Fitness seascapes and adaptive evolution of the influenza virus

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The seasonal human influenza A virus undergoes rapid genome evolution. This process is triggered by interactions with the host immune system and produces significant year-to-year sequence turnover in the population of circulating viral strains. We develop a dynamical fitness model that predicts the evolution of the viral population from one year to the next. Two factors are shown to determine the fitness of a viral strain: adaptive changes, which are under positive selection, and deleterious mutations, which affect conserved viral functions such as protein stability. Combined with the influenza strain tree, this fitness model maps the adaptive history of influenza A. We discuss the implications of our results for the statistical theory of adaptive evolution in asexual populations. Based on this and related systems, we touch upon the fundamental question of when evolution can be predicted.

[1]Joint work with Marta Luksza, Columbia University