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Description

Cancer is one of the leading causes for disease and death in Europe with millions of people being diagnosed or dying because of it. In addition, billions of euros need to be injected into the system to fight these diseases. Cancer tumours are extremely heterogeneous entities with complex subclonal structures that interact with normal cells surrounding them. This complexity causes that many patients to not respond to treatment or become resistant to it shortly after it is initiated, causing profound suffering to them and their families. Single cell RNA sequencing (scRNA-seq) and other single cell technologies have revolutionised the field of molecular biology opening up unforeseen chances to investigate the cellular heterogeneity of tissues, organs and even full organisms.

Numerous studies have applied these technologies to unveil the heterogeneity behind different types of cancer tumours deciphering their cell type composition, metabolic pathways that are altered and normal cellular components that are surrounding the malignant tissue. We propose to go a step further by using single cell multi-omics data to parametrise patient specific tumour models and simulate their temporal, dynamic behaviour. We aim to investigate the complex dynamics among competing subclones and the ability of tumours to relapse after treatment. Also, we want to simulate the effect of therapeutic targets modulation, by virtually modifying the expression of specific genes identified from multi-omics and interpret the impact of such modification as a function of time. Furthermore, we can investigate the effect of modifying relative subclonal abundances and understand competition mechanisms and the relapse ability of some subclones and the gain of resistance to therapies.

We think that this project can be of importance to develop novel computational frameworks that can be applied in the clinic to assist health professionals to make decisions about how to treat patients.

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Source URL (retrieved on 22 jun 2024 - 18:16): <https://www.bsc.es/ca/research-and-development/projects/sc2cancermods-sello-excelencia-gonzalo-parra-single-cell-multi>