

BIOINFORMATICS SCIENTIST

Introduction:

Sciome LLC is an innovative research and technology consulting company providing state of the art informatics solutions for the life sciences industry. We specialize in developing and deploying novel bioinformatics, text mining and cheminformatics solutions for researchers in the government, academic and private sector organizations. We have a small team (PhD/Masters/Bachelors level scientists and developers) and we are growing!

One of our main areas of expertise is in *biological data mining*. In this domain, we specialize in developing and deploying computational methodologies for 'omics data mining. We routinely use open source bioinformatics techniques, develop novel statistical approaches and perform data analysis in a collaborative fashion. We have an opening for a **bioinformatician**. This is a new growth opportunity and it is a great time to join our growing team. This position promises an impactful career in a fun and relaxed work environment with flexible work hours. We provide a complete compensation package including competitive base salary, 401(k), medical, dental and disability coverage.

Job description: Bioinformatics Scientist

Sciome consults with leading researchers in the field and provides bioinformatics support for experiments generating 'omics data from a variety of health and environmental projects. Sciome has an opportunity for a bioinformatics analyst to conduct analyses in support of a variety of genomics studies that investigate the role of genetic and environmental factors on biological systems. The candidate will have a unique chance to work with leading scientists having wide ranging perspectives on scientific issues and to progress his/her career in a growing organization.

The successful candidate will participate in the analysis of large, high-throughput 'omics datasets such as those generated by next generation sequencing and microarray platforms via the application of bioinformatics and statistical methods. Projects may also include analyses of toxicological, environmental and other biological data types in addition to genomics data. Typical projects investigate changes in chromatin marks (ChIP-Seq, ChIP-Chip), gene expression (mRNA-Seq, Microarray), and the influence of genetic variations (SNPs, genetic rearrangements, etc.) in response to environmental stressors. Data analysis will be carried out using off the shelf bioinformatics analyses techniques as well as in house methodologies. Data management, analysis, interpretation, and documentation leading up to publications will be necessary for successful progression of projects.

Education: Masters or PhD degree in Bioinformatics / Computational Biology / Computer Science / Statistics or closely related field.

Key responsibilities:

- Bioinformatics analysis of genomics data arising from next generation sequencing and microarray platforms. Specific data types include Exome-seq, ChIP-seq, ChIP-on-Chip, mRNA-seq, DNA-Seq and microarray gene expression or genotype data.
- Perform statistical analysis of genomic datasets and participate in methods development while working with Sciome team members. Utilize appropriate off-the-shelf tools or in-house methods and keep up with the literature on rapidly evolving next generation sequence data analysis tool sets.
- Contribute towards the management of large biological datasets and maintaining data analysis workflows as necessary for analysis of sequencing and microarray data.



- Participate in drafting data analysis plans per project needs, perform bioinformatics analysis of the data, interpret results and communicate the results with clients and researchers.
- Document analysis workflows and methods for further report generation and/or scientific publication in peer reviewed journals.

Desired Skillset:

- Hands-on experience with analysis of Exome-seq, DNA-Seq, ChIP-seq, ChIP-Chip, mRNA-seq and microarray datasets.
- Understanding of the wide range of bioinformatics tools and methods for analysis of data originating from next generation sequencing and microarray platforms.
- Experience with applying appropriate statistical and/or bioinformatics analyses to large molecular biological datasets.
- Experience with the use of statistical packages in R and experience in scripting languages such as Perl, Python or Matlab.
- Software coding experience in multiple languages is preferred.
- Strong communication and writing skills in English are essential.
- The ideal candidate will have a proven track record of scientific publication in the fields of bioinformatics, genomics and/or the life sciences.
- Must be eligible to work in the U.S.

How to apply:

Please send your detailed CV via email to [jobs {at} sciome {dot} com](mailto:jobs@sciome.com)

Please refer to **Bioinformatics Scientist** position and include your accurate contact information.

Benefits:

Comprehensive Health Insurance plans compatible with H.S.A.

Health Savings Account with employer contribution

Dental Insurance

Life Short-term and Long-term disability Insurance

Generous 401k retirement plan with employer match

Other ancillary benefits