We seek a talented and highly motivated Bioinformatician to join our dynamic, collaborative team focused on high-throughput sequencing (HTS) applications. This position involves novel integrated multimodal analyses of single cell datasets in blood immune cells and tissue. The candidate will develop and apply bioinformatics workflows to support both standard and custom data analysis for transcriptomics, epigenomics and multi-omics projects. This role provides a unique and rewarding opportunity to conduct research with broad scientific and technical impact and make a profound impact on human health. A faculty appointment at the rank of Instructor at Harvard Medical School will be proposed. Applicants will be involved in the teaching of pre- and post-doctoral trainees from Harvard Medical School.

About us
The Tsibris Laboratory studies the biology of HIV latency and its reversal in the context of human disease. The guiding principle of our work is a cure for HIV. The Tsibris lab is located in Cambridge, MA, an area rich in world-class academic centers, pioneering biotechnology and pharmaceutical companies, and a diverse, welcoming, and inclusive community. More information about the Tsibris Lab may be found at tsibrislab.bwh.harvard.edu.

The Harvard Chan Bioinformatics Core (HBC) is a center for bioinformatics research at the Harvard T.H. Chan School of Public Health. We work closely with biomedical scientists across Harvard to implement approaches for analysis, interpretation, visualization, and dissemination of scientific discoveries using high-throughput omics data. The HBC emphasizes teamwork and a supportive environment where we learn from each other. More information about the HBC may be found at bioinformatics.sph.harvard.edu.

About you
You have a background in biomedical or quantitative science and a strong interest in working with biomedical researchers. You thrive on scientific challenges and enjoy collaborating with an interdisciplinary team. You can combine your knowledge of biology and computation to communicate effectively with programmers and wet-lab scientists alike. Experience with single cell datasets and an interest in Immunology and/or HIV pathogenesis are a plus. You are an independent learner, are keen to explore and apply new methods, and are motivated to continually expand your skills. You follow best practices for code and data management, have good organization skills, and are capable of simultaneously working on different projects and deadlines. You are experienced with high-throughput sequencing analysis and are comfortable mentoring junior researchers.

Duties
The Bioinformatician will support research projects within the Tsibris Lab and interact with the HBC. They will work with a team of bioinformaticians to develop and apply bioinformatics workflows to support both standard and custom data analysis for variant calling, transcriptomics, epigenomics and multi-omics projects. They will provide expertise in the use of specialized bioinformatics tools and analysis methods. They will collaborate with the Tsibris Lab to design, analyze and interpret experiments.

Coordinating with experienced HBC staff, the candidate will analyze incoming data using existing analytical approaches and assess/develop new methods where appropriate. They will

document their work thoroughly, adhere to NIH requirements for data management, and provide manuscript-level reporting of final analyses and results. They will summarize, analyze, and visualize data using advanced techniques, and present it clearly to collaborators.

The Appointment is anticipated for two years, with renewal after the first year contingent upon satisfactory performance.

Qualifications
- Ph.D. in Bioinformatics, Computational Biology, Genomics, Biostatistics or Biological Sciences with working knowledge of molecular biology.
- At least 2 years of postdoctoral experience in academia or industry using a broad range of current bioinformatics approaches for common applications. Expertise in at least one of the following HTS applications is required:
  - Transcriptomics (bulk, small or single cell RNA-seq)
  - Epigenomics (ChIP-seq or ATAC-seq)
- Demonstrable ability to apply statistical approaches to analyze data, interpret and present results.
- Excellent analytical and programming skills.
- Excellent communication and time management skills.

Additional
- Knowledge of and experience with immunology and/or virus datasets is a plus.
- Ability to produce reproducible code (R Markdown, Latex, Jupyter notebooks, etc).
- GitHub repositories and publications that can showcase your skills.
- A strong interest in sharing expertise and/or teaching.

Interested candidates should email a cover letter, detailed curriculum vitae, and research interests as a single PDF to:

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We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability status, protected veteran status, gender identity, sexual orientation, pregnancy and pregnancy-related conditions or any other characteristic protected by law.