

Title: Computational modelling of cancer sequencing data

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Cancer is a complex evolutionary process characterised by several type of somatic alterations, spanning from simple somatic mutations to more complex chromosomal alterations. Next generation sequencing technologies provide the mean to measure such lesions at a good resolution. We can therefore use such measurements to understand the genetic organisation of a tumour, its makeup in terms of lesions and use this information to understand its dynamical patterns of growth. In this lectures you will be introduced to common analyses in the field of bioinformatics and machine learning applied to cancer genomics, trying to reduce the complexity of the cancer to the key ingredients of its evolutionary process. Practical data-analysis sessions will be carried out in R.

Requirements: RStudio.