

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 WGS and WES 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 chromatin remodeler complex ATRX in the regulation of aberrant transcriptional programs associated with Neuroblastoma, utilizing enhancers analysis, transcriptomic analysis, open chromatin analysis and transcription factor network analysis; in another project, we are working to understand a computational classifier to stratify HIV positive anal precancer patients to high-, and low-risk, utilizing Ultra Low Coverage WGS and ML approaches. We are integrating whole exome sequencing data into this project as well to further identify cancer driver mutations in high risk tumors. 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; the effects of DNA reorganization on cancer progression; 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 pipelines for the analysis of Copy Number Variations, coding and non-coding SNPs, and transcriptomics using existing analysis pipelines.
 - Use somatic mutation calling pipelines such as GATK Best Practices
 - Use CNV calling tools such as GATK CNV, PureCN, CNVkit
 - Assess validity and function of mutations using databases such as COSMIC, ClinVar and previous publically available datasets
 - Assess quality and tumor purity of WES samples
- 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 and pipelines 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 WGS and WES (i.e. genomics, transcriptomics or epigenomics datasets).
- 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, GATK Mutect2, GATK CNV, PureCN, IchorCNA, IGV and the UCSC genome browser).
- Knowledge of cancer biology, chromatin biology, and technologies such as qPCR and next-generation sequencing.
- 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
Director Bioinformatics for Next Generation Sequencing core
Hess Center for Science and Medicine
1470 Madison Avenue, 6th Fl., Rm. 302
Email: dan.hasson@mssm.edu