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Inferring the Phylogeny of Cancer Cells

Cancer cells accumulate large amounts of genetic aberrations as they proliferate, inducing an evolutionary process inside the tumour. Recent advances in sequencing technology allow us to probe intra-tumour heterogeneity, with the objective of elucidating the evolutionary dynamics of cancer.

I will outline the unique challenges of cancer phylogenetics and describe two approaches we have developed in this area. The first approach uses a Bayesian nonparametric model to deconvolve cancer cell subpopulations from bulk sequencing data. The second approach is a tree reconstruction method tailored to cancer evolution.