Quantifying the evolutionary dynamics of cancer

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about

- Wednesday
- Building 5 Paraninfo (Envases de Cartón)
- 12:00 – 13:00

Cancer results from a stochastic evolutionary process characterized by the accumulation of mutations that are responsible for tumor initiation, progression, immune escape, and drug resistance, as well as mutations with no effect on the phenotype. Mathematical modeling, combined with clinical, sequencing and epidemiological data, can be used to describe the dynamics of tumor cell populations and to obtain insights into the hidden evolutionary processes leading to cancer. I will present recent approaches for quantifying the evolutionary dynamics of cancer in patients, and their implications for deciphering cancer heterogeneity and response to therapy.

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