

Abstract Submitted
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Low-dimensional clustering reveals new influenza strains before they become dominant JIANKUI HE, MICHAEL DEEM, Rice University — Influenza A virus has been circulating in the human population and has caused three pandemics in the last century (1918 H1N1, 1957 H2N2, 1968 H3N2). The newly appeared 2009 A(H1N1) has been classified by the World Health Organization (WHO) as the fourth pandemic virus strain. We here consider an approach for early detection of new dominant strains. We first construct a network model and apply it to the evolution of the 2009 A(H1N1) virus. By clustering the sequence data, we found two main clusters. We then define a metric to detect the emergence of dominant strains. We show on historical H3N2 data that this method is able to find a cluster around an incipient dominant strain before it becomes dominant. For example, for H3N2 as of 30 March 2009, we see the cluster for the new A/BritishColumbia/RV1222/2009 strain. Turning to H1N1 and the 2009 A(H1N1), we do not see evidence for antigenically novel 2009 A(H1N1) strains as of August 2009. This strain detection tool combines a projection operator with a density estimation.

Jiankui He
Rice University

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