

Bioinformatician in single cell spatial transcriptomics

We are looking for a highly motivated and creative researcher to study the epi-transcriptomic landscape of pediatric and adult tumors at single cell and spatial resolution under the supervision of Prof Matteo Cereda within the Cancer Genomics and Bioinformatics laboratory at the Italian Institute for Genomic Medicine (IIGM) and the University of Milan.

Research. The main objective is characterized epi-transcriptional regulation of different cancer types, including prostate, breast, lung and sarcomas in young and adult patients. To achieve this goal, our research program will exploit spatial and single cell transcriptomic sequencing approaches at short- and long-read levels. Patients will be tracked from the point of diagnosis with data including longitudinal and multi-tumour site sequencing. The research will include applying computational approaches to define the epi-transcriptional regulation of RNA processing in cancer and identify molecular markers favoring the design of personalized treatments and the development of novel cancer therapies, especially in light of RNA-based therapeutics.

Role. The post holders will be responsible for the development and optimization of spatial and single cell multi-omics data analysis at short- and long- read sequencing levels to assess epigenetic and transcriptional regulation of RNA processing. A key mission will be to ensure the delivery of computational analyses to identify actionable targets generated by RNA processing mis-regulation. RNA-based therapeutic approaches will be evaluated against these alterations within a clinical context. To achieve these goals, the candidate will also be expected to contribute to the development of new algorithms and bioinformatics approaches. Robustness and reproducibility of bioinformatics analyses will be at the core of this role.

Requirements.

- Master's degree in a relevant subject (e.g., physics, computational biology, computer science, bioinformatics, bioengineering or in a related field of the life sciences). Ph.D. is a significant plus.
- Knowledge of programming languages as R, bash, python
- Prior experience in working with NGS, particularly in single-cell and long-read sequencing, is a significant plus.
- Experience in standardised and modular bioinformatics workflows.
- Ability to present the results in oral presentations at meetings and in publications in top ranked journals relevant to the field.

IIGM - Italian Institute for Genomic Medicine

Sede legale: Piazza Bernini 5 - 10138 - Torino; Sede Operativa: c/o IRCCS, SP 142 km. 3,95 - 10060 - Candiolo (TO)

- Ability to report research progress on a regular basis
- Fluency in English.
- Proven communication and problem-solving skills.
- Strong interpersonal skills demonstrated by the ability to gain the assistance and cooperation of others in a team endeavour.
- Ability to build trust through operating with transparency and creating an open and positive environment.
- Commitment to oncological research.

IIGM is a private research institute located within the FPO Candiolo Cancer Research center. The institutional goal is to foster and develop excellence in human genomic research and education, with special reference to genomic variability in multifactorial diseases, as cancer. The institute provides high-level scientific education and access to state-of-the-art research facilities (*e.g.* Illumina, Oxford Nanopore sequencers). Further information on the CGB laboratory are available at: <u>http://www.ceredalab.com/</u>

References. Del Giudice M. *et al.*, Cell Reports (2022); Lauria A., Peirone S., Del Giudice M. *et al.*, Nucleic Acid Research (2020); Cereda M., Gambardella G., Benedetti L., *et al.*, Nature Communication (2016).

Application. To apply for this position please submit a cover letter in English, describing research experience and motivation, CV in English, and contact information of 2 references to: <u>matteo.cereda@iigm.it</u>

The position is available immediately.