

JOBIM 2024 - Mini-symposium
Thursday June 27th 2024, 16h30-18h30

Unraveling Cellular Landscapes: Advances in Spatial Transcriptomics

Organizers

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Abstract

In the ever-evolving landscape of omics approaches, spatial transcriptomics has emerged as a revolutionary tool. While single-cell transcriptomics analyses offer unprecedented insight into the granularity of cell-specific gene expression patterns, they lack the spatial context crucial for understanding the intricacies of specific biological questions, such as developmental processes, tumor invasion, or insights into biological structures or rare cell types obtained from histology and fluorescence. Integrating near single-cell granular transcriptomic profiling and histological characterization of tissues allows for a comprehensive exploration of cellular heterogeneity and a nuanced understanding of molecular landscapes.

However, spatial transcriptomics data analysis poses unique challenges in bioinformatic analysis that also rely strongly on new developments in data management, statistics and image analysis. Bioinformatic analyses need to address issues of scalability, data normalization, batch effect correction (*e.g.*, between slides). At the same time, robust image processing and analysis are required to deal with image artefacts and deploy cutting-edge deep learning techniques for cell-segmentation and phenotyping based on large dataset and AI models.

The objective of this symposium is to share insights from various experiences in managing all aspects of spatial transcriptomics data, perspectives on how to effectively integrate them, and scientific illustrations of how spatial considerations can prove relevant to biology. Presentations of analyses methods and pipelines from two core facilities will be followed by illustrations with talks on specific scientific topics.



Program

16h30-17h

Presentations of methods from analysis platforms

Yad Ghavi-Helm, Sergio Sarnataro

Spatial-Cell-ID, ENS, Lyon

Marie Coutelier, Stephen Whitmarsh

Data Analysis Core, Paris Brain Institute, Paris

17h-18h

Presentations of scientific projects

Isaias Hernandez

Centre de Recherche des Cordeliers, Paris

Intratumoral GABA synthesis is associated with immunosuppression and non-response to immune checkpoint inhibitors in TLS positive RCC tumors

Emeline Cherchame

Data Analysis Core, Paris Brain Institute, Paris

Investigation of the impact of Growth Hormone Receptor activation on Glioblastoma progression: a Visium spatial transcriptomics analysis of Xenograft models of GBM cells in the mouse brain

Kevin Lebrigand

Bioinformatics Hub, Institut Pharmacologie Moléculaire et Cellulaire, Sophia-Antipolis

Spatial isoform Transcriptomics

Baptiste Alberti

Institut de Génomique Fonctionnelle (IGFL), Ecole Normale Supérieure, Lyon

Reconstructing spatiotemporal gene expression and enhancer activity in Drosophila embryos using scRNA-Seq and optimal transport

18h-18h30

Open table and discussion