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South African Computer Journal - Detection of recombination in variable number tandem repeat sequences

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- Abstract

Tandem repeats are repeated sequences whose copies are adjacent along the chromosomes. They account for large portion of eukaryotic genomes and are found in all types of living organisms. Among tandem repeats, those with repeat unit of middle size are called minisatellites. These loci depart from classical loci because of the propensity to vary in size due to the addition or the removal of one or more repeat units. Due to this polymorphism, they prove useful in genetic mapping, in population genetics, and forensic medicine. Moreover, some specific tandem repeat loci are involved in diseases, like the insulin minisatellite, which is implicated in type I diabetes and obesity. Those loci also undergo complex recombination events. Presently, some programs to compare tandem repeats alleles exist and yield good results when recombination is absent, but none correctly handles recombinant alleles. Our goal is to develop an adequate tool for the detection of recombinant among a set of minisatellite sequences. By combining a multiple alignment tool and a method based on phylogenetic profiling, we design a first solution, called MS_PhylPro, for this task. The method has been implemented, tested on real data sets from the insulin minisatellite, and proven to detect recombinant alleles.

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