

Intercellular communication orchestrates important tissue processes in all multicellular organisms. Recent advantages in single-cell and spatial transcriptomics unveil new possibilities in analysing cell-cell communication. Up-to-date workflows of both revolutionary methods are described and complemented with relevant novel tools. By merging detailed genome-wide single-cell sequencing information with preserved spatial context, it is possible to capture tissue organisation in great detail. Knowledge-graph-based tool SpaTalk is used to reveal signalling pathways in mouse brain after cerebral ischaemia. The results show significant role of adhesion-related and tissue-densification-related signalling events in the intercellular communication at the lesion border. Detailed signalling mechanisms among proliferating microglia, astrocytes, and oligodendrocytes ongoing in the lesion are also revealed.