

Titel:

Bioinformatics challenges in the analysis of single-cell RNAseq data

Abstract:

In these last few years, single-cell RNA sequencing (scRNA-seq) techniques have become widely used thanks to the advantages they offer, for example, compared to bulk RNA-seq or microarray. Scientists can interrogate the transcriptome of each single cell composing a tissue, obtaining information at a resolution that was impossible before. Due to the different nature of this data, several new algorithms and tools have been developed to address challenges and opportunities specific of scRNA-seq. Here we present a detailed view of the main steps composing the analysis of scRNA-seq data. We will consider a real dataset generated from a medulloblastoma mouse model by the Pediatric Oncology Clinic of the UKM. In particular, we will focus on the methodological aspects of the analysis as well as the different tools and algorithms that can be used to leverage the opportunities of this data type. Starting from a sparse matrix of gene expression, it is possible to investigate the data in terms of cellular heterogeneity, presence of specific cell types, identification of tumoral vs. non-tumoral cells, differential expression between cell clusters and many others. Finally, we will show how scRNA-seq can help the investigation of the biological mechanisms driving medulloblastoma tumors and can be successfully applied in different medical settings.