

Computational Biologist

Job ID: 00414649

Job Function

Research

Schedule

Full-time

Location

United States-California
South San Francisco

Job type

Regular Employee

Company/Division

Pharmaceutical

Job Level

Experienced

Who We Are

At the Roche Group, about 80,000 people across 150 countries are pushing back the frontiers of healthcare. Working together, we've become one of the world's leading research-focused healthcare groups. A member of the Roche Group, Genentech has been at the forefront of the biotechnology industry for more than 30 years, using human genetic information to develop novel medicines for serious and life-threatening diseases. The headquarters for Roche pharmaceutical operations in the United States, Genentech has multiple therapies on the market for cancer and other serious illnesses. Please take this opportunity to learn about Genentech, where we believe that our employees are our most important asset and are dedicated to remaining a great place to work.

The Position

Genentech seeks a talented and highly motivated Computational Biologist to pursue research projects in collaboration with our Department of Oncology Biomarker Development. The primary focus is translation of complex biomarker data into useful diagnostic tools that can guide our understanding of drug activity in patient tumors and identify subsets of patients who may benefit from specific therapeutic interventions.

A successful candidate will work with interdisciplinary teams (including biomarker, clinical, biostatistics and bioinformatics scientists), will carry out data analysis and integration across various domains, and will develop novel methods for identifying diagnostic and prognostic biomarkers. Regular publication of scientific and methodological results is strongly encouraged. Finally, the successful candidate must be able to effectively present complex results in a clear and concise manner — to other bioinformaticians as well as to audiences without a computational or statistical background.

Who You Are

Requirements:

- PhD in bioinformatics, biostatistics, computational biology or similar, with a strong publication record. Alternately, a PhD in molecular biology combined with a very strong record of high-throughput data analysis, supported by publication in this area.

- Extensive experience with data generated by a variety of high-throughput molecular assays: microarrays, next-generation sequencing, multiplexed qPCR, mass spectrometry proteomics, etc.
- A strong understanding of the statistical principles behind current best practices in the field. Experience with biomarker discovery and evaluation is a plus.
- Expertise in the use of a high-level programming language such as R, Python or Perl for complex data analysis. Low-level programming, web application programming, or relational database experience are pluses.
- A solid understanding of the relevant concepts in cancer biology and genetics.
- Exceptionally strong communication, data presentation and visualization skills.
- Ability to work both independently and collaboratively, and to handle several concurrent, fast-paced projects.

Genentech is an Equal Opportunity Employer.