

# Cologne Evolution Colloquium

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## **Modelling influenza population dynamics: the role of selection in global and single-host viral populations**

Influenza is a global disease, yet its evolution is driven by individual infection and transmission events. RNA segments of the influenza virus very rarely undergo recombination, such that interference effects between selected mutations at different loci greatly affect viral evolution. We here describe two approaches to understanding the role of selection in the evolution of the influenza virus, each accounting for interference between alleles. Analysing the global evolution of the H3N2 influenza strain, we describe a model of allele frequency dynamics given additive selection across multiple loci. We find that substitutions in the haemagglutinin gene of the virus are driven more by interference effects between alleles than by the inherent effects of selection. Next, considering data at the within-host level, we examine sequence data from a transmission study of H1N1 influenza in pigs. Applying a coarse-grained quasi-species model to time-resolved sequence data, we infer what was the role of selection during the course of an individual infection.

Wednesday, January 29, 2014, 17:00  
University of Cologne, Institute for Genetics  
Seminar Room 0.46

Hosted by Michael Lässig

Molecular Basis of  
Evolutionary Innovations

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