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Mathematical model for cancer evolution from whole-genome sequencing data

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Mathematical model for cancer evolution from whole-genome sequencing data
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A hallmark of cancer is its heterogeneity in molecular signatures. During the course of disease, the tumor might include a diverse collection of genetically distinct subpopulations across disease sites or temporal variations in the mutational makeup of single cells. The medical intervention may further change the mutational landscape of the tumor and disease progression. Because of this, there is a need for an accurate assessment of tumor heterogeneity for the development of effective therapies and prognosis. We discuss the mathematical theory for inferring the cancer growth structure from whole-genome sequencing (WGS) data. The theory takes into account the sampling process and data preprocessing procedures, both of which are integral to the production and analysis of sequencing data yet so far has not been considered from a mathematical viewpoint. We present the results from fitting data from 19 WGS samples of colon cancer with mutator phenotype, and 10,000 WGS samples of different cancer subtypes (data from The Cancer Genome Atlas). Inference of the tumor growth from these results will also be discussed.