Development of new bioinformatic tools to analyze the HLA genetic system - (session: Novel Algorithms for Bioinformatics)

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In the human genome, the HLA genetic system is characterized by the highest complexity level and SNPs density among humans. Our group at CRIBI has developed many bioinformatic tools useful to build and maintain a database containing most of the official sequences for the WHO Nomenclature Committee For Factors of the HLA System.

Our tools have been envisaged to analyze and make the public HLA sequences more informative and to make easier the detection of short oligonucleotides useful as typing PCR primers.

First of all, we have produced a database that represents a good starting point for HLA sequence data analysis. In fact, one of the first finding was the detection of several inaccuracies in the IMGT/HLA database, that is the best immunogenetic resource publicly available.

The most innovative feature is a new aligning method among oligonucleotidic and allelic sequences based on ibridisation thermodinamic parameters. This program calculates these parameters using the most reliable algorithms, predicting the melting temperature of the hybrid also in case of mismatches.

This method allowed to develop a specific program that finds out all putative reaction probes or primers, which are then selected on the bases of their capability to identify groups of alleles, permitting to realize full typing kits. Another program simulates, on a thermal gradient, a PCR-based typing reaction against all HLA alleles, also revealing non-specific allele amplification that may produce wrong typing interpretation.

Some other utilities are available at our web address http://grup.cribi.unipd.it/projects/HLA