

Combining CS and Biology: Algorithms for comparing and summarizing tumor trees

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Tumors evolve as part of an evolutionary process where distinct sets of genomic mutations accumulate in different cell lineages descending from an original founder cell. A better understanding of how such tumor lineages evolve over time, which mutations occur together or separately, and in what order these mutations were gained may yield important insight into cancer and how to treat it. Thus, in recent years there has been an increased interest in computationally inferring the *evolutionary history* of a tumor – that is, a rooted tree where vertices represent populations of cells that have a unique complement of somatic mutations and edges that represent ancestral relationships between these populations. However, accurately inferring these trees is often a challenging process. In this talk, I will discuss several methods designed in my lab that address issues related to the inference of tumor evolution. This includes methods to compare these trees that take into account the unique structure of tumor evolution and both graph and optimization based methods that are able to create a consensus tree from a set of conflicting tumor evolutionary histories.

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