McGill University Research Centre on Complex Traits
MRCCT

Dr. Vladimir Reinharz, PhD

Department of Computer Science, Ben-Gurion University, Beer-Sheva, Israel

Title : "HCV and HBV Virus Dynamics and Parameters Estimation in a Multiscale Model with Age, with and without Treatment"

Thursday, October 4, 2018

Karp Amphitheater | Room 501, 1:00 PM

Bellini Bldg - *Goodman Cancer Research Centre*

"Mathematical modeling of Hepatitis C (HCV) dynamics provides important insights to the process of HCV infection. It has improved our understanding of intracellular viral genome dynamics. The standard biphasic model for HCV kinetics during treatment has profoundly contributed to our assessment of the effectiveness and to our knowledge of the mechanism of action of interferon-alpha (IFN) and ribavirin as well as a comprehensive understanding of the nature of viral kinetic patterns observed in patients under treatment. Multiscale models for HCV kinetics are an extension to the classical biphasic model.
The multiscale models consider the intercellular viral RNA in an additional equation for the variable (R), with the introduction of age-dependency in addition to time-dependency, making it a partial differential equation (PDE) model. They are considerably more difficult to solve and to perform parameter estimation on compared to the biphasic model. We developed an efficient numerical solution to solve the multiscale model. We follow this strategy by providing a parameter estimation method.
In contrast from previous approaches, our strategy does not rely on any canned method but we fully implements our own Levenberg–Marquardt routine, thus making it suitable to our multiscale model equations by modifications inside the routine and an early preparation of the multiscale equations by taking their derivatives with respect to the parameters we would like to estimate. We show how our method can reproduce known HCV viral dynamics with and without treatment and estimate the parameters of the treatment. Finally, we extend our method to the Hepatitis B virus (HBV) with has different dynamics. We show that Agent Based Modelling and our method can reproduce some of the kinetic patterns but not the non-multiscale models"

LOCATION: Karp Amphitheater - Room #501, 1:00 PM

HOSTED BY Dr Jérôme Waldispühl