Monthly Webinars

To help you use IRD/ViPR more effectively, we are hosting monthly webinars.

- August 7, 2018: Sequence Feature Variant Type analysis
- Please register here.

News & Events

- August 26-31, 2018: 23rd International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology (VEME), Berlin, Germany. We will teach part of this training workshop.

Influenza Research Database (IRD)

New Features in IRD

Sequence Search API

The IRD/ViPR team has been continuously enhancing the application programming interface (API) into the IRD/ViPR database. The newest version of the API now supports sequence search by sequence-associated metadata. In addition to searching by GenBank metadata fields, such as virus species and collection year, searching by IRD/ViPR annotations are also supported, including:

- IRD/ViPR-annotated subtypes/genotypes for Dengue Virus, Hepatitis C Virus and Rotavirus A
- IRD/ViPR-annotated mature peptides for viruses that encode polyproteins
- IRD/ViPR-annotated genome segments for segmented viruses

Details are described at Support > IRD/ViPR APIs.

Host Factor Visualization with Cytoscape

In the previous release, we added the functionality that allows visualization and analysis of host factor co-expression networks using Cytoscape. Built upon this infrastructure, in this release, 22 more host factor experiments now have pre-computed Cytoscape networks.

To recap, key functionalities provided for host factor data analysis include:

- Gene enrichment analysis: Users can use the CLASSIFI algorithm to determine whether any pathway or biological process is over-represented in a host factor bioset, expression pattern group, or WGCNA module.
- Clustering of genes based on co-expression: Across different experimental samples, genes that are highly correlated in expression levels are clustered into data modules using WGCNA.
- Correlation between WGCNA gene module and associated metadata: WGCNA gene module-metadata (trait) correlations are represented in a heatmap.

Cytoscape visualization of WGCNA gene modules: Each WGCNA module is represented as a separate network, in which host factors are the nodes and edges represent the strength of expression correlation. Users can interact with the networks and highlight each individual node’s edges. These module-specific networks are accessible via Host Factor Experiment > Data Models > Model 2: WGCNA module-metadata correlation heatmap > Choose a model > Data Model Gene Significance page > Visualize as Cytoscape Network.

In future releases, we will add functionalities to support analysis of the computed Cytoscape networks.

The July 2018 release of IRD is now available, visit www.fludb.org

Users can highlight individual nodes’ edges in the Cytoscape network.