

Postdoctoral research topic

- Title of the proposed topic: **AI for Single-cell and Spatial full-length RNA profiling.**
 - Research axis of the 3iA: Theme 3 "AI for Computational Biology and Bio-Inspired AI"
 - Supervisor: Kevin Lebrigand, PhD, IPMC, CNRS, lebrigand@ipmc.cnrs.fr
 - Potential co-supervisor (name, affiliation):
 - The laboratory and/or research group: IPMC, "Physiological Genomics Group", Dr. Pascal Barbry.
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Apply by sending an email directly to the supervisor.

The application will include:

- Letter of recommendation of the supervisor indicated above
 - Curriculum vitae including the list of the scientific publications
 - Motivation letter
 - Letter of recommendation of the thesis supervisor
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- **Description of the topic:**

We are currently looking for a highly motivated postdoctoral computational biologist interested by the study of RNA isoform usage at single cell and spatial resolution. The position is geared toward the development of innovative bioinformatics machine learning approaches to fully explore novel methodological approaches that have been developed by our group, and which combine the isolation of thousands cells by a microfluidics device with RNA long read sequencing based on the Oxford Nanopore Technology.

Single-cell technologies are becoming essential in many research projects to analyze complex biological systems. Single cell and spatial transcriptomics assays are becoming instrumental to develop approaches in system's biology. The technological solution that was used so far was based on short-read sequencers. While this provides a well-adapted solution to describe gene expression at a cellular level, it does not detail the modifications of RNA structure by splicing, editing, etc... Our team provided last year the first bioinformatic workflow to analyze full-length transcription at single-cell and spatial resolutions after using long-read Nanopore sequencers (Lebrigand et al, Nat. Comm., 2020; Lebrigand, bioRxiv, 2020). We are now aiming at better defining and exploring splicing usage, bi-allelic expression and splicing quantitative trait loci (sQTL) in complex biological samples at the single-cell and spatial resolution. The postdoctoral fellow will develop innovative computational approaches based on machine learning to explore and decipher the biology of those mechanisms.

The postdoc will join the laboratory of Pascal Barbry at IPMC (Sophia Antipolis, France), involved in the Human Cell Atlas (HCA) consortium. He/she will work in close collaboration with UCAGenomiX platform researchers on the elaboration of the Human Lung Cell Atlas, using data derived from the Human Developmental Cell Atlas project (INSERM), and from EU and CZI-funded projects. UCAGenomiX, node of the "France Genomique" Network develops innovative methodological developments for the academic field, with a specialization in single cell and spatial transcriptomics experiments.

The ideal candidate would have a background in computational/bioinformatics approaches in RNA biology. Capacity to interact directly with biologists is important to develop AI-based tools that can be closely developed with them and be transferred to a larger audience. Datasets already exist but additional experiments will be generated in collaboration with the biological laboratory during the course of this postdoctoral fellowship.

Background:

- M Deprez, LE Zaragosi, et al. 2020. A single-cell atlas of the human healthy airways. *American journal of respiratory and critical care medicine* 202 (12), 1636-1645
- K Lebrigand et al. 2020. The spatial landscape of gene expression isoforms in tissue sections. *Biorxiv*.
- K Lebrigand, V Magnone, P Barbry, R Waldmann. 2020. High throughput error corrected Nanopore single cell transcriptome sequencing. *Nature communications* 11 (1), 1-8