

## Intern - Bioinformatics and Computational Biology

Job ID: 00451644

Job Function  
Internship/ Trainee Development

### Schedule

Full-time

### Location

United States - California  
South San Francisco

### Job type

Internship / Student

### Company/Division

Full-time

### Job Level

Entry Level

## Who We Are

A member of the Roche Group, Genentech has been at the forefront of the biotechnology industry for more than 40 years, using human genetic information to develop novel medicines for serious and life-threatening diseases. Genentech has multiple therapies on the market for cancer & other serious illnesses. Please take this opportunity to learn about Genentech where we believe that our employees are our most important asset & are dedicated to remaining a great place to work.

## The Position

The mission of the group is to provide the information systems including the methods, software, databases, infrastructure, and training required for Research to access and analyze DNA and protein sequence information and related biological data. To utilize these information systems to analyze biological information and to identify genes of therapeutic interest.

The successful candidate will explore the impact of gene regulatory networks and gene co-expression networks on clinical outcomes such as survival, response to treatment, etc. using external gene expression and mutation databases as well as internal clinical trial datasets. The co-expression networks will be further explored for prioritization of novel biomarkers and targets that associate with clinical outcome. This will be a collaborative effort between the intern candidate and the Oncology Biomarker Development research team. These data will eventually feed into mathematical models of gene networks in collaboration with gRED Quantitative Systems Pharmacology (QSP). Ultimate goal will be to build a R package that will incorporate these analyses that can be broadly applied to any new clinical trial datasets in the future.

## Who You Are

- Pursuing a PhD
- Background in bioinformatics, biostatistics, computational biology, systems biology, computer science, genetics, genomics, engineering or related field.

- Proficiency in R is required, skills with other high-level programming languages and experience in standard bioinformatics toolkits and programs highly desired.
- Familiarity with Linux working environment and high performance computing highly preferred.
- Applicants with good understanding of concepts in cancer biology/genomics and/or familiarity with high-throughput sequencing technologies will be prioritized.

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