Phenotypic Sequence Feature Variant Type (SFVT) Annotation Tool

Influenza sequences in IRD are annotated with 3,445 experimentally characterized regions termed “Sequence Features” (SF), as well as the predicted phenotypic effects of selected sequence variations. In this release, a new tool has been added that allows users to annotate their personal sequences with the locations of Sequence Features and to determine if their sequences carry particular Phenotypic Variant Types (PVT) in which particular sequence substitutions are predicted to give phenotypic effects, such as increased virulence or antiviral drug resistance. To access this annotation tool, mouse over the “Analyze & Visualize” drop-down menu and click “Identify Sequence Features in Segments”.

New Host Factor Data

In collaboration with the Michael Katze Laboratory, Department of Microbiology, University of Washington in Seattle, IRD has released two more host factor studies within the Host Factor Experiments component. Both studies evaluated the transcriptional response to influenza virus (H7N9, H7N7, H3N2, H1N1, and H5N1 subtypes) infection by microarray analysis, using either human cell line or mouse models. Details of the studies are reported in PMIDs 24496798 and 24991006. These data can be further explored in IRD using various analysis tools, for example, expression pattern summaries, host factor comparisons across biosets or experiments, and GO and pathway enrichment analysis.

Linkouts to Influenza Outbreak Events in EMPRES-i

In collaboration with the Swiss Institute of Bioinformatics and the U.N. Food and Agriculture Organization (FAO), influenza strains and sequences in IRD are now linked to influenza events (e.g. outbreaks) present in EMPRES-i Global Animal Disease Information System and to isolate records present in OpenFlu. To access disease information, follow the EMPRES-I Disease Event ID link on the Strain Details page.

Swine H1 Clade Classification

In collaboration with Tavis Anderson from Georgia Southern University and other swine influenza experts at the USDA the IRD team has developed an algorithm to classify the phylogenetic lineages of all North American swine HA (H1) sequences in IRD. This algorithm uses phylogenetic analysis to classify HA sequences according to the USDA classification scheme and has been verified as highly accurate (>98%) for HA1 sequences > 300 nt. See the SOP document for more details. This classification tool is also available for annotating user provided sequences.

New Features in IRD

IRD Strain Details page linked to Disease Event information at EMPRES-i.

News & Events

Outbreak Events

- June 8-11, 2015: IRD workshop at the Symposium of Computational Resources for Swine Viral Diseases, USDA NCAH campus, Ames, IA
- June 24, 2015: IRD/VIPR Hands-on Workshop, University of Texas Medical Branch, Galveston, TX
- July 11-15, 2015: American Society for Virology 34th Annual Meeting, London, Ontario, Canada. IRD will give talks and host an exhibit booth at the meeting.

Recent IRD Publications