Algorithms for Inferring Evolution and Migration of Tumors

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Cancer is an evolutionary process driven by somatic mutations that accumulate in a population of cells that form a primary tumor. In later stages of cancer progression, cells migrate from a primary tumor and seed metastases at distant anatomical sites. I will describe algorithms to reconstruct this evolutionary process from DNA sequencing data of tumors. These algorithms address challenges that distinguish the tumor phylogeny problem from classical phylogenetic tree reconstruction, including challenges due to mixed samples and complex migration patterns.