Detecting genomic alteration in genomic profiles: the infinite population case

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Résumé

Two states Markov Jump process can be used to model alterations in genomic profiles along a chromosom (0 for normal state and 1 for alteration) in a normal cell. Detecting recurrent alterations among a set of patients based on genomic profiles help to identify genomic regions and potentially genes involved in the disease process. This may be formalized within a statistical test procedure and require to characterize the lengths of the excursions above a given threshold for the process of the cumulated profiles. This work has been done when the size of the cohort is small. When the size of the population increases, we prove that the cumulated process tends to an Ornstein Uhlenbeck (OU) process and we have a bound for the rate of convergence. We prove that this rate of convergence also holds for the convergence of the longest excursion.

Mots-Clés: Ornstein Uhlenbeck, excursion, Geomic Alteration

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