

## **Title: Spatial transcriptomics in neurological research**

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**Abstract:** The structural and functional complexity of the central nervous system presents a profound challenge for neuroscience. Traditional transcriptomic methods, while powerful, require tissue dissociation, which strips away the crucial spatial context of gene expression. Because the precise architectural organization of heterogeneous cell types dictates neural circuitry, function, and pathology, preserving this spatial topography is essential. In recent years, high resolution spatial transcriptomics has emerged as a transformative paradigm, bridging the gap between high-throughput molecular profiling and classical histology. By preserving the spatial context, these technologies allow researchers to identify distinct cellular subpopulations, map cell-cell interactions, and trace subtle gene expression gradients within their native anatomical microenvironments. We will discuss how these spatial insights advance our understanding of both healthy brain architecture and the mechanisms driving complex neurological disorders.



**Short Bio:** Koen De Gelas is working as a Scientific Technical Advisor for 10x Genomics covering single cell and spatial applications. He is interested in facilitating the use of novel “omics” technologies to accelerate scientific discoveries and to advance human health. Koen received his MSC in Biology and a PhD in molecular genetics from KULeuven, Belgium.

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