New virus portals for Nairoviridae and Hantaviridae

With the reclassification of the Bunyaviridae family as Bunyavirales order, five genera (Hantavirus, Nairovirus, Orthobunyavirus, Phlebovirus, Tospovirus) in the former Bunyaviridae are now novel virus families. To better facilitate the study of these viruses, the ViPR team has been building new virus family collections reflecting these taxonomic changes. In this release, new Nairovirus and Hantaviridae families are now available. The remaining seven new virus families will be available in the September release. Within each virus family site, you can easily search, retrieve, and analyze virus data for the family.

- access integrated data: genomes/segments, proteins, immune epitopes and 3D protein structures.
- use a suite of analysis tools: multiple sequence alignment, phylogenetic tree construction and visualization, metadata-driven comparative analysis, sequence variation analysis, BLAST, short peptide search, PCR primer design, genome annotation, etc.
- store and share data via your Workbench

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 biotset, 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.