

Título:

Estimation of HIV models using nature-inspired optimization methods and black-box modeling tools

Enquadramento (Indicar adicionalmente Ramo/Área de Especialidade caso aplicável):

Considerable attention has been devoted to the modeling of HIV infection in order to provide tools that can assist in analyzing and predicting the evolution of the disease [1]. HIV infected patients require a life time therapy since the virus cannot be eradicated to date. In real life, therapy interruptions may occur, due to heavy secondary effects. Such therapeutic interruptions may be planned to minimize the secondary effects by using the mathematical tools and models.

Nature-inspired algorithms (Genetic Algorithms, Particle Swarm Optimization, Ant Colony) are state-of-the-art techniques to deliver heuristic optimization tools without requiring explicit knowledge of the gradient of the problem to be optimized. These optimization techniques are being applied in different fields such as forecasting, feature selection, logistics, among others. In the present work these optimization tools are going to be applied for mathematical modeling of HIV dynamics. The infection dynamics are modeled by mathematical (differential) equations which represent the main kinetics of the infection: the viral load, the healthy and the infected CD4+ T-cells kinetics. The model parameters are then tuned using optimization algorithms with real patient data. The modeling is used for individual HIV patients to help for an early diagnosis of the evolution of the infection.

Protease Inhibitors (PI) are common therapy drugs used to treat HIV infection. An inevitable consequence of the virus high mutability rate is the emergence of drug resistant variants. Drug resistance represents a foremost barrier to the successful treatment of HIV patients and clinical awareness of HIV drug resistance is a major issue towards an efficient antiretroviral therapy. In this work black-box modeling techniques, such as fuzzy modeling, artificial neural networks and support vector machines will be used to model the mechanism governing the interaction between the PI drug and virus susceptible parts.

The competences required for these tasks come from mathematical modeling and gradient free optimization that are typically taught in the Intelligent Systems area.

Objetivos:

The work of this thesis consists of the application of mathematical modeling to the HIV virus in a twofold approach:

- modeling the HIV infection dynamics using nature-inspired optimization tools, such as Genetic Algorithms, Particle Swarm Optimization and Ant Colony;
- modeling of docking mechanisms, which consisting of virus/drug interaction, using black-box modeling tools, such as Neural Networks, Fuzzy Models and Support Vector Machines.

Based on the latter tasks , a *consensus approach* tool will be designed using a Fuzzy Inference Systems to provide a decision support system that can help prescribing a given drug therapy.

[1] Lengauer, T. & Sing, T. Bioinformatics-assisted anti-HIV therapy. Nature Reviews Microbiology(4) 790-797, 2006.

Requisitos (e.g. média, disciplinas concluídas):

Sistemas Inteligentes, Controlo Óptimos, Sistemas Estocásticos, conhecimentos de Matlab e domínio da língua inglesa.

Resultado esperado:

- Pre-processing of patient data. Definition of an optimization problem for the HIV infection model. Implementation of nature-inspired optimization algorithms for parameter estimation. Simulation and validation of model using suitable criteria.
- Definition of modeling problem for the HIV / PI interaction mechanisms using black-box models. Implementation of black-box modeling tools for model estimation. Comparison of model quality using suitable criteria.
- Development of software toolbox.

Observações:

Trabalho de tese atribuído ao aluno Gonçalo Farinha.

Localização da realização da dissertação:

IST - Centro de Sistemas Inteligentes/IDMEC