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Prediction of amino acid substitutions on the hemagglutinin molecules of influenza A viruses

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概要

Human influenza viruses mutate from time to time, causing annual epidemics worldwide. Given the high mutation rate of the viral gene, it is difficult to select an effective vaccine strain prior to each influenza season. In order to elucidate the pattern of viral evolution, we introduce a bioinformatics technology that analyzes a large number of epidemic strains in a multidimensional space. We found that the relative sequence distances among past epidemic strains could be predicted by a mathematical model. Retrospective tests for 12 years showed that the model could predict the direction of viral evolution with high accuracy. Through these technologies, we investigate the past, current and future evolution of influenza A viruses.