the role. We feel that BiNGS presents a unique opportunity for junior bioinformaticians who seek to expand their data analysis skills; their understanding of transcriptional and epigenetic programs and their role in driving cancer initiation, progression and metastasis, and other diseases; their ability to communicate science clearly and efficiently; and their involvement in reducing racial bias in science through mentorship of URMiS. We are happy to sponsor US working visa to qualified candidates.

### **Job responsibilities will include but not be limited to:**

- Execute computational analysis for scRNA- and scATAC-seq, bulk RNA- and ATAC-seq, ChIP-seq, Cut&Run, and HiC/Hi-ChIP and promoter capture, using existing analysis pipelines.
- Integrate multiple datatypes and data from publicly available resources (e.g. ENCODE, PCAWG, TCGA, ICGC and GTEx).
- Provide analyses and visualization for presentations and publications.
- Participate in development of new software tools to process, analyze and visualize high-throughput multidimensional sequencing data.
- Manage the core online database and interactive tools on local HPC and commercially available clouds preferably Amazon Web Services.
- Tracking and reporting of ongoing projects.
- Provide training to TCI investigators and trainees.

## Requirements

- MSc in Bioinformatics or Computational biology with a focus on genomics or related discipline.
- Experience in analyzing and integrating various NGS datatypes preferably ATAC-seq and scRNA-seq (i.e. genomics, transcriptomics or epigenomics datasets).
- Knowledge of cancer biology, chromatin biology, and technologies such as qPCR and next-generation sequencing.
- Proven experience with Perl, R and Unix. Additional experience with standard genomics tools for high-throughput sequencing data analysis is preferred (e.g., Bowtie2, deepTools, Samtools, and the UCSC genome browser).
- Experience in batch HPC cluster environment with a parallel file system.
- Ability to research, analyze, recommend, communicate and implement data analysis solutions.
- Must be able to work as an individual while part of a small team.

We will adjust immigration status as needed

Please send your CV and a cover letter that specifically addresses this job description to:

Dan Hasson, Ph.D  
Associate Professor  
Icahn School of Medicine at Mount Sinai  
Department of Oncological Sciences and Dermatology  
Hess Center for Science and Medicine  
1470 Madison Avenue, 6th Fl., Rm. 302  
Email: [dan.hasson@mssm.edu](mailto:dan.hasson@mssm.edu)