Wednesday, March 6, 2013

Stochastic models of cell populations with hierarchical structure and latently cell activation and viral blip generation in HIV-1 patients

Daniel Sanchez Taltavull. Centre de Recerca Matemàtica (CRM)

In this talk I will present the work I have done during my thesis. In the first part I will show you a stochastic model of cell differentiation.

Tissues in higher organisms exhibit a hierarchical structure where only a small number of stem cells have the potential for indefinite division. The descendants of the stem cell population undergo a process of maturation where, after a series of intermediate differentiation steps, a fully matured cellular type emerges. In general, mature cells have no replicative potential whereas cells belonging to the intermediate stages gradually loose their stem cell-like properties. Acquiring a proper understanding of this process is important for many reasons but one of the more pressing issues is related to the fact that disregulation of the maturation process leads to cancer. However, many questions related to the regulation of this process remain unclear. Our aim is to examine some of these open questions.

In second part I will show you a model of the behaviour of the HIV-1 when therapy is applied. Although potent combination therapy is usually able to suppress plasma viral loads in HIV-1 patients to below the detection limit of conventional clinical assays, a low level of viremia frequently can be detected in plasma by more sensitive assays. Moreover, many patients experience transient episodes of viremia above the detection limit, termed viral blips, even after being on highly suppressive therapy for many years. An obstacle to viral erradication is the persistence of a latent reservoir for HIV-1 in resting memory CD4+T cells. Motivated by viral persistence in HIV+ patients, we present a stochastic model of HIV viral dynamics, considering the diffussion of virus and cells in the blood stream.