

# Computational oncology: from biomedical data to models and back

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Cancer is a disease responsible for around 8 million deaths per year (around 13% of all deaths in 2008), and whose worldwide impact is projected to continue rising, with an estimated 13 million deaths in 2030 (as of an estimate by the World Health Organization). Finding a cure to cancer is definitely challenging, as there are as many different types of cancer as human cells, and the progression of the disease is heterogenous across individuals. Often, histologically identical tumors have few genetic features in common, and thus reconciling heterogeneity across tumour types and patients is one of the main areas of research in the community.

In the last years, thanks to the development of new high throughput sequencing technologies that measure the genomic content of cancer cells at different resolutions, the new field of Cancer Evolution has emerged. In this field, carcinogenesis is described as an evolutionary process driven by the accumulation of genomic aberrations, and complex methodologies are used to retrieve the life history of analyzed tumours. At a broad level, this opens up for the opportunity to create models that recapitulate heterogeneity, and that elucidate how genomic events orchestrate diseases initiation and progression. So doing, we can anticipate a cancer's next step, and eventually implement personalized treatment strategies that are tailored to each patient.

Computational modelling is one of the key methodologies used in Cancer Evolution. In this talk, I will give a brief introduction to the problems in the field, from a computer science perspective. I will overview some of the major computational challenges, and the kind of data can be used to approach them. The talk will span from (very basic) cell/ cancer biology, to a discussion of what types of mathematical models can be used to describe cancer growth/ therapy, and what Data Science challenges we have to face to implement successful strategies for cancer data analysis.