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Efficient Algorithms for Computing the Transformation Distance Between Minisatellites

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Minisatellites are genomic subsequences commonly used to understand the dynamic of mutations in particular for inter-allelic gene conversion-like processes at autosomal loci. Jobling et al. have characterized the Y-specific locus MSY1, a haploid minisatellite, which is composed of 48 to 114 copies of a repeat unit of length 25, rich in AT and predicted to form stable hairpin structures. These sequences are of great interest since they constitute markers for Y chromosome diversity: therefore they allow to trace male descendence proximity in populations. We show how to compute efficiently the evolution distance between these loci.