

1 Spatial Transcriptomics Visualization (przestrzenna wizualizacja transkryptoniki) using Representation Learning

In this laboratory, we will explore how to visualize spatial transcriptomics data using dimensionality reduction techniques and neural network representations.

1.1 Introduction

Spatial transcriptomics is an emerging technology (nowoczesna technologia) that preserves the spatial locations of cells while measuring their gene expression (ekspresji genów). This approach provides valuable insights (cennych informacji) into tissue architecture (architektury tkanek), cellular interactions (interakcji komórkowych), and spatial patterns (przestrzennych wzorców) of gene expression that are lost in dissociated single-cell methods. (pojedynczych komórek opartych na dysocjacji)

In this exercise, we'll visualize spatial transcriptomics data using techniques like UMAP, t-SNE, TriMAP, and PaCMAP. We'll enhance (ulepszymy) these visualizations by leveraging neural network representations, exploring how the activations of hidden layers can improve our ability to identify distinct (odrębnych) tissue regions (obszarów tkankowych) and cell types.

By the end of this laboratory, you'll understand how representation learning can be applied to spatial transcriptomics data to extract meaningful (istotne) biological insights about tissue organization. (organizacji tkanek)

Does this structure work for you? (Czy taka struktura Ci odpowiada) Each file follows the format of your previous labs while creating a focused laboratory on spatial transcriptomics visualization. I've created separate MDX files for setup (do konfiguracji), data loading, preprocessing, neural network training, and two specific (konkretnych) exercises.