

Computational Biologist

Job ID: 00410610

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

The Department of Bioinformatics and Computational Biology in Genentech Research is seeking a motivated individual to lead the development of software methods and infrastructure for the analysis of high-throughput biological data. This work will be in close collaboration with other computational researchers, as well as the broader community of Genentech scientists, who are together seeking novel therapies for unmet medical needs. Much of the software will be developed in R, as it is our primary data analysis environment. Interesting challenges include the scale of the data and the need for agility in a fast-paced, dynamic research environment. Publishing of methods and software is encouraged, and there is potential for collaboration with open-source projects. There is also opportunity for investigating open scientific problems in computational biology, such as variant calling, functional assessment of non-coding transcripts, and the relationship between copy number variation and expression.

Who You Are

A masters or preferably PhD in computer science, statistics, computational biology or similar field is required. Must have a strong command of R, with 5+ years experience and knowledge of S4 classes,

parallel computing and the R/C interface. A successful applicant will very likely have contributed to one or more R packages available from the CRAN or Bioconductor repositories. Additional experience in languages like C/C++ and Python would be a strong plus. Must be at home in a UNIX environment. Scientific competence should be demonstrated by publications in high-profile journals. You will have excellent communication skills, a very strong background in software engineering, quantitative skills and an ability to work in teams.

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