

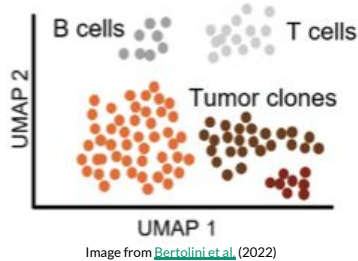
# Exploiting the spatial dimension

## The power of single cell spatial transcriptomics

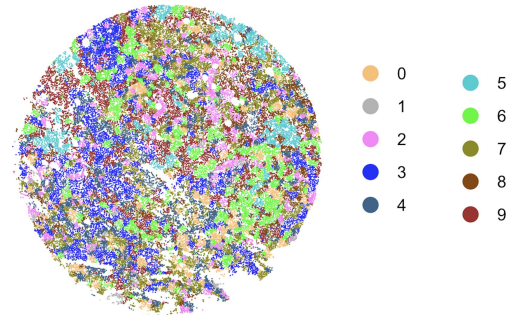


### From single cells & and their spatial location to characterization of tissues

Composition of detected genes → Cell types

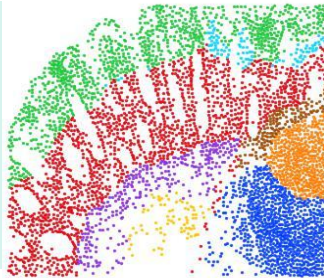


Composition of cell types → Spatial niches

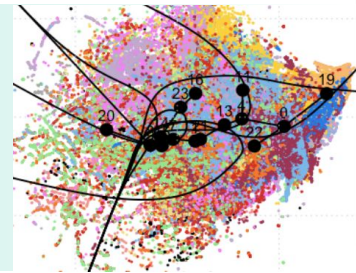


### Further analyses to unravel biological insights

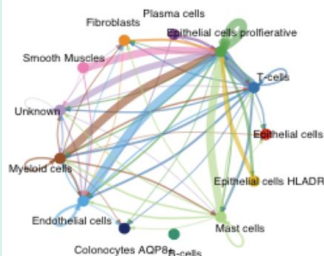
Profile tissue remodeling by comparing identified spatial niches across conditions



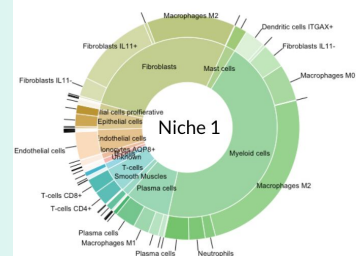
Trajectory analysis: relationships between niches (e.g. associations with healthy vs diseased samples)



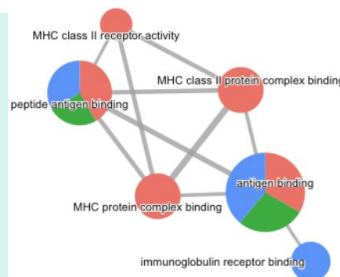
Compare cell-cell communication (e.g. which cell types or niches interact) across samples



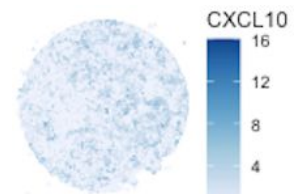
Cell type characterisation taking into account spatial dimension



Perform GO, KEGG, GSEA on genes from different clusters, trajectory lineages across conditions



Identify and characterize gene markers (e.g. most spatially variable genes)



Supported ST technologies: Visium (HD), Xenium, CosMx among others

Additional services: gene panel design, cell segmentation, integration with scRNA-seq, & more

