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Inferring epidemiological dynamics of infectious diseases using Tajima's D statistic on nucleotide sequences of pathogens .

The estimation of the basic reproduction number is essential to understand epidemic dynamics, and time series data of infected individuals are usually used for the estimation. However, such data are not always available. Methods to estimate the basic reproduction number using genealogy constructed from nucleotide sequences of pathogens have been proposed so far. Here, we propose a new method to estimate epidemiological parameters of outbreaks using the time series change of Tajima's D statistic on the nucleotide sequences of pathogens.