Spatial-Cell-ID

The Spatio-temporal transcriptome of single cells in their tissue*

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Imaging

RNA detection by multiplexed single-molecule Fluorescence *In-Situ* Hybridization (smFISH) techniques

Precise quantification at a very high spatial resolution of a small (1-30, smFISH) to large (30-10000, MERFISH) number of transcripts *in vivo*

Resources:

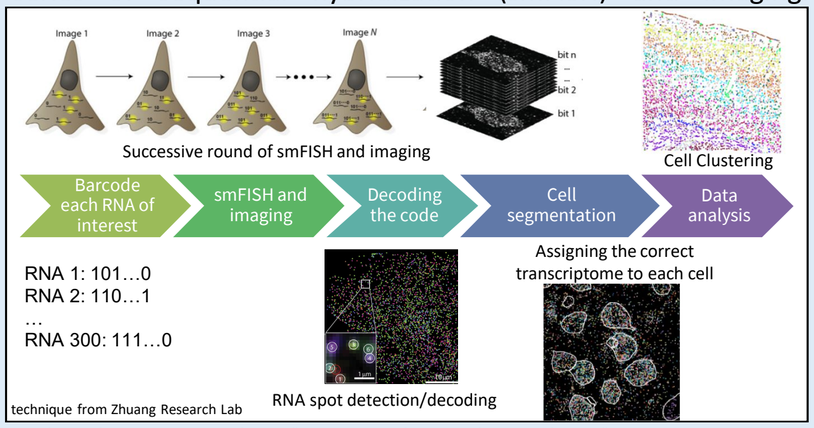
STELLARIS 8 tau-STED - Leica
Home-made microfluidics for multiplexed FISH
Dedicated engineer (3 years)

Location:

PLATIM @ UAR Biosciences

MERFISH principle:

Combinatorial labeling approach to associate unique barcodes with individual RNA species. Barcodes are then read through a series of sequential hybridization (smFISH) and imaging.



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Imaging

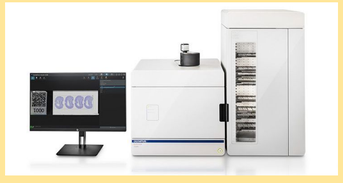
Slide-seq

Quantify the expression pattern of a large number of transcripts (~5000) with a high spatial resolution

Genomics

Resources:

Slide scanner VS200 - Olympus
IncuCyte S3 - Sartorius

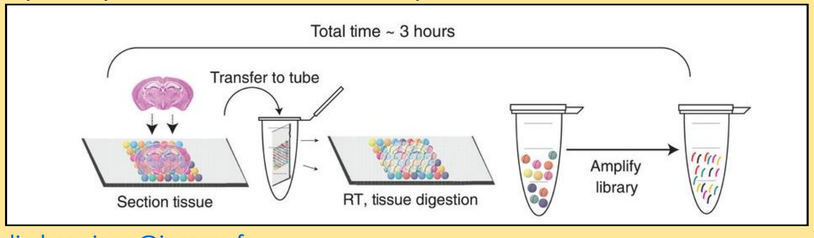


Location:

PrimaStem/Connectomics @ SBRI

Slide-seq principle:

The tissue section is placed onto a transcriptomic slide that contains spatially barcoded DNA. The captured and barcode RNAs are amplified and sequenced. The barcodes are used to spatially reconstruct the transcriptome.



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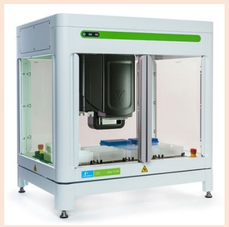
Genomics

Spatial single-cell RNA-sequencing (scRNAseq)

Quantify the full transcriptome of single cells isolated from complex tissue samples and reconstruct their spatial location *a posteriori*

Resources:

Aurora cell sorter - Cytek
CellenONE cell sorter - Cellenion
Chromium controller - 10x genomics
Zephyr G3 NGS workstation

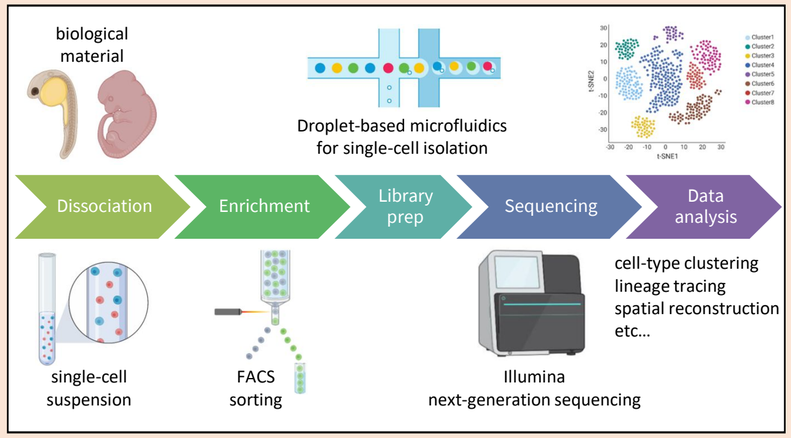


Location:

CyLE & ProfileXpert @ SFR Lyon Est
Cytometry @ UAR Biosciences
PSI @ IGFL

Spatial scRNAseq principle:

Cells from complex biological samples are dissociated into a single-cell suspension. The viable cell type(s) of interest can be enriched by FACS before their encapsulation in micro-droplets. scRNAseq libraries are then prepared automatically and sequenced. The single-cell transcriptomes are used to map back each cell's spatial location within the biological material of origin.



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Data analysis

Data analysis

Hardware, software and human resources for computational biology and artificial intelligence applied to image analysis of MERFISH data and spatial reconstruction of single-cell sequencing data

Resources:

HPC@theEdge workstations
Computing clusters
Data storage server
Software:
ARIVIS, Amira 3D, IMARIS
Dedicated engineer (8 years)

Location:

Data center of the ENSL @ PSMN/CBP
PLATIM @ UAR Biosciences
PSI @ IGFL

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Data analysis principle:

image analysis: segmentation, deconvolution, RNA spot detection, RNA spot corrections, RNA spot assignation, MERFISH barcode analysis.

Single-cell sequencing analysis: Cell-type clustering, lineage tracing, spatial reconstruction

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