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Random Sequences and Genomic Analysis

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April 2, 2001

Abstract

A crucial problem in genomic analysis is to distinguish "biologically significant" signals in sequences from those that are part of the ground noise. To this end, biological sequences are compared with those expected to be met "by chance." Models of random sequences frequently used in this perspective will be briefly described, as will be analytical methods (developped notably in the Algorithms Project at Inria!) and experimental methods (random sequence generation) used to solve these problems. Then, recent works on random sequence generation according to a model that is more constrained that those studied so far will be presented, together with a framework in which it applies to the study of genomic sequences.