Manual

HIVE

Handy Integration and Visualisation
of multimodal Experimental Data

http://vanted.org/hive/
1 HIVE Overview

HIVE is an Add-on for the VANTED system. VANTED is a graph editor extended for the visualisation and analysis of biological experimental data in context of pathways/networks. HIVE extends the functionality by adding the handling of volumes and images, together with a workspace approach, allowing one to integrate data of different biological data domains. HIVE is written in Java and Java3D and utilize Software Design patterns such as the Model-View-Controller concept. To understand how the application can be used, it is highly advised to watch the introdution-video.

The main tasks of HIVE are:

- handling of omics data, networks, images and volumes
- integration of different data types using a graph-based workspace
- combining biological data in different ways and
- manifold visualisations of combined data

1.1 Short Introduction

This section gives you a very short work flow of what can be done with this application. It is highly advised to additionally watch the video (and eventually read the paper). In the section 1.2 you may look up more detailed information. This is advised if you already got a feeling of the structure and interactions in the application.

1.1.1 Importing Data

- use drag and drop directly from the file system or use the tab “Data Sources” (here you have access to a set of example data and several databases)
- if no graph is open or the graph is not saved yet you will be prompted for saving the Integration graph, as it will be the basis of the workspace (all data will be saved in the same directory)
- if the data is not annotated yet, you will be prompted to fill out the metadata of the data files
- the data gets imported into the Metadata View and the Mapping View
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Figure 1.1: Screenshot of the application HIVE, which allows to integrate, combine and visualize data from different biological domains, resulting in views on integrated data. (1): MetadataGraph integrating data at metadata level, (2): MappingGraph integrating data at raw data level, (3): IntegrationViews visualizing combined data, (4): Tab with controls working on the active view.
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1.1.2 Visualising Data

- switch to the Mapping View (Button at the top-left corner of the MetadataView or using the menu “Window”) and select exactly one node
- the “Visualise and Map” tab will show all views able to visualise this raw data
- click at one button and choose a subset of the raw data you want to visualise

1.1.3 Combining Data

- select any number of nodes in the MappingView
- all the data contained in this nodes will be extracted and all mapping functions able to use a subset of this data are shown in the “Visualise and Map” tab
- click at one button and choose a subset of the raw data you want to use as an input and the correct parameter values
- if you selected enough data needed for this mapping function as input a new mapping node will appear in the graph
- resulting mappings can be used again as an input for mapping functions (you may reconstruct a volume from some images and use this volume and an image from another node to perform a Multimodal Alignment, see also Fig. 1.2)

1.1.4 Selecting Data/Working Sets

- switch to the MetadataView (Button at the top-left corner of the Mapping View or using the menu “Window”) and select any number of metadata nodes
- in the “Navigation” tab you will find buttons to extend this selection by selecting all nodes above this node (predecessor nodes) or below this node (successor nodes)
- the button “select paths” will perform both, which allows you to easily select all data contained in an experiment or belonging to a condition
- selected nodes can be hidden or all other nodes can be hidden
- the hiding of nodes will also result in the hiding of nodes in the Mapping View, if the data contained in the node contains metadata equal to the hidden
- mapping nodes are hidden, but still can be visualised and used as input for mapping functions
- raw data import nodes (the four coloured ones) will allow only to map/visualise the selected data (as indicated by the two numbers at the bottom left corner)
Figure 1.2: Two mappings and its indicators: Rounded Rectangles inside the mapping node indicate the type (colour) and number of raw data, which is combined in the mapping. Similarly edges indicate the type and number of raw data, which was used to create the mapping. The left mapping was created under use of 30 omics values and one image. This raw data is copied into the mapping and may be altered according to the mapping functions operations (this means that the image does not necessarily look similar and so on). The right mapping was created under use of 12 images and contains 1 volume. The input images are gone, just the volume remains, as it is the result of applying the mapping function. This volume can be used for other mappings again, as indicated by the rightmost edge.
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Figure 1.3: Dialog to select raw data used as input for mapping functions or visualisations of raw data import nodes: Raw data is coloured according to the type and a tool-tip shows the metadata of this raw data.

1.1.5 Raw Data Indicators

- a colour code is used consistently throughout the application, by linking the data type to a colour
  - volume = blue, omics = red, network = yellow, image = green
  - edges in the MappingView are coloured according to the type of data (see Fig. 1.2)
  - the buttons to execute a mapping functions is coloured according to the type of data needed for this mapping (see Fig. 1.1/4)
  - raw data lists are also coloured (see Fig. 1.3)

- mapping nodes visualise the type of raw data contained in the mapping by using a rounded and coloured rectangle with a number for each data type (see Fig. 1.2)

- if a mapping is visualised and opened in a window, all the raw data contained in the visualised mapping is highlighted in the MappingView (mapping node) and MetadataView (all nodes representing the metadata of the raw data are highlighted). The highlighting is a blue or grey border, depending on the activation of the window the raw data is visualised in (see Fig. 1.4)

1.2 TODO: Details

- for some mapping visualisations there is an additional Tab shown, allowing a user to change mapping-relevant attributes (e.g. network-distance for the Network Stack-
Figure 1.4: When visualising a mapping one can track the tackled raw data by observing the highlighting in the MappingView (not shown) and MetadataView. In later the nodes representing the metadata of the raw data are highlighted. Blue border indicates the metadata of active windows, grey border indicates that this metadata is part of a mapping, which is open in a non-active window.
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• Stereoscopic devices may be used (anaglyphs and polarisation) by accessing the Menu “Window” → “Show Stereodialog”

• 4 buttons in the toolbar with red, green and blue arrow, indicating components to be able to reset the viewpoint of a 3D view

• right-click at the list of models in the control tab, if a 3D view is open → allows you to set the GUI to the selected model, select or deselect all models or delete a model

1.3 Extension of HIVE

Like VANTED, HIVE is also implemented under use of the MVC-concept and therefore quite flexible to be extended. One can create a new mapping function by creating a new subclass of the AbstractMappingAlgorithm. The new class has to implement some methods and will automatically be registered at runtime into a list of all mapping functions. Similarly, this works for AbstractMappingVisualisationAlgorithms. Also due to the plugin-structure of VANTED it is possible to add views, tabs, GUI-components and algorithms by creating a VANTED Plugin or Add-on and adding it when running HIVE. If you plan to extend HIVE please contact Hendrik Rohn (rohn@ipk-gatersleben.de).

VANTED Add-ons may be created on basis of the Exemplary Add-on (Add-on-Example) available at http://vanted.cvs.sourceforge.net/viewvc/vanted/. The HIVE source is also available (Hive Add-on).