

Position	Scientist, Computational Biology
Supervisor	Luis Barrera, PhD
Department	Biology
Prerequisites	PhD in Computational Biology, Bioinformatics, Computer Science, or Statistics (or equivalent experience)

Position Summary:

The mission of Arrakis Therapeutics is to extend small molecule medicines into new realms of biology by discovering and developing compounds that selectively target RNA. By targeting distinct RNA structures, Arrakis is generating drug candidates with novel mechanisms of action for molecular targets that are challenging to drug in therapeutic indications with high unmet need.

Bioinformatics and computational biology are critical parts of the Arrakis platform. We are developing novel, sequencing-based assays to investigate RNA structure and function and characterize the effects of small molecules on cellular RNAs. We are also employing a wide range of genomic data types to inform our target selection and therapeutic strategy.

We are seeking a scientist to further develop our computational platform by writing software pipelines, improving algorithms for RNA computational biology, and working closely with experimental scientists to analyze, interpret, and visualize data from sequencing assays.

Responsibilities:

The responsibilities of this position include the following:

1. Develop and use computational tools that optimally incorporate experimental data (e.g., SHAPE-MaP) to inform RNA structure prediction.
2. Write and deploy RNA-seq analysis pipelines to identify differentially expressed genes, quantify transcript levels, and characterize alternative splicing events.
3. Employ and develop methods to characterize the binding preferences and functions of RNA-binding proteins (e.g., analyzing CLIP data).
4. Participate in building a scalable, cloud-based computing infrastructure that automates analyses and generates reproducible results in a timely manner.
5. Follow best practices for collaborative software development, such as using repositories for version control and participating in code reviews.
6. Contribute to a culture of effective collaboration between experimental and computational scientists.
7. Survey the scientific literature to stay informed of the latest tools and databases.

Experience/Skills/Knowledge Required:

1. PhD in Computational Biology, Bioinformatics, Computer Science, or Statistics (or equivalent experience).
2. Extensive programming experience in at least one appropriate language for bioinformatics and data analysis, such as Python, R, or Java
3. Familiarity with scientific software development in Linux or UNIX environments.
4. Demonstrated ability to access and mine large sequencing datasets to address biological questions and generate hypotheses. Examples of relevant data types include RNA-seq, CLIP-seq, ChIP-seq, ribosome profiling, and SHAPE-MaP.
5. Thorough understanding of statistical methods relevant to the life sciences.
6. Ability to effectively communicate methodologies and results with colleagues, including bench scientists, research management, and project team leaders.
7. Strong problem solving and trouble-shooting skills.
8. Excellent oral communication and writing skills.
9. Ability to work in a dynamic and fast-paced environment.

Experience/Skills/Knowledge Preferred:

1. Deep understanding of RNA molecular biology and experience working with data types that are relevant for the study of RNA.
2. Experience deploying software and performing analyses in a cloud-computing environment, such as Amazon Web Services, Microsoft Azure or Google Cloud.
3. Familiarity with frameworks that can be used to develop web-based tools and visualization apps, such as Shiny, D3.js, or Plotly.