Analyzing resistance phenomena in HIV with bioinformatics methods

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ABSTRACT

We report on research that is targeted towards understanding the resistance phenomena that HIV undergoes in the presence of selective pressure presented by combination drug therapies. The ultimate goal of this research is to support the physician with helpful models for HIV resistance and to aid his decision as to how to adapt his therapy to the resistance phenomena observed in a patient.

The talk will present the medical background of the problem and the following major results:

1. The Arevir database collecting data on HIV resistance. The data are derived from two sources, namely from genotyped patients (wrt to the dominant HIV strain observed in their blood serum) together with their medical history and from in-vitro measurements of the resistance of many HIV strains against single HIV drugs.

2. Statistical learning methods for predicting the resistance of a given HIV strain against single HIV drugs. This software is available via the geno2pheno server on the internet under http://www.genafor.org

3. New bioinformatics contributions that present a model of HIV resistance against combination drug therapies and makes suggestions for therapy adaption that take estimated future mutational path of the virus into account.

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REFERENCES


