

Bento: A Toolkit for Subcellular Analysis of Spatial Transcriptomics Data

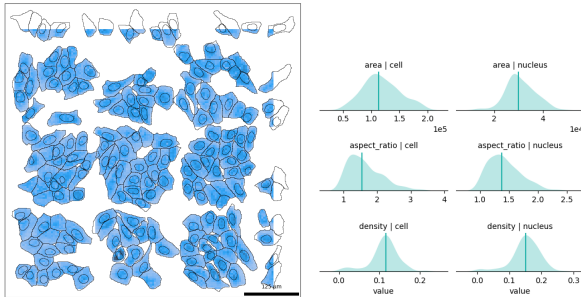
Anjali Jangir

2024

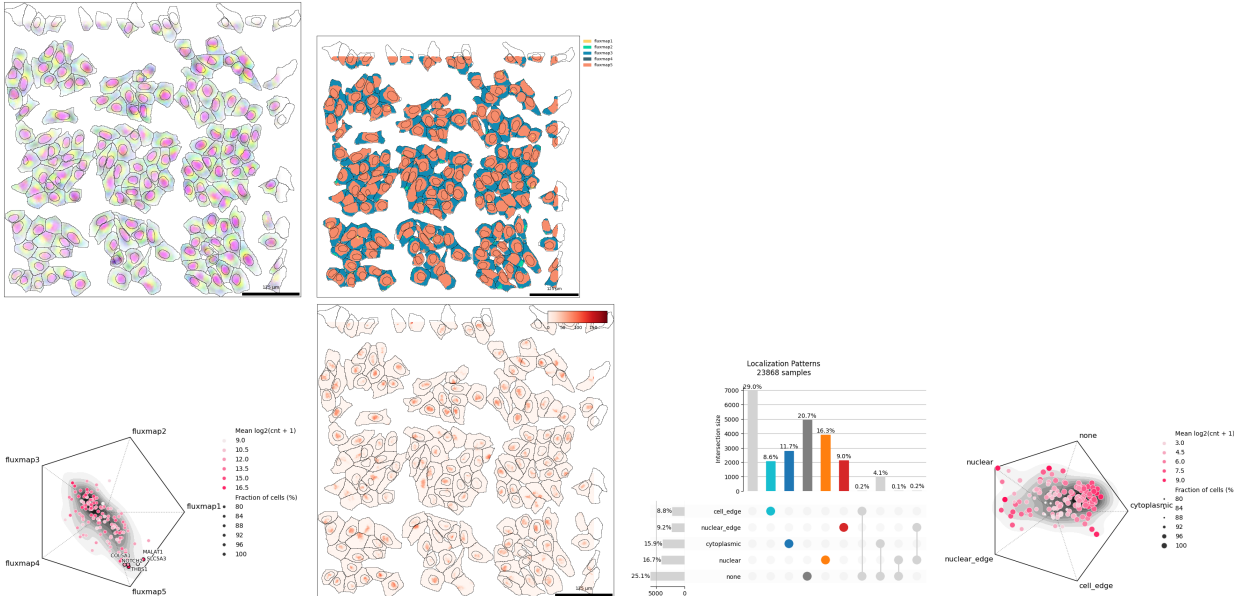
1 Results

Bento was evaluated on MERFISH and seqFISH+ datasets, showing that RNA localization patterns correlate with gene functions. For instance, nuclear-localized RNA supports specific nuclear functions, while cytoplasmic localization aligns with cell membrane functions.

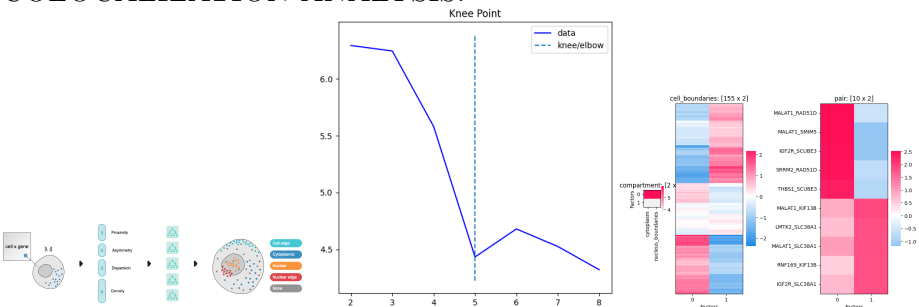
SPATIAL SUMMARY STATISTICS:



RNAflux: Semantic Segmentation of subcellular domains:



COLOCALIZATION ANALYSIS:



TRAINING RESULTS:

