Variation app for Cytoscape 3

Hacking variation-cytoscape3-app from git mirror

Install

- Git, http://git-scm.com/
- JDK 1.6 or later, http://openjdk.java.net
- Apache Maven 3.2.2 or later, http://maven.apache.org

Clone the git mirror repository

```
$ git clone https://github.com/heuermh/variation-cytoscape3-app.git
```

(or fork using the Github web interface and clone the fork)

Install

```
$ cd variation-cytoscape3-app
$ mvn install
```

Package variation-cytoscape3-app

```
$ mvn package
```

Load target/dsh-variation-cytoscape3-app-2.0-SNAPSHOT.jar in Cytoscape 3.1.x or later

Apps → App Manager → Install from File...

Note the git mirror builds, installs, and packages as version 2.0-SNAPSHOT

Hacking variation-cytoscape3-app from svn trunk

Install

- Subversion, http://subversion.apache.org
- JDK 1.7 or later, http://openjdk.java.net
- Apache Maven 3.2.2 or later, http://maven.apache.org

Checkout the dishevelled.org repository

```
$ svn checkout https://svn.code.sf.net/p/dishevelled/code/trunk dishevelled-trunk
```

Install the entire lot (will take a few minutes)

```
$ cd dishevelled-trunk
$ mvn install
```

Package variation-cytoscape3-app

```
$ cd variation-cytoscape3-app
$ mvn package
```

Load target/dsh-variation-cytoscape3-app-1.0-SNAPSHOT.jar in Cytoscape 3.1.x or later

Apps → App Manager → Install from File...

Note svn trunk builds, installs, and packages as version 1.0-SNAPSHOT

Using Variation app for Cytoscape 3

Install from Cytoscape App Store
http://apps.cytoscape.org/apps/variation

Video walkthrough
http://www.youtube.com/watch?v=FIjW0pgL5OY

Retrieve features task

Given a network with nodes annotated with Ensembl gene ids

Apps → Variation

On Config tab set Ensembl gene id column: field to correct node table column

On Config tab set Feature service: combo box to desired implementation

Click the Apply button if any configuration settings change

Click Retrieve features... tool bar button

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

Add variations task

Given a network with nodes annotated with Ensembl gene ids

Apps → Variation

On Config tab set Ensembl gene id column: field to correct node table column

On Config tab set Feature service: combo box to desired implementation

On Config tab set Variation service: combo box to desired implementation

Click the Apply button if any configuration settings change

Click Add variations... tool bar button

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

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 task

Given a network with nodes annotated with Ensembl gene ids

Apps → Variation

On Config tab set Ensembl gene id column: field to correct node table column

On Config tab set Feature service: combo box to desired implementation

On Config tab set Variation service: combo box to desired implementation

On Config tab set Consequence service: combo box to desired implementation

Click the Apply button if any configuration settings change

Click Annotate variation consequences... tool bar button

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

All variations associated with the genomic features associated with the nodes in the current network are displayed in the Variation view

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 task

Given a network with nodes annotated with Ensembl gene ids

Apps → Variation

On Config tab set Ensembl gene id column: field to correct node table column

On Config tab set Feature service: combo box to desired implementation

On Config tab set Variation service: combo box to desired implementation

On Config tab set Consequence prediction service: combo box to desired implementation

Click the Apply button if any configuration settings change

Click Annotate variation consequences... tool bar button

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

All variations associated with the genomic features associated with the nodes in the current network are displayed in the Variation view

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

Visual Mapping tasks

Apps → Variation

Perform any of add variation, annotate variation consequences, or predict variation consequences tasks as described above

On Visual Mapping check visual mapping(s) to perform

Click Apply button to perform visual mapping(s)