KÖLNER Theoretisch-Physikalisches KOLLOQUIUM Cologne Evolution Colloquium

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Evolution of influenza: Statistical genetics far from equilibrium

The human flu virus undergoes rapid evolution, which is driven by interactions with its host immune system. We describe the evolution of viral genomes in terms of a non-equilibrium statistical mechanics model. This model successfully predicts the evolution of influenza one year into the future. Thus, evolutionary analysis transcends its traditional role of reconstructing past history. This has important consequences for public health: evolutionary predictions can inform the selection of influenza vaccine strains. We discuss the conditions of predictability and its links to cooperative phenomena and universality. These links highlight the key role of statistical mechanics in making evolutionary biology a predictive science.

Friday, April 25, 2014, 16.30 h Theoretical Physics Seminar Room

Coffee is served at 16.10 h in the library.