The Reconstruction of Cancer Phylogenies

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Cancer is an evolutionary process. As tumours grow, they acquire mutations, some of which may give individual cells a selective advantage and lead to clonal expansion of descendant cells. The presence of multiple competing lineages leads to widespread intra-tumour heterogeneity in treatment naïve tumours, although selective pressures may reduce the level of heterogeneity at key evolutionary bottlenecks, such as the acquisition of treatment resistance or the ability to metastasise to secondary sites.

The advent of Next Generation Sequencing (NGS) has enabled the detailed study of the genomics of cancer evolution, usually through multi-sampling of tumours across either the spatial or temporal dimension. However, which is the best method for inferring and visualising cancer phylogenies is controversial.

I will compare the various methods that have been used to reconstruct tumour phylogenies and describe the advantages and disadvantages of different visualisations. I will also describe attempts to benchmark methods for phylogeny reconstruction. Finally, I will outline extensions that enable the tracking of cancer cell populations during invasion and metastasis.