

Birth and Death Models with Time Dependent Rates Applied to Virus Phylogenies

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Abstract

In this thesis we use a modified birth and death process to model phylogenetic trees reconstructed from sequence data that has been sampled at different times. This is common in organisms where major evolutionary changes can occur in a short period of time, such as viruses, and therefore the dating of the sampling is of great importance. Our main focus is on birth and death processes with time dependent rates, instead of previously used constant rates. Here we apply our model on eight phylogenetic trees reconstructed from different genome segments of influenza A virus. The evolution of influenza virus is affected by the interplay with our immune system, which makes it possible to infer epidemiological parameters from its sequence data. For example the effective reproductive number over time, which is the average number that one infected individual will infect in a population consisting of not only susceptible individuals. It is known that influenza outbreaks have a seasonal behaviour. Our aim with this thesis is to investigate if this seasonal behaviour can be detected using birth and death processes with periodic rate functions on the phylogenetic trees of the influenza A virus. Furthermore, we also want to infer the effective reproductive number. As a main result, models with periodic rate functions have a better fit to the data than constant rate models.

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