Division of Statistics and Machine Learning
Department of Computer and Information Science
Linköping University

Master thesis project ”Transfer learning for mRNA data integration ”

Background

One of the key problems in medical care is that many patients do not respond to treatment. One of reasons is that mRNA data which are traditionally used in biological analyses contain relatively few observations: while many thousand genes are measured, only a few hundreds of observations are available in the largest datasets. One solution might be merging the data sets from different studies but one problem is that often different measuring techniques are used in different mRNA data which leads to so called batch effects in the data

Deep transfer learning models are commonly used for transferring knowledge between data sets coming from similar, but not exactly same conditions. Your task will be investigating the performance of two classes of such models: universal domain adaptation models and supervised domain adaptation models in merging two or more mRNA data.

Data

- mRNA datasets withs few hundred observations and thousands of genes, each observation labelled by cell type, for example data sets from R package “celldex”.

Research Questions

- Assuming that cell types (labels) are available only for the source data but target data cell types might be different, which universal domain adaptation method shall be used and what performance will it have on mRNA data?
- How big is the uncertainty of the estimated target gene expressions in the merged target data?
- If time permits: Assuming that cell type information is available in both source and target data, which supervised domain adaptation method is efficient for merging of mRNA data?
- If time permits: How much does the accuracy of the supervised approach differ from the accuracy of the universal approach?

Prerequisites

- Good knowledge of Machine learning, specifically Deep Learning, and Statistics
- Good programming skills

Research Team

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