

Bioinformatics Scientist

MedGenome Inc. is a leading genomics services provider. We are dedicated to accelerating scientific discovery, as well as to developing and delivering innovative solutions for basic research, translational medicine and healthcare by leveraging our deep expertise and experience in biology and bioinformatics. MedGenome has built strong partnerships with leading academic, pharmaceutical, biotechnology, government, and clinical institutions by delivering on its promise to deliver high-quality data and technical support.

About this role

We are seeking a committed and driven Bioinformatics Scientist for our Research Services team. The candidate will be working on analyzing high-throughput, large-scale genomic data, including but not limited to sequencing data from multiple technologies as well as develop bioinformatics analysis pipelines for research and commercial projects.

Responsibilities

The candidate will support data analysis efforts for both internal and external studies. Candidates with experience in exome and genome sequencing, bulk or single-cell RNA sequencing, bioinformatics, or data algorithms including machine learning will be preferred. The candidate will be expected to work closely in collaboration with the NGS laboratory and assay development team to develop analysis pipelines for new genomics-based assays. The candidate will also work with interdisciplinary teams including R&D to work on different areas of research including cancer genomics, immunology, and drug target discovery. Regular publication of scientific or methodological papers resulting from such work is an important outcome expected of this position [please see recent publications in *Nature* (December, 2019); *Nature Genetics*, (January, 2020); *Nature Communications*, (August, 2020); *Scientific Reports*, (November, 2020)]. Success critically depends on possessing creativity, attention to detail, and an ability to effectively present complex techniques and results in a clear and concise manner to a diverse audience of scientists.

Who you are

- You have a Ph.D. with 0-2 years of work experience and a background in bioinformatics, computer science or a related life sciences field with experience in bioinformatics
- You have hands-on experience with analysis of NGS-based technologies (e.g. single cell sequencing, whole genome, transcriptome and exome data, long-read sequencing, proteomics data, etc.)
- You enjoy using creative and novel informatic approaches to bring new insights to biological problems and bring a competitive edge to our research service offerings, and then working closely with biomarker scientists to develop those ideas experimentally.
- You have demonstrated competence in a programming language such as R or Python, experience with version control systems, and familiarity with high-performance computing environments.
- You have experience in pipeline development for DNA, Bulk & Single-cell RNA Sequencing data analysis using containerization (Docker, Conda, etc) or Nextflow
- You have in-depth experience in secondary analysis tools/algorithms/databases for sequencing data.
- You have strong writing and communication skills as evidenced by a solid scientific publication record
- You are a team player, self-motivated and detail-oriented.

Please e-mail your CV to careers-us@medgenome.com

Get in touch

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