

A LINEAR ALGORITHM FOR THE DETECTION OF EVOLUTIVE TANDEM REPEATS¹

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ABSTRACT

We present here a linear algorithm for the detection of evolutive tandem repeats. An evolutive tandem repeat consists in a series of almost contiguous copies, every copy being similar (using Hamming distance in this article) to its predecessor and successor. From a global view point, evolutive tandem repeats extend the traditional approximate tandem repeat where each copy has to be in a neighbourhood of a given model. Due to the lack of algorithms, these repeats have been discovered in genomic sequences only recently. In this article, we present a two-stage algorithm, where we first compute an array containing all the Hamming distances between candidates, then we visit this array to build a complete evolutive tandem repeat from insulated pairs of copies. Moreover, we explain how it is still consistent with the usual technique devoted to dynamic programming which consists in filling a comparison matrix and backtracking through it to find an optimal alignment.

Keywords: Linear algorithm, evolutive tandem repeats, Hamming distance

1. Introduction

The notion of approximate tandem repeat is generally well-defined, from the formal view point [2, 12], it uses a consensus model, every copy participating to this repeat

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