

Postdoctoral position - Bioinformatics Scientist in Lung Cancer Genomics at NCI/UCSD

Position Overview

Exposure to house dust mites (HDM), an indoor aeroallergen found in almost every home in the world, can generate allergic reactions and inflammation in the lungs. Based on our recent investigations (see <https://pubmed.ncbi.nlm.nih.gov/36670473/>), we hypothesize that chronic exposure to certain aeroallergens such as HDM could promote lung cancer and be a risk factor for lung cancer in never smokers (LCINS), a cancer type with largely unknown etiology. Our group at the University of California in San Diego (UCSD) is pioneering research in understanding the effects of HDM exposure on lung cancer development. A particular focus lies on chronic exposure to HDM and its potential role in reshaping the lung's microenvironment, driving cancer progression, and influencing therapeutic efficacy.

While our preliminary insights underline the role of HDM in inducing chronic lung inflammation, we are broadening our scope and seeking a postdoc to analyze multi-omics data 1) to investigate how allergen exposure and chronic lung inflammation change the lung microenvironment and make it conducive to lung cancer development, 2) to identify mutational signatures linked to allergen exposure and chronic lung inflammation in preclinical lung cancer models, and 3) to translate these findings to human lung cancer patients by identifying the composition of the lung tumor microenvironment and the mutational signature profiles in LCINS patients who have signs of prior exposure to environmental allergens. Ultimately, our goal is to increase public awareness of the risk that chronic exposure to certain aeroallergens poses for the development of lung cancer and to develop preventive strategies to mitigate such exposures.

The successful candidate will work on publicly available datasets (e.g. TOPmed) and lung cancer genomic data generated by our collaborator, Dr. Maria Teresa Landi, at the National Cancer Institute (NCI). For example, Dr. Landi initiated the *Sherlock-Lung* study, which includes deep whole-genome sequencing (WGS) data from >1,400 tumor/normal samples and RNA-seq and methylation tumor/normal data from >1,800 samples from lung cancer patients (see <https://pubmed.ncbi.nlm.nih.gov/33712835/> and <https://pubmed.ncbi.nlm.nih.gov/34493867/>). Using these available lung cancer genomic data, the successful candidate and Dr. Landi's team will investigate the effects of HDM exposure and chronic lung inflammation on somatic mutagenesis and cancer.

The bioinformatics scientist will be responsible for performing both standard and complex integrative analyses of large-scale multi-omics data. Related tasks include, but are not limited to, data manipulation, algorithmic implementation, statistical programming, genetic/genomic data analyses, data visualization, manuscript drafting, and presentation of results to the scientific community. This position will also require investigation of publicly available cancer genomic databases and bioinformatics pipelines for different data types, including DNA sequencing, and transcriptome, methylation, and microbiome profiling.

Qualifications

Required

1. Doctorate degree in bioinformatics, computational biology, computer science, biostatistics, applied mathematics, or a related field, with a minimum of 3 years of working experience in bioinformatics.
2. Extensive experience in programming using different languages (including bash and R and Python), high-performance computing clusters, and job submission Engines (e.g., SLURM).
3. Team-oriented with excellent written, presentation, and verbal communication skills, with demonstrated ability to learn and adopt bioinformatics techniques and resources.
4. Extensive experience in data processing and visualization, and strong familiarity with statistical methods and analyses for biological data.
5. Familiarity with cancer genomics-related data analysis or experience in performing studies related to cancer genomics.
6. Strong publication record.

Preferred

1. Strong experience in advanced genomic analysis (somatic analysis for different genomic alterations, mutational signature analysis, genomic assembly, pathway analysis etc.) for different types of omics sequencing data (WGS, RNA-Seq, etc.).
2. Expert knowledge of relevant bioinformatics tools for NGS data and genetic databases for processing, analysis, and visualization.
3. Familiarity and working knowledge of tools to explore and investigate cancer genomics with publicly available data sources (such as TOPmed, dbGaP, TCGA, ENCODE, 1000 Genomes, GTEX, gnomAD, cBioPortal, ICGC, UKBB).
4. Experience in performing statistical analysis of large datasets by running open-source and custom-developed analysis pipelines in R or Python.
5. Experience in developing R shiny app and complex data visualization based on popular R packages (e.g., ggplot2).
6. Working knowledge of lung cancer, inflammation, or dust mites. Significant experience in Omic-data analysis pertaining to these topics.
7. Experience in preparing manuscripts based on original research to be published in peer-reviewed journals.

Additional Details

Our team is looking for a motivated Ph.D. bioinformatician with 0-2 years of prior postdoctoral experience interested in a postdoctoral position for a minimum of 2 years (depending on funding available, project progress, and performance of the candidate). The position will require the candidate to work with Dr. Landi on the NCI campus in Rockville, MD to get access to the WGS datasets necessary for this project. The candidate will be hired and supported financially by UCSD, but work 100% on site in Rockville, MD. Pay is commensurate with qualifications and includes a comprehensive benefit package. This is a full-time position with a competitive salary (starting at \$64,480-69,342 per year based on level of experience, see <https://www.ucop.edu/academic-personnel-programs/files/2023-24/oct-2023-acad-salary-scales/t23.pdf>) and full benefits package (see <https://postdoc.ucsd.edu/postdocs/benefits-services.html>).

To Apply

Please send a resume and cover letter addressing your qualifications for the position to Dr. Samuel Bertin (sbertin@ucsd.edu), with "Bioinformatics Scientist Application" in the subject line. The position is available immediately and will remain open until filled.