Wednesday, December 5  
4:00 p.m. – SWIG Boardroom (CIT 241)  

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"A predictive fitness model for influenza"  

The seasonal human influenza A (H3N2) virus undergoes rapid evolution, which produces significant year-to-year sequence turnover in the population of circulating viral strains. Adaptive mutations occur primarily in antigenic epitopes, the antibody-binding domains of the viral surface protein haemagglutinin. Here we develop a fitness model for haemagglutinin sequences that predicts frequency changes in the viral population from one year to the next. In particular, the model accurately predicts influenza's characteristic punctuated pattern of epitope amino acid substitutions. We discuss consequences for the epidemiology of influenza and other fast-evolving pathogens.  

Hosted by Daniel Weinreich