

Biozentrum





Basel Computational Biology Seminar

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Revealing the brain's molecular anatomy with single-cell and tomography-based spatial transcriptomics

I will present our comprehensive single-cell transcriptome atlas of mouse brain development spanning from gastrulation to birth. In this atlasing effort, we identified almost a thousand distinct cellular states, including the initial emergence of the neuroepithelium, different glioblasts, and a rich set of region-specific secondary organizers that we localize spatially. In this context, I will provide an example of how the spatially-resolved transcriptomic data can be particularly useful to interpret the complexity of such complex atlases.

Continuing in this direction, I will show the approach that we recently proposed as a general way to spatially resolve different types of next-generation sequencing data. We designed an imaging-free framework to localize high throughput readouts within a tissue by combining compressive sampling and image reconstruction. Our first implementation of this framework transformed a low-input RNA sequencing protocol into an imaging-free spatial transcriptomics technique (STRP-seq).

Finally, I will showcase the technique with the profiling of the brain of the Australian bearded dragon Pogona vitticeps. With this analysis, we revealed the molecular anatomy of the telencephalon of this lizard and provided evidence for a marked regionalization of the reptilian pallium and subpallium.

Date: Monday, May 10th 2021

Time: 16:00 h Zoom Link:

https://unibas.zoom.us/j/98301836128?pwd=dkZCbDVZQmFzTkNyT0JpakFBTjRyQT09

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