European Molecular Biology Laboratory

Multi-omics interrogation of mouse brain tissue at single-cell and spatial resolution

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Background

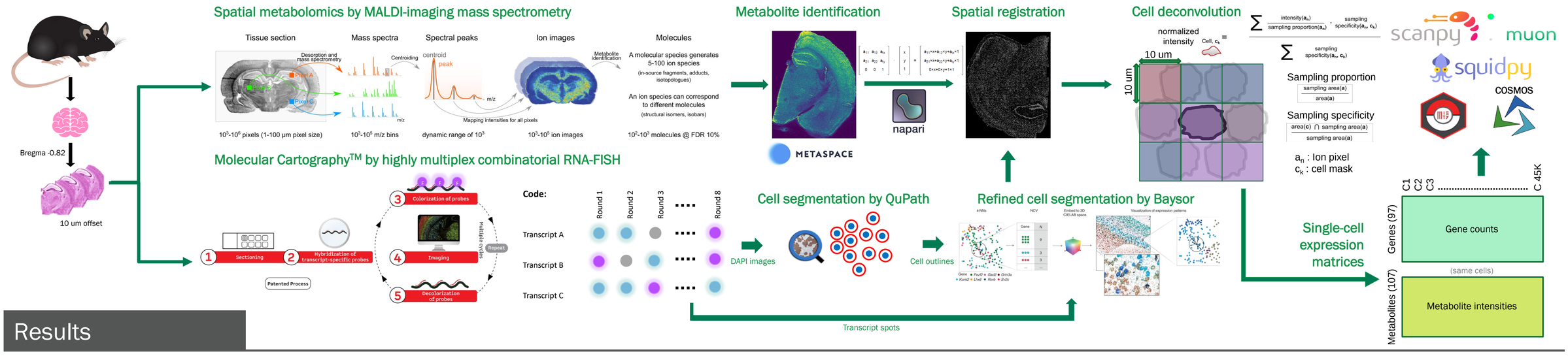
Introduction

Recently emerged spatial omics technologies provide unprecedented insights into spatial aspects of gene expression, protein localization, and metabolite concentrations in tissues. Advancing in this direction requires both novel multi-omics experimental methods and novel computational methods able to link information across omics, molecularly and spatially. Here we provide the first multi-omics dataset combining spatial transcriptomics and metabolomics at single cell resolution. The uniqueness of the provided data supplied with demos will facilitate rapid uptake and data re-use by computational biologists, thus boosting the field of spatial multi-omics.

Aims

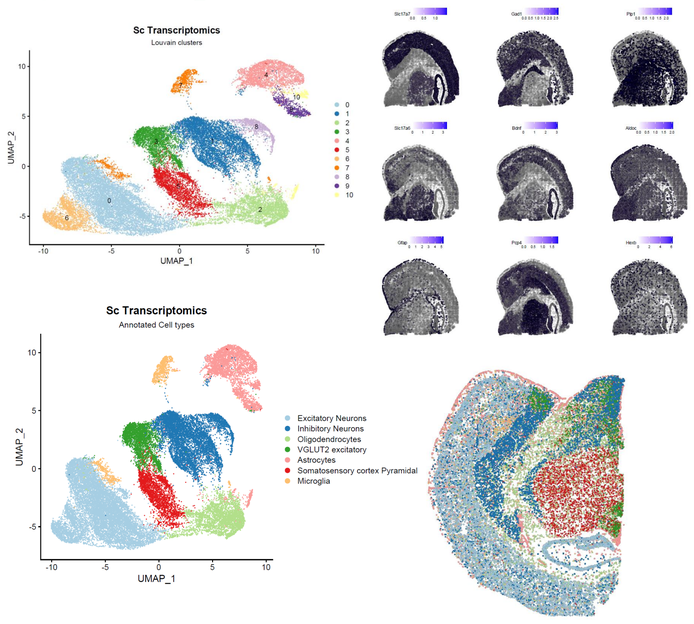
- Providing the first public spatial multi-omics data combining highly-multiplex RNA FISH (Resolve Biosciences) and spatial metabolomics by MALDI-imaging mass spectrometry from consecutive sections of the mouse brain.
- Showcase how the data can be interrogated by the recently emerged software for single cell and spatial multi-omics.

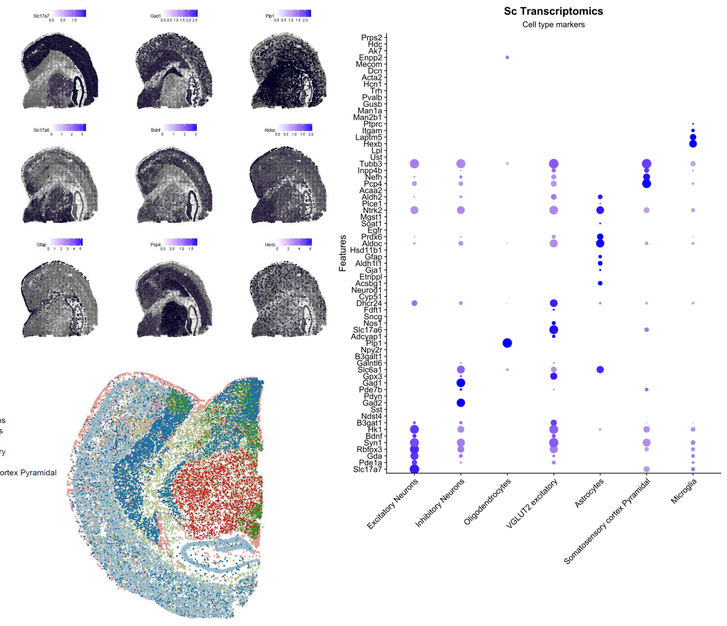
Methods



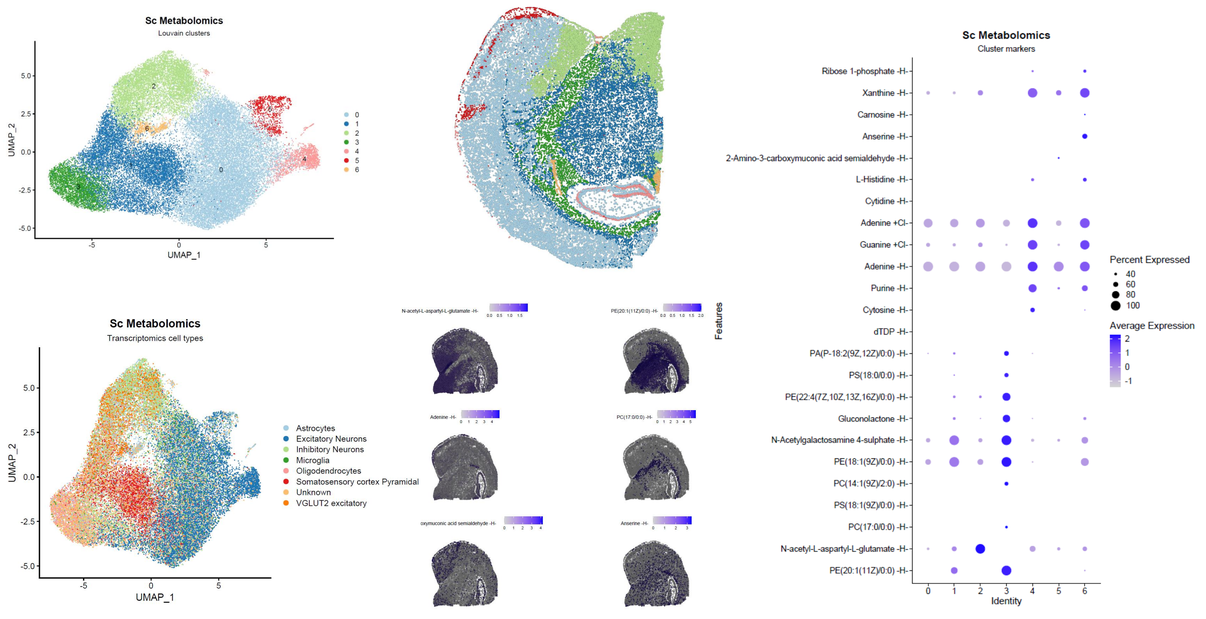
Results

Spatial single-cell transcriptomics



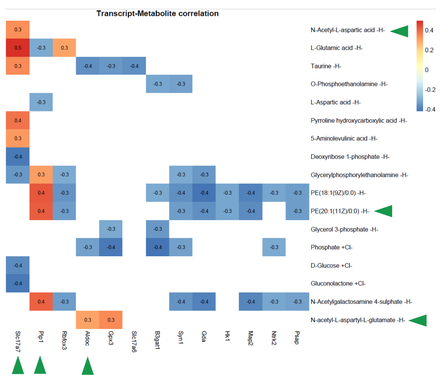


Spatial single-cell metabolomics

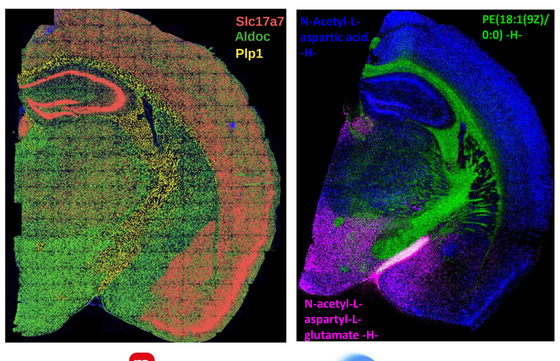


Multi-omics joint analysis

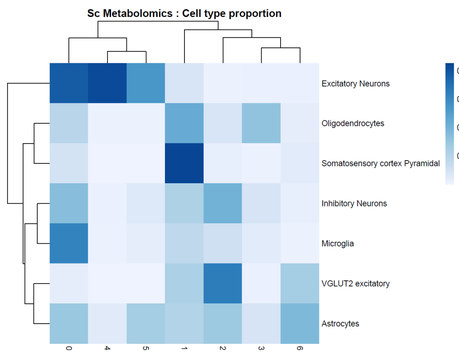
Transcript-Metabolite correlation



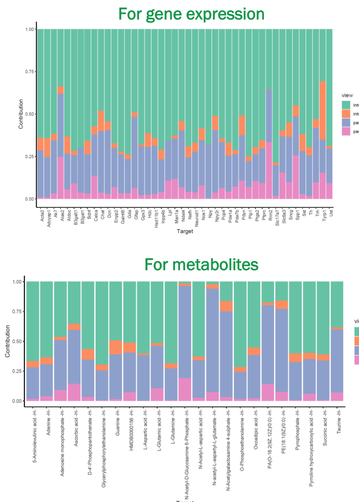
Spatial localization of correlated transcripts and metabolites



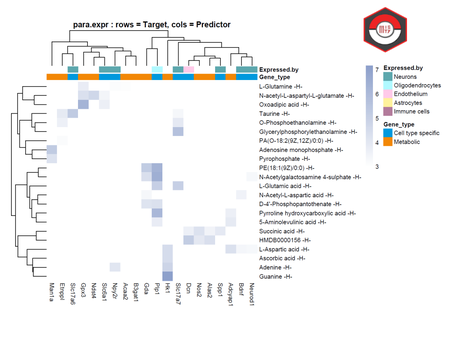
Cell types in metabolic clusters



Explaining by spatial and intra views



Explaining importance of spatial gene expression on metabolite abundance



Conclusions

- Spatial multi-omics dataset: spatial single-cell transcriptomics and spatial near-single-cell metabolomics
- Mapped metabolites to the same single cells detected by transcriptional composition
- Detected spatially localized cellular clusters for both modalities with a high degree of overlap
- Found high concordance between transcriptionally identified cell types and metabolic cellular populations
- Found moderate-high correlations between gene expression and metabolites
- Marker interactions between both modalities were partly explained by both spatial and intrinsic expression

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