

A Bayesian Non Parametric Model for the Characterization and Clustering of Antigenic Variability in Influenza

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Resumo/Abstract:

Vaccination is one of our main tools against Influenza, however the continuous evolution of viral immunogenic proteins to evade human immunity, known as antigenic drift, is one of the major challenges for this strategy. Thus, every year, a new vaccine must be designed to take into account the influenza strains of the following flu season. To this end, a better understanding of the process of antigenic drift and characterization of seasonal antigenic variability in Influenza is paramount. The phylogenetic Chinese restaurant process is a Bayesian non parametric model that integrates information from viral molecular evolution and reactivity of immunogenic proteins to characterize clusters of viral variability. The model is used to evaluate the effect of genetic evolution on viral antigenicity. Additionally, it is compared to different methods for the same type of data.