## An advanced expert rule system for HIV drug resistance prediction in the BioNumerics<sup>®</sup> Software

D. Michielsen, K. Janssens, P. Vauterin, B. Pot, L. Vauterin Applied Maths NV, Keistraat 120, B-9830 Sint-Martens-Latern, Belgium

**INTRODUCTION:** The Human Immunodeficiency Virus (HIV), the causative agent of AIDS, is a highly mutable lentivirus, a member of the Retroviridae, with a RNA encoded genome. HIV has the *gag/pol/env* gene organization typical of retroviruses. Automated drug resistance predictions, based on mutation rules for the *pol* gene, are frequently used for HIV. Unfortunately, resistance rules are often trapped in closed systems, hiding which rules are fired and what events causes them to fire. Within the BioNumerics® software environment, we developed an open expert system that allows researchers to create, adapt and (re)evaluate their own expert rules in combination with publicly available rule sets. The flexibility and power of this tool can easily be demonstrated with publicly available HIV data<sup>1</sup> and drug resistance algorithms<sup>1,2</sup> which allow the prediction of (combinations of) successful anti-retroviral drug therapies, based on the known SNPs in the HIV *pol* gene.



Applied Maths NV; http://www.applied-maths.com; info@applied-maths.com; tel: +32-9-2222100

1) http://hivdb.stanford.edu/ 2) http://www.kuleuven.be/rega/cev/links/rega\_algorithm/index.htm