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Analysis of the copy number profiles of several tumor samples from the same patient reveals the successive steps in tumorigenesis

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Cancers arise from an accumulation of genetic and epigenetic alterations, through which cells acquire the properties required for malignancy. Unraveling the sequence of alterations driving tumorigenesis is crucial to understand the biological mechanisms underlying tumor initiation, invasive progression and metastasis. The idea of analyzing several tumor samples, such as recurrences or metastases, from a single patient has recently gained popularity in the cancer research community [1,2].

Here, we present a computational method, TuMult, for reconstructing the sequence of copy number changes driving carcinogenesis, based on the analysis of several tumor samples from the same patient. We demonstrate the reliability of the method with simulated data, and describe applications to three different cancers, showing that TuMult is a valuable tool for the establishment of clonal relationships between tumor samples and the identification of chromosome aberrations occurring at crucial steps in cancer progression. This work was recently published in Genome Biology [3].

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