Visualizing consequences of genetic variation in biological networks

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Summary

The Variation app for Cytoscape 3 establishes a genomic location for genes on nodes in a biological network, associates variations with those genes from a variety of local or remote resources, and then sources or predicts consequences of those variations for further analysis and visual mapping.

Features

- Feature view
- Variation view
- Variation consequence view
- Visual mappings
- Discrete color mapping for Sequence Ontology (SO)-annotated consequence terms

Resources

- Ensembl REST APIs
- SnpEff-annotated VCF files
- Ensembl VEP-annotated VCF files
- Global Alliance for Genomics and Health APIs
- Google Genomics APIs

Google Summer of Code (GSoC) 2014

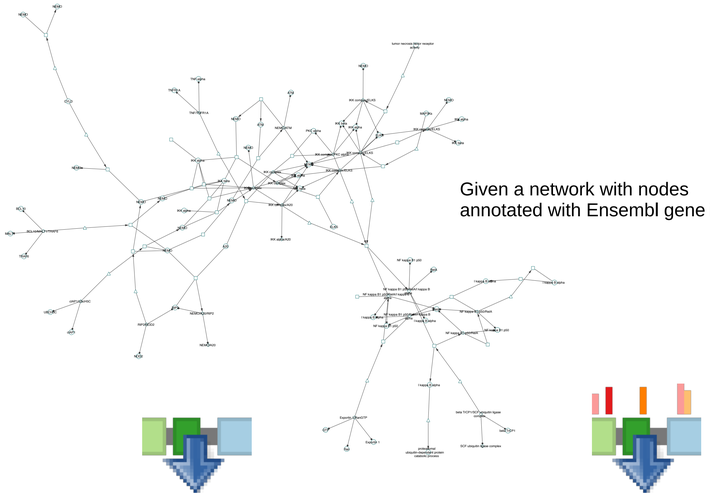
Under the 2014 National Resource for Network Biology (NRNB) GSoC program:

- Support for ADAM genome analysis system
- Additional compound visual mappings

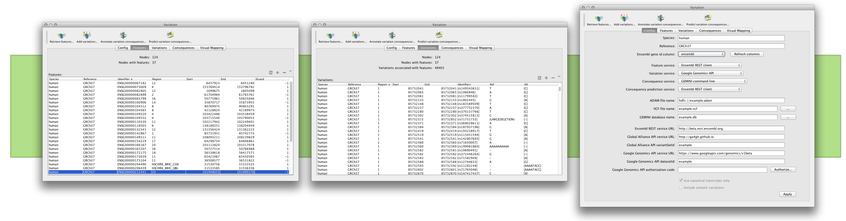
Availability

The Variation app for Cytoscape 3 is licensed GNU Lesser General Public License (LGPL), version 3 or later.

Versions 1.0 and later are available on the Cytoscape 3 App Store at http://apps.cytoscape.org/apps/variation.



Given a network with nodes annotated with Ensembl gene ids



Retrieve features

- All genomic features associated with the nodes in the current network are displayed in the Feature view

Add variations

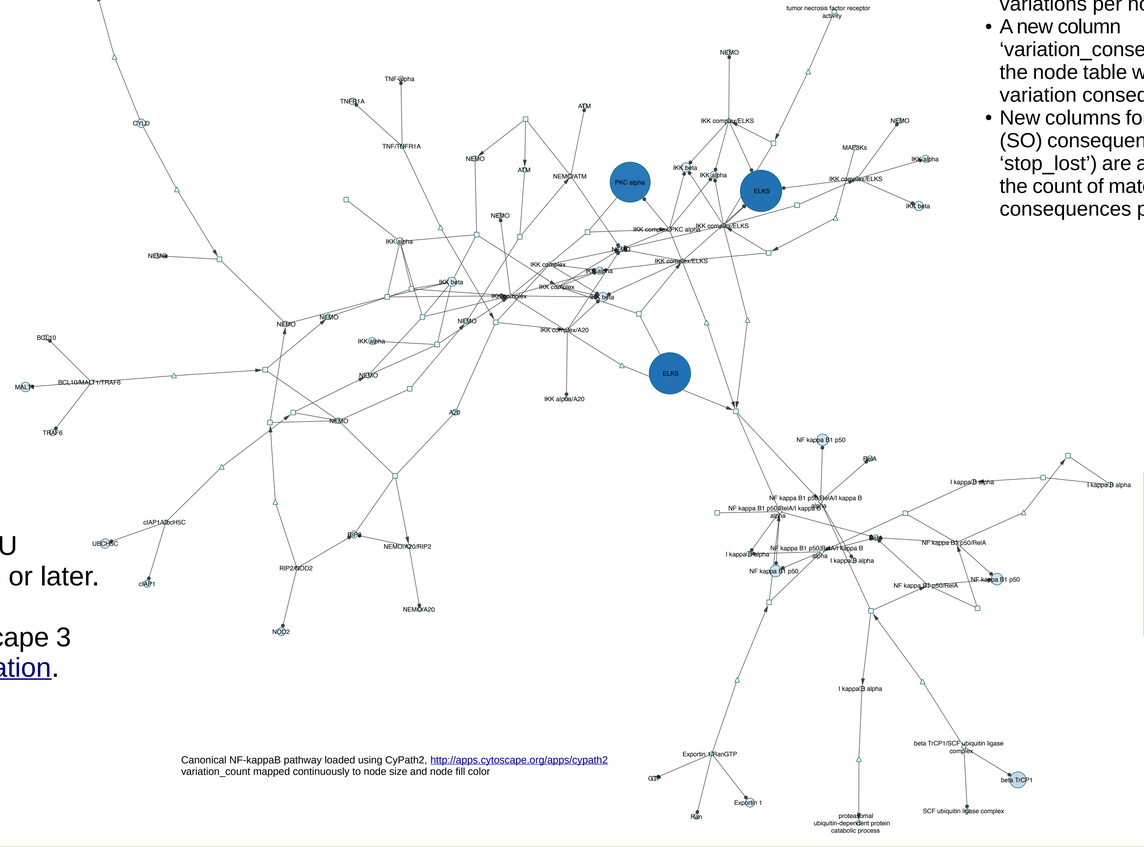
- All variations associated with the genomic features associated with the nodes in the current network are displayed in the Variation view
- A new column ‘variation_count’ is added to the node table with the aggregate count of variations per node

Annotate variation consequences

- All variation consequences for all variations associated with the genomic features associated with the nodes in the current network are displayed in the Consequence view
- A new column ‘variation_count’ is added to the node table with the aggregate count of variations per node
- A new column ‘variation_consequence_count’ is added to the node table with the aggregate count of variation consequences per node
- New columns for each Sequence Ontology (SO) consequence term (e.g. ‘stop_gained’, ‘stop_lost’) are added to the node table with the count of matching variation consequences per node

Predict variation consequences

- All newly predicted variation consequences for all variations associated with the genomic features associated with the nodes in the current network are displayed in the Consequence view
- A new column ‘variation_count’ is added to the node table with the aggregate count of variations per node
- A new column ‘variation_consequence_count’ is added to the node table with the aggregate count of newly predicted variation consequences per node
- New columns for each Sequence Ontology (SO) consequence term (e.g. ‘stop_gained’, ‘stop_lost’) are added to the node table with the count of matching newly predicted variation consequences per node



Canonical NF-kappaB pathway loaded using CyPath2, http://apps.cytoscape.org/apps/cypath2
variation_count mapped continuously to node size and node fill color