

Bioinformatics Analyst(Contract Position)



Beverly, MA

Send your resume to careers@seqwell.com

Join the seqWell journey!

Do you enjoy the challenge of figuring out how to accelerate research by creatively leveraging your resources and expertise? Our mission at seqWell is simple. We strive to unlock the full potential and efficiency of modern NGS instrumentation through a transformative library prep technology called plexWell™. Our workflow enables scalable multiplexing with fewer steps and cost-consuming normalization to achieve greater efficiency, cost savings, and minimize time to results.

What we are looking for:

seqWell is seeking a talented and motivated individual for a contract position of Bioinformatics Analyst. This part-time contract position is based out of the company's primary laboratory and offices in near Boston in Beverly, MA. The Bioinformatics Analyst position will report to seqWell's Director of Bioinformatics and work to support the company's R&D team with by providing analysis reports and tools on a range of sequencing data sets and applications. As member of the company's product development team, the ideal candidate will help realize the company's mission to engineer enhanced library preparation solution sand streamlined application workflows that redefine the standards for throughput, quality, and utility across NGS

What you will bring:

- Experience with high-throughput sequencing analysis using established pipelines as well as adjusting deliverables to meet the needs of lab scientists.
- A desire to collaborate and communicated with wet lab scientists and to create reproducible, accessible analyses and clear writing skills is a must.
- Familiarity with pipeline tools (e.g. Nextflow) or developing new pipelines; experience using and/or streamlining cloud architecture and automated pipelines
- Working knowledge and comfort working on Linux command line and fluency in at least one scripting language, preferably Python.
- Experience with standard command line high-throughput sequencing bioinformatic tools is required, including tools for RNAseq analysis.
- Experience with software development best practices such as version control.
- Initial availability of 20 hours per week

Required skills:

- fluency in a scripting language such as Python or R
- experience working with command-line bioinformatics tools (bwa, samtools, picard, bedtools, STAR, salmon, or similar)
- proficiency in a Linux command-line environment

Desired skills:

- familiarity with pipeline software, ideally Nextflow
- experience with AWS services (EC2, S3, Batch, Lambda) and the AWS CLI
- containerization using Docker