

Abstract

This bachelor's thesis is focused on the use of machine learning and deep learning methods in an attempt to automate the annotation of cells based on their gene expression (single-cell data). In particular, it is focused on the use of transformers and architectures derived from them, such as performers. The main part of the work is devoted to the description and explanation of how these architectures work in their basic form, the description of the models created for cell annotation and their comparison.