

# Abstract

Spatially resolved transcriptomics is a novel method that enables the study of gene expression in tissue samples without loss of spatial context. It can be used to map the distribution of mRNA to individual cells as well as subcellular locations. Data obtained using this method provide important insights into various aspects of biology, including embryology, oncology, or immunology. The functioning and mutual interaction of individual cells cannot be fully explained without knowledge of their exact location in the tissue.

Due to the novelty of the method, reconciling the obtained information on gene expression and spatial arrangement of cells is currently a major challenge and bioinformatics approaches are still being established. The aim of this work is to map the current algorithms for the normalisation of spatially resolved transcriptomics data and to compare these algorithms based on available data sets. Eventually, selected algorithms will be implemented and integrated into the workflow used at IMG CAS. The work includes

- i. survey of available solutions,
- ii. selection of a suitable solution or design of a new one,
- iii. implementation of the solution and its testing on available data.