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“Characterisation and modelling of the tumour micro-environment”

Abstract:

Given the recent discoveries about the importance of specific interactions between immune and cancer cells, understanding the spatial properties of tumors at single-cell resolution becomes crucial. We have recently developed computational tools to describe spatial patterns and clustering of specific cell types in tissues using network theory. These approaches allow us to extract statistical properties from imaging or spatial-omics datasets that can be used as biomarkers. We will describe software to extract cellular networks from imaging or spatial-omics datasets and analyze spatial patterns by defining cellular neighborhood states across lung cancer samples. Some of the identified patterns can constitute biomarkers and aid in prediction of response to immunotherapy.

Finally, we will discuss our planned strategy to achieve an understanding of the dynamics of cellular interactions and phenotype transitions that can help us better target therapies in a personalized medicine approach. These models involve a combination of agent-based and logic modeling to represent processes at play in the tumor microenvironment at different levels. A major challenge remains in bridging the gap between literature based model construction and purely data-driven approaches, which are necessary to make the models patient-specific and clinically relevant.