

VIROLAB: a Distributed Decision Support System for Viral Disease Treatment

Peter M.A. Sloot¹, Alfredo Tirado-Ramos¹, Gokhan Ertaylan¹,
Breannan O Nuallain¹, D. van de Vijver², Charles A. Boucher²,
and Marian Bubak^{3,4,1}

¹ Section Computational Science, Faculty of Science, University of Amsterdam,
Kruislaan 403, 1098 SJ Amsterdam, The Netherlands

² Utrecht University Medical Center, The Netherlands

³ AGH University of Science and Technology, Krakow, Poland

⁴ ACC Cyfronet AGH, Krakow, Poland

emails: [sloot,alfredo,gokhan,bon]@science.uva.nl,
C.Boucher@azu.nl, bubak@agh.edu.pl

Abstract

The HIV drug-resistance interpretation systems are used routinely throughout the world in a clinical setting. More knowledge is rapidly becoming available upon which clinical decisions could be made. This knowledge, information, data and evidence from many sources are combined within a Decision Support System (DSS) to provide coherent judgements on drug-susceptibility. At the core of the DSS is a HIV drug-resistance interpretation system incorporating knowledge from the principal systems (Stanford HIVdb, Rega, ANRS, Virolab) in use throughout the world.

We describe an improved rule-based language which has adequate expressiveness and enjoys a fully-specified, formal semantics, allowing for automated reasoning over rule sets. Among the questions which can be addressed are:

- Ambiguity: Is the rule set internally ambiguous? Does it allow more than one interpretation?
- Completeness: Does the rule set have complete coverage?
- Consistency: Are there rules in the set which make contradictory predictions?
- Redundancy: Do some rules of a rule set subsume others?
- Dissonance: How do rule sets differ in their predictions?
- Predictive power: Can one rule set make more specific predictions than another or can it make predictions in cases where the other is silent?

The formal language which we present has a well-defined semantics that will allow for making judgements of the above kinds using reasoning that is either completely automated or at least semi-automated.

Furthermore recent findings have revealed the need to express multiplicative effects of certain mutations on drugs. The state of the art language for specifying HIV drug interpretation rules, ASI, in its present form, is limited to linear combinations of effects.

In future work we will use Bayesian hierarchical modelling to make predictive distributions in the presence of uncertainty. The full chain of analysis will combine Bayesian hierarchical modelling with probabilistic decision analysis based on utility attribution and/or multi-objective optimisation of such quantities as cost, chance and duration of survival or quality-adjusted life years.

Acknowledgements. This work was done within the Virolab project using the Virolab Virtual Laboratory experimental environment (see www.virolab.org). For more details see: P.M.A. Sloot, A. Tirado-Ramos, I. Altintas, M.T. Bubak, and C.A. Boucher: *From Molecule to Man: Decision Support in Individualized E-Health*, IEEE Computer, (Cover feature) vol. 39, nr 11, pp. 40-46. November 2006.