Junior Bioinformatics Developer

Fusion Genomics is looking to hire a full-time Junior Bioinformatics Developer to join our team in an exciting and highly dynamic start-up environment. The successful applicant will participate in developing, improving and maintaining bioinformatics tools that will advance our next-generation sequencing assays. The job will entail conducting analysis and interpretation of assay results from large-scale clinical genomic and metagenomic datasets, developing computational methods involving machine learning, and lending analysis support to our colleagues and external collaborators. The successful candidate will work independently but will interact with our bioinformatics scientists and laboratory personnel. This role requires a general knowledge of bioinformatics, statistics, and programming, as well as effective communication skills, meticulous attention to detail, and ability to work under pressure.

Key Responsibilities:
- Maintain a production bioinformatics analysis pipeline.

- Understand and provide bioinformatics support for clinical/analytical validation of genomic assays.

- Test and validate new data analysis software and techniques.

- Foster effective and collaborative working relationships with fellow employees, management and external partners.

- Produce thorough but concise written documentation of algorithms, validations, SOPs, and other processes and procedures as required.

- Contribute to drafting of manuscripts for peer-reviewed journals.

Qualifications:
- Undergraduate degree in a quantitative field with strong programming experience (bioinformatics, computational biology, data science, statistics, applied math, computer science, or engineering). Master's degree in a quantitative field is preferred.

- Proficiency in Python, R, C/C++, and/or other high-level languages.

- Proficiency in distributed version control systems, such as git.

- Experience in working with standard NGS data analysis tools (such as samtools/bcftools and bwa/bowtie2/minimap2) and pipeline management frameworks (such as nextflow or snakemake).

- Experience in implementing and validating bioinformatics methods, in particular for next-generation sequencing analysis.

- Experience in working in a UNIX environment, including experience with shell scripting and common command-line tools.

- Experience in machine learning algorithms to analyze biological data is a plus.

- Basic understanding of molecular biology (infectious diseases and metagenomics are a plus).

- Demonstrated ability to effectively communicate in spoken and written English.

- Demonstrated ability to efficiently organize work assignments and establish priorities.

- Proven interpersonal skills with the ability to work collaboratively as a member of cross-functional team.

Location: Burnaby, BC, Canada.

This position comes with a competitive package. Fusion Genomics is an equal opportunity employer. To apply, send a resume and short cover email to jobs@fusiongenomics.com Please note that only short-listed candidates will be contacted.

Fusion Genomics Corporation is a molecular diagnostic company that innovates disruptive diagnostics assays based on next-generation sequencing technologies to characterize infectious disease agents of global importance, including SARS-CoV-2. Fusion assays are based on its novel DNA/RNA capture and informatics technologies and when commercialized will help prevent unnecessary deaths from infectious disease and halting the growing problem of outbreaks (pandemics) and drug resistance.