



Hamilton Institute

A Phylogenetic Hidden Markov Model for
Immune Epitope Discovery

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Abstract

We describe a phylogenetic model of protein-coding sequence evolution that includes environmental variables. We apply it to a set of viral sequences from individuals with known human leukocyte antigen (HLA) genotype and include parameters to model selective pressures affecting mutations within immunogenic (epitope) regions that facilitate viral evasion of immune responses. We combine this evolutionary model with a hidden Markov model to identify regions of the HIV-1 genome that evolve under immune pressure in the presence of specific HLA class I alleles and may therefore represent potential T cell epitopes. This phylogenetic hidden Markov model (phylo-HMM) provides a probabilistic framework that can be combined with sequence or structural information to enhance epitope prediction.

Venue: Seminar Room, Hamilton Institute, Rye Hall, NUI Maynooth

Time: 2.00 - 3.00pm (followed by tea/coffee)

Travel directions are available at www.hamilton.ie

