Job Announcement: Computational Scientist - Chromatin Conformation Analyses

The **Genomic Architecture of Cancer** laboratory is seeking an enthusiastic and talented **Computational Scientist** to investigate the role of chromatin conformation in cancer. Our dynamic team is exploring how epigenetic elements are impacting cell functions across normal and malignant development, with a focus on drug resistance. Our models are primary patient samples, that we analyze through multi-omics technologies, including single cell approaches and genome-wide screenings.

Who we are:
Our laboratory is located at the **Candiolo Cancer Institute** in Turin, Italy. We are a Comprehensive Cancer Center and a National referral center for cancer therapy and research (I.R.C.C.S.). We additionally work in close partnership with the **Applied Bioinformatics Lab** (ABL) at the New York University School of Medicine. Our goal is to understand the key mechanisms that drive tumor biology and translate these discoveries into better treatments for cancer patients.

Position Overview:
As a Computational Scientist specializing in chromatin conformation analyses, you will play a pivotal role in unraveling the three-dimensional structure of chromatin and deciphering its functional implications. Leveraging your expertise in computational biology, bioinformatics, and statistical analysis, you will develop innovative algorithms and computational models to interrogate large-scale genomic datasets. Your insights will contribute to a deeper understanding of chromatin dynamics and its role in gene regulation, with profound implications for human health and disease.

Key Responsibilities:
- Employ computational methods to analyze high-throughput sequencing data, including Hi-C, ChIP-seq, and ATAC-seq, to characterize chromatin conformation landscapes.
- Develop and implement novel algorithms and software tools for the integration and interpretation of multi-omics datasets related to chromatin structure and function.
- Collaborate closely with experimental biologists and bioinformaticians to design experiments and validate computational findings.
- Stay abreast of the latest advancements in computational biology and genomics, applying innovative approaches to address complex scientific questions.

Qualifications:
- Ph.D. or equivalent experience in computational biology, bioinformatics, genomics, or a related field. Younger candidates (postgrad) with a solid computational track are also encouraged to apply.
- Proficiency in programming languages such as Python and R, preferably with experience in developing bioinformatics pipelines and tools.
- Strong background in statistical analysis applied to biological datasets.
- Previous experience with genomic data analysis, particularly in the context of chromatin conformation assays (e.g., Hi-C, ChIP-seq, ATAC-seq) is desirable, but not mandatory.
- Excellent communication skills and ability to collaborate effectively within a multidisciplinary team environment. Given the international nature of our team, English is the official language.

Benefits:
- Competitive salary, adjusted for your level of experience.
- Numerous openings for professional development and career advancement.
- Allocated funds for 3-year long projects, further extendable upon satisfactory performance review.
- Multi-disciplinary teamwork, with access to cutting-edge technologies and state-of-the-art facilities.
- Opportunity to work with our ABL team in New York, learning innovative and highly marketable skills.
- International visibility, with the opportunity to present your work at national and international meetings.
- Collaborative and inclusive work culture, fostering creativity and innovation.

How to apply:
Please submit your C.V., a cover letter outlining your scientific interests and relevant experience, and contact information of two referees to francesco.boccalatte@ircc.it

https://www.med.nyu.edu/faculty/francesco-boccalatte