

Looking for marker genes in healthy and cancer tissues.

Marker genes are genes that have expression profiles able to distinguish the sub-populations of cells present in the data. They are used to annotate cell types and “understand” their biology. In cancerous tissues they are used to identify cancer subtypes and thus to fine-tune therapies. Complex pathologies (in particular cancer) are characterized by strong variability at the molecular level. Each patient has a different way of developing cancer. A precise tailoring of therapies requires rapid identification of the particular cancer subtype and of the altered pathways of the patient. This is typically done using marker genes which are often themselves the targets of the therapy. However marker genes are typically selected using clustering algorithms and their choice is strongly influenced by the choice of the algorithm, with large uncertainties and, in some cases, contradictory results. A physicist’s point of view in this game can greatly improve the quality of the results and enhance their robustness. In this talk I will discuss a few results obtained in this context in our group in the past few years. In particular I will discuss the use of probabilistic models and of algorithms based on a hierarchical version of stochastic block modelling to identify marker genes.

Role

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