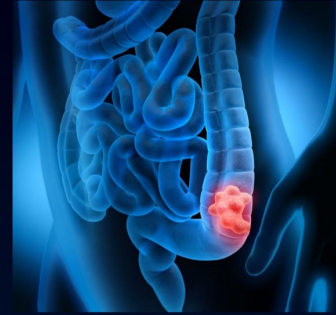# Gene expression signal deconvolution for cell population estimation in tissue

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Introduction

It is well known that cancer is a heterogeneous disease. Due to the heterogeneity, tumors contain different mixtures of individual cell types, which vary, inter alia, according to morphological region and patient. This problem leads to different responses to treatment in individual patients.

Deconvolution of gene profiles is a tool that is able to detect differences in gene expression between several cell populations, which can also be presented in small proportions. The aim of this study is, based on the gene profiles of individual colorectal cancer (CRC) cell types, to estimate the tissue mixture of tumor samples, to build gene patterns which could characterize cell types in the mixtures that will be leading to individual treatment improvement, and to create a complete tool to analyze tumor samples automatically.
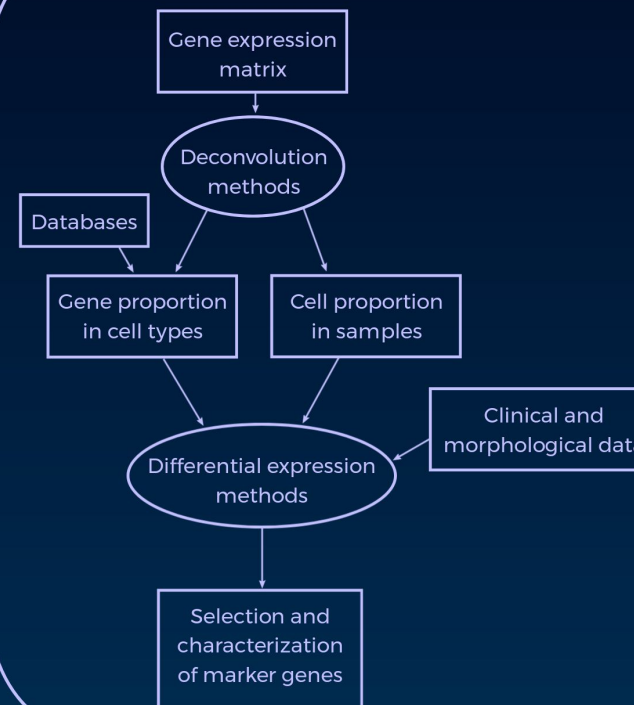
Material

The analysed data contains gene expression of human CRC:
- samples from small macrodisected colorectal regions
- samples with different morphological patterns

serrated

desmoplastic
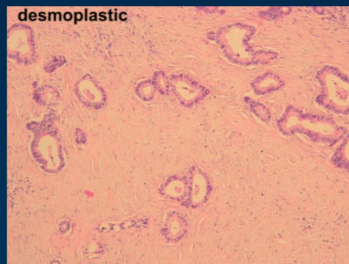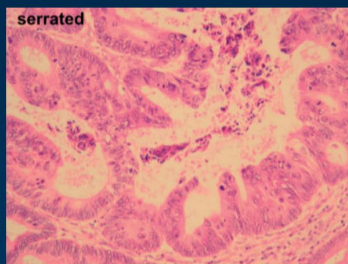
Workflow

Applying deconvolution methods to gene expression data, the proportion of cell types in tumor samples and the proportion of genes in each cell type will be estimated.

Using databases, known marker genes for cell types will be characterized.

Applying differential expression methods and clinical and morphological data to the results, new marker genes will be selected and gene patterns for morphological regions will be created.

References

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