Cornell University Library

We gratefully acknowledge supporting institutions

arXiv.org > q-bio > arXiv:1204.6313

Search or Article-id

(Help | Advanced search)

All papers | Go!

Quantitative Biology > Populations and Evolution

Low-dimensional clustering detects incipient dominant influenza strain clusters

Jiankui He, Michael W. Deem

(Submitted on 27 Apr 2012)

Influenza has been circulating in the human population and has caused three pandemics in the last century (1918 H1N1, 1957 H2N2, 1968 H3N2). The 2009 A(H1N1) was classified by the World Health Organization (WHO) as the fourth pandemic. Influenza has a high evolution rate, which makes vaccine design challenging. We here consider an approach for early detection of new dominant strains. By clustering the 2009 A(H1N1) 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 identify a cluster around an incipient dominant strain before it becomes dominant. For example, for H3N2 as of March 30, 2009, the method detects the cluster for the new A/British Columbia/RV1222/2009 strain. This strain detection tool would appear to be useful for annual influenza vaccine selection.

Download:

- PDF
- Other formats

Current browse context:
q-bio.PE
< prev | next >
new | recent | 1204

Change to browse by:
q-bio

References & Citations

- NASA ADS

Bookmark (what is this?)

ScienceWISE

Submission history

Which authors of this paper are endorsers?