

FIRST WORKSHOP

"DYNAMICAL SYSTEMS APPLIED TO
BIOLOGY AND NATURAL SCIENCES "

1-3 FEBRUARY 2010
CMAF, LISBON UNIVERSITY

ABSTRACT | Jaime Combadão

Title

Long term evolution of viral virulence, a model based on HIV characteristics

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Abstract

The Human immunodeficiency virus (HIV) has an interesting infection profile. It reaches a high viral load soon after infecting a new host, declining rapidly to a latent stage, that has a lower viral load. Importantly, the viral load in this latent stage has a correlation with the duration of this stage. In the end, a highly infective late stage is reached, with a high viral load but with a short time window of activity. The pattern of viral genetic variation changes in each of these stages, being the latent stage the one that is bounded by a stronger selective force by the host immune system. By individual based, stochastic models, we have studied the evolution of virulence on homogeneous populations, where each individual has a number of evolving viral sequences. We studied the pattern of neutral genetic variation and some simple models of adaptive genetic variation, and compare these quantities with the HIV epidemics characteristics. Particularly, we followed the sequence genetic signature related with the evolution of virulence and R_0 .

