LETTER TO THE EDITOR

Bioinformatic methods to analyze annual perspective changes of influenza viruses

To the Editor,

The recent report on "bioinformatic methods to analyze annual perspective changes of influenza viruses" is very interesting.1 Hu et al1 "designed a systemic analysis method to evaluate annual perspective sequence changes of influenza virus strains" and further used a tool, "PHYLIP 3.69," for epitope search; they concluded that the proposed combinatorial bioinformatics method was effective. In fact, the usefulness of bioinformatic tools in treating infectious and tropical diseases has been confirmed.2 Focusing on the present report, the selected tools seem to be appropriate and good for prediction purpose. However, several tools are available for tracing annual perspective change and finding epitopes. Specifically focusing on annual perspective change, Google Flu Trends, a tool that is widely used presently, should be mentioned.3 This tool (Google Flu Trends) can be easily assessed using Google and the updated current situation can be seen.3 Nevertheless, any computational bioinformatic tool has its limitation.4 Focusing on PHYLIP, there are many upgraded applications to increase the ability of this tool. A good example is WebPHYLIP, which allows Internet manipulation of PHYLIP.4

References


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