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Evolution of Influenza H3N2: A random walk in high dimensions

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Abstract

Influenza H3N2 has been circulating in human populations since the 1960s. After infection, individuals become resistant to the infecting strain, but become susceptible to reinfection when the virus mutates. The hemagglutination inhibition (HAI) assay measures the distance between two strains by testing how well antibodies generated from the first strain can inhibit the second strain. Multi-dimensional scaling (MDS) is a technique for finding a set of points in a low dimensional space based upon their pairwise distances. Using MDS, researchers have shown that HAI data can be represented in only two dimensions with very little error. Does this mean that the underlying evolutionary dynamics of influenza are two dimensional? Sadly, no. As I will show, the observed data is likely generated by a random walk of very high dimensions.