



BiRC talk– open to all

Speaker: Matthew Hartfield, MIVEGEC-Centre IRD de Montpellier, France
Title: The effect of individual variation on evolutionary emergence of pathogens
Time: Wednesday 13 November 2013, 14:15 - 15:00
Venue: Bioinformatics Research Centre, Build.1110-Aud 223, C.F. Møllers Allé 8, 8000 Aarhus C

Abstract:

Pathogens can rapidly evolve due to their high mutation rates and replication ability. This immense variation, particularly at the individual level, can have a huge impact on the emergence probability of new epidemic strains, or can act to maintain already established chronic strains in the population. In this seminar I will present aspects of my current work, both theoretical and empirical, on this current topic. First, I will describe a phylogenetic method to determine to what extent infection outcomes caused by Hepatitis C are affected by variation in genotypes. We show that for HCV subtypes 1 and 3a, phylogenetic differences in the virus can explain around 65% of variation in infection outcomes, once host effects have been accounted for. Next, I will describe a mathematical model for investigating the probability that weakly-spreading pathogenic strains can mutate and trigger larger outbreaks. The existence of the first strain can interfere and limit emergence of secondary, mutated strains, and we highlight this outcome with an application of our model to a Chikungunya virus outbreak on La Réunion island.

After the talk there will be beer/soda/coffee and chips in the coffee room on the 4th floor.

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