Overview

Influenza Research Database (IRD, www.fludb.org), funded by the National Institute of Allergy and Infectious Diseases, serves as a single publicly-accessible repository of integrated datasets and analysis tools for influenza virus research.

IRD Integrates Data from External Sources and Generates Novel Data from Internal Computational Pipelines

- Influenza Strain Details page shows that the HA sequence of the A/jiangsu/4/2007 strain carries the 110N PVT substitution which has been shown to increase binding to alpha 2-6 receptor in the publication cited.

- Novel Sequence Annotation and Analysis Tools in the Influenza Research Database (IRD)

- Integrated with IRD analysis tools including Sequence Variation Analysis and metadata-driven Comparative Analysis Tool for Sequences (meta-CATS)

- Provides comprehensive enriched influenza virus sequence annotations
- Supports custom sequence annotation, analysis, and visualization

HA Subtype Numbering Conversion

- Based on the HA subtype numbering scheme by Burke and Smith (2014)  
- Automatically convert the coordinates of any HA protein sequences to coordinates of any other subtypes, in order to map functional domains or phenotype markers across subtypes

- Integrated with IRD analysis tools including Sequence Variation Analysis and metadata-driven Comparative Analysis Tool for Sequences (meta-CATS)

Custom Metadata Capturing

- New utility for capturing user-provided sequence associated metadata
- Analyze and visualize user-provided sequence data and metadata along with IRD data using any IRD tools

Figure 4. A phylogenetic tree constructed from a combination of user-provided (downloaded from GISAID) and IRD sequences. Tree leaves colored-coded by subtype. User-provided sequences are highlighted in green.

References


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