

Job Description Example: Genomic Data Scientist

Yoh is a seeking a **Genomics Data Scientist** to support a San Francisco Bay Area based startup company in the biotechnology industry. You will have the opportunity to help develop the new age of regenerative medicine.

Title: Genomics Data Scientist **Location**: San Francisco Bay Area

Type: Permanent

Industry: Biotechnology

Pay: Competitive, depends on experience

RESPONSIBILITIES

- Analyze data from experiments including CRISPR pooled screens, scRNA-seq, scATAC-seq, Perturb-seq type screens, among others.
- Work with biologists, bioengineers, and wet lab scientists to design experiments to ensure that our experiments can obtain actionable insights.
- Propose and develop new models and methodologies to analyze novel data types that we are generating in house.

REQUIREMENTS

- Masters in Statistics, Computer Science, Computational Biology, Bioinformatics, Bioengineering, or a related field with 2+ years of experience in academia or industry; or a BS in one of the above fields with 4+ years in academia or industry.
- Experience in analyzing and obtaining actionable insights from high throughput sequencing (HTS/NGS) data is required. Some examples include RNA-seq, ATAC-seq, WGS, scRNA-seq, among the many other types of HTS data.
- Knowledge in experimental design and experience working with teams in designing experiments.
- Experience with deep learning and the practice of model evaluation on real world data.
- Knowledge of either Python or R is required, and both is a plus.
- Familiarity and experience with CRISPR screening data is preferred.
- Able to communicate research results effectively to non-data scientists

For more information, reach out to Caitlin.Noll@Yoh.com



Resume Example: Genomic Data Scientist

SKILLS

- Genomics research
- Data analysis
- Machine learning
- Atlas of mouse and human cells (immune, cancer, stem etc.)
- High-throughput sequencing data
- R programming

- Python programming
- Deep learning
- Keras
- Tensorflow
- Genomics UIs & Visualizations
- Nautilus Cloud

Timeframe of Employment

Cross-functional collaboration

EXPERIENCE

Accredited University
Genetics Department, Research Lab

Data Analyst

- Developed neural network aligned novel motif search algorithm
- Collaborated with in scientists to integrate data analysis strategies
- Collaborated with in scientists, computational biologists, bioinformaticians to integrate data analysis and interactive visualization objectives

Project Leadership

- Planned, coordinated and executed a workflow to build an atlas of functional regulatory motifs from mouse chromatin data
- Handled processing of large volumes of NGS data such as RNASeq, DNaseSeq, ChIPSeq, ATACSeq data on remote HPC clusters and cloud platforms
- Led and supervised the development of a Meta method for batch effect detection in bulk and single cell RNASeq data.

Software/Pipeline Development

- Led development and management of web applications for visualizing browsers tracks, metadata information, associated functional motifs etc. for 100s of mouse chromatin data
- Developed app for tracking dynamic importance from neural network and labeling transcription factors by experts

Accredited University

Timeframe of Experience

Graduate Research Assistant

Computer Science Department, Research Lab

- Identified drawbacks of building ML (Machine learning) methods after classic batch correction strategies. Designed a method for batch effect removal in cancer data.
- Designed, developed and executed a study of identifying cell type specific cofactors in human ChIPSeq data using ML methods (decision tree, gradient boosting etc.)
- Developed and executed a study of transcriptional regulator detection pertaining to hypomethylation boundaries in colorectal cancer (used Random Forest)
- Collaborated with physicists to integrate machine learning objectives to study patient specific transcriptomics for hypertension (used SVM)

EDUCATION

Accredited University
PhD, Computer Science

Year of Completion