

MINERVA platform: manual

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MINERVA platform: User's manual

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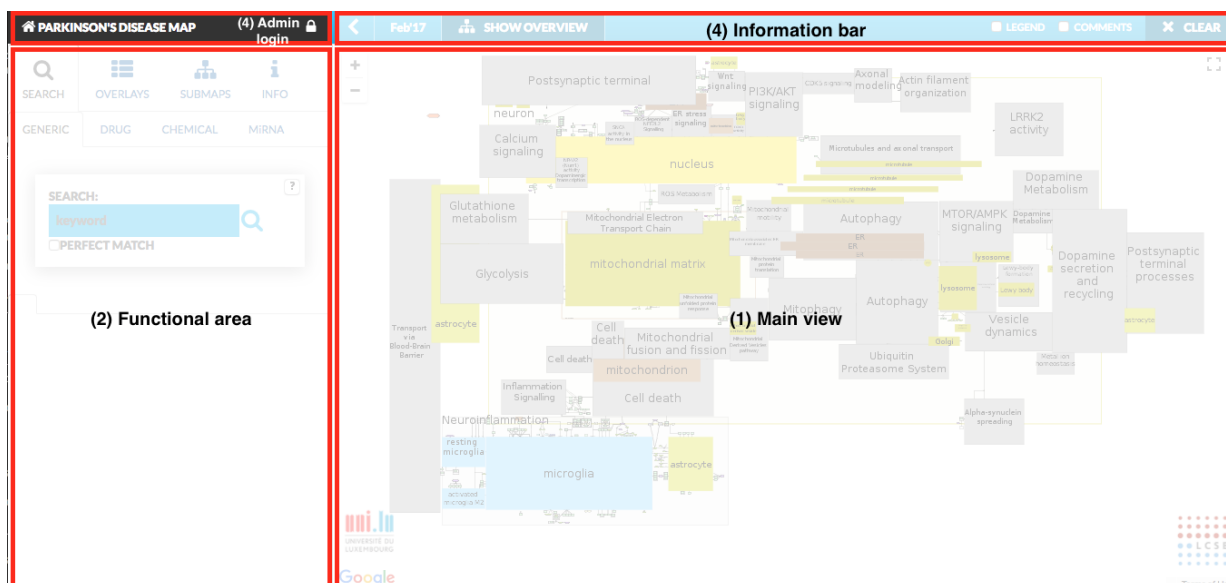
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User view refers to the visualization and functionalities accessed by users of the content hosted by your MINERVA instance.

You can also see the summary of this page in [the MINERVA Quick Reference Guide](#).

Main view

The main view of the MINERVA platform is summarized in the figure below.



Main components of this view are

- **Display area (1)**: where the contents of the projects are visualized
- **Functional area (2)**: allowing for advanced interaction with explored content
- **Information bar (3)**: containing additional overlay functions
- **Admin login (4)**: allowing administrator login. To login as user go to Overlays or Info tab

Accessing the project

Your instance of MINERVA platform can host many projects, which are uploaded via the administrator view (see [Admin manual - Add project](#)). They are accessed by a provided, dedicated web address.

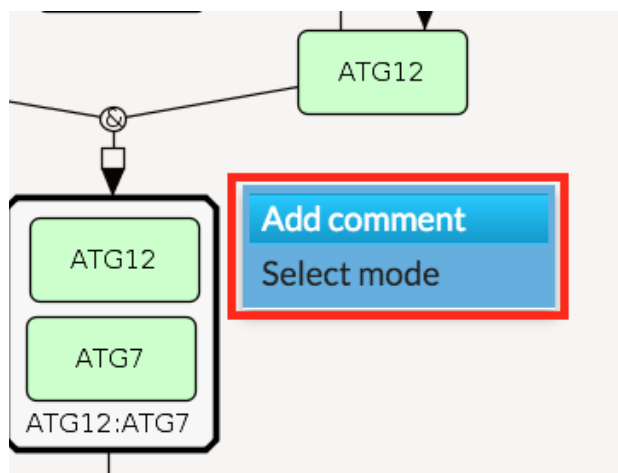
Exploring the display area

The content is visualized using Google Maps API, and allows similar pan and zoom functionalities. The content is interactive, the user can click on an element or interaction to examine additional details displayed in the left panel (functional area).

The content is by default displayed in a semantic zoom mode, where compartments and areas in the submitted file cover underlying elements on higher levels of zoom. This view is generated procedurally, directly from the uploaded content. This view is generated automatically from the layout of the CellDesigner file. MINERVA platform calculates coverage of bigger areas by smaller, and assigns them to appropriate zoom levels. For more details see [Section Content curation](#). You can turn off the semantic zoom view by going to the **Overlays** tab in the left panel (functional area), and changing the view to **Network** (see also [Section Overlays](#)).

Annotating, selecting and downloading the display area

Right-click in the display area invokes a contextual menu with two options - (see below).



Add comment

This functionality allows to annotate contents in the display area. Clicking the **Add comment** button invokes a form that can be filled out by the user and sent to the administrators of the project. The field **Pinned** controls, whether the comment will be visible in the map (see below, left).

COMMENT

Type: Protein: ATG7

Pinned: Yes

Name: Marek

Email: marek.ostaszewski@uni.lj

Content: Review the interaction between SIRT1 and ATG7

Send

COMMENT

Type: <General>

Pinned:

Name: Reaction: re3338

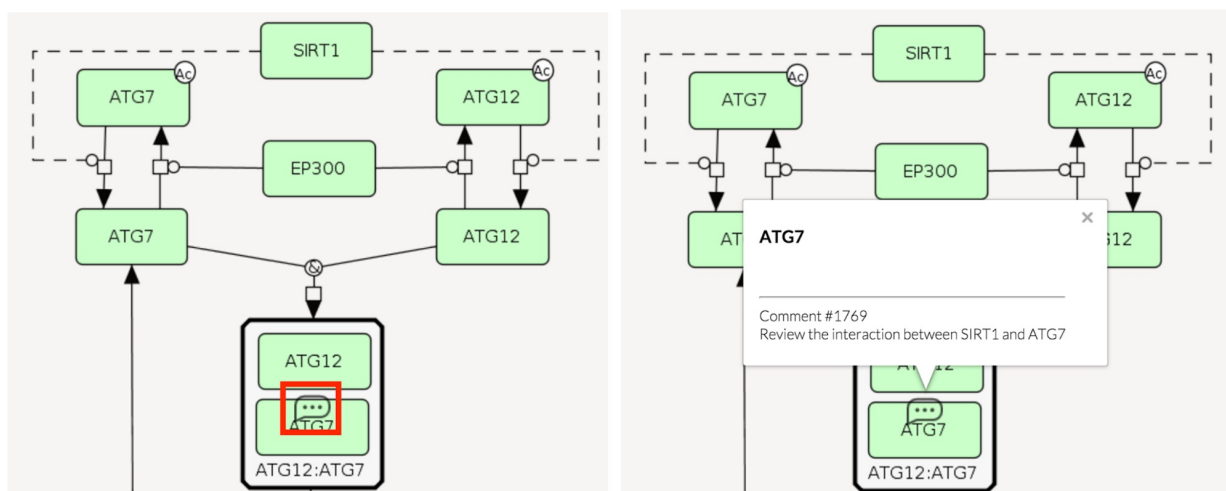
Email: Protein: ATG7

Content:

Send

Type field is a drop-down menu, listing elements nearby to the click location. This allows to choose and attach the comment to a particular element or interaction (see above, right).

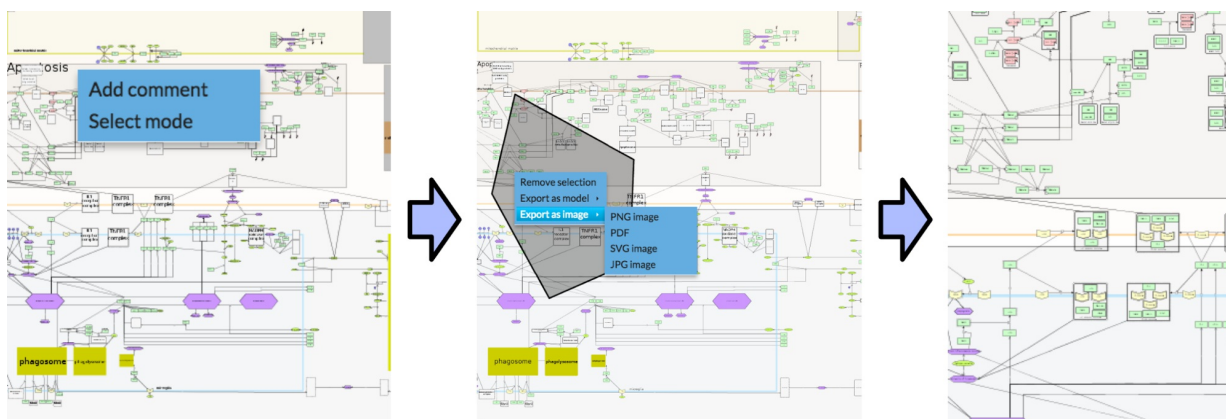
After sending, and if the field **Pinned** was set to **Yes**, the comment becomes visible in the display area, as shown below, to the left (after checking the **Comments** checkbox, see [Comments](#)).



Clicking on the comment bubble displays annotated element and the text of the comment (see above, right). Name and email are not disclosed, they will be accessible only to project and platform administrators (see [Admin manual - Comments](#)).

Select mode

Clicking the **Select mode** enables the functionality supported by Google Maps API, allowing to select an arbitrary shape in the display area. The shape then can be downloaded in various formats, either as a model (.xml file) or as an image (see below).



- **Export as model** produces a file acceptable by either CellDesigner, or pure SBGN editors, containing the editable fragment of the selected display area. Importantly, in the case of CellDesigner export, all additional annotations provided by MINERVA platform are downloaded as well.
- **Export as image** produces a rectangular image containing the selection. Export to vector graphics is supported, allowing to modify and enhance the downloaded image.

Content curation

MINERVA framework handles SBGN-compliant format, produced either by CellDesigner (<http://www.celldesigner.org>) or SBGN editors, like SBGN-ED (<https://immersive-analytics.infotech.monash.edu/vanted/addons/sbgn-ed>). MINERVA relies on such externally curated content.

Moreover, a number of additional functionalities of MINERVA operates on metadata that can be provided in the SBGN-compliant file itself. These are the following:

- **Processing of existing annotations:** annotations to elements or interactions embedded within CellDesigner file (MIRIAM > Add relation) are automatically parsed and processed. They can be used to extensively annotate elements (see [Admin manual - Configure automatic annotation](#)) and they can be verified by MINERVA platform against a set of predefined content-governing rules (see [Admin manual - Configure automatic verification](#)).
- **Procedural generation of semantic zoom** : information on complexes and overlaying compartments is extracted from SBGN-compliant files to generate **Pathways and compartments** view, where on the high level of zoom bigger compartments overlay smaller ones, and on the middle levels of zoom contents of complexes are masked. Moreover, in CellDesigner, TextArea elements can be used to draw named rectangles covering functionally important areas. These will be incorporated into the generation of the semantic zoom as well. For this, you will need to create an additional area by
 - clicking **Edit > Add layer**
 - enabling **Layer** toolbox by checking **View > Change toolbar visible > Layer**
 - drawing **TextArea** objects using a corresponding button
- **Cross-platform SBGN translation:** CellDesigner files can be uploaded to be displayed in pure SBGN notation (see [Admin manual - Fields of the Add project window](#)), and SBGN-displayed content can be downloaded as a pure SBGN file.

For explanation and examples on content curation and annotation, see [Examples - CellDesigner file upload and annotation](#).

Functional area

Functional area (the panel to the left from the display area) displays additional information about selected elements and interactions, allows to query the content, generate custom overlays and browse submaps.

Search tab

Search tab allows to search for particular elements or interactions in the displayed map. Also, under this tab, the panel displays detailed information on selected elements or interactions (see below).

The screenshot shows the MINERVA interface with the Search tab active. On the left, a search panel displays results for 'PINK1' and 'Parkin'. The main area shows a detailed biological network diagram with various cellular components like microtubules, ER, mitochondria, and lysosomes. The search results on the left include details for Protein: PINK1, such as full name, symbol, former symbols, and annotations from Entrez Gene, UniProt, HGNC, and RefSeq.

There are four subtabs available in the **Search** tab, offering different scopes: * **GENERIC** for regular search * **DRUG** for drug target search * **CHEMICAL** for chemical target search * **MIRNA** for miRNA target search

Generic

The generic scope works as follows:

- **Search field:** Type your search query here, separating multiple elements with a semicolon ';'. Searches for separate terms will be visible in separate tabs. Search will look for similar names and synonyms of elements in the map. To search for an identifier of an interaction, you need to add **reaction:** prefix to the searched identifier. The **search** pins indicate hits in the display area. They have different colors for multiple search items and are clickable, showing information as in the left panel.
- **Perfect match** tick box: If this box is ticked, terms with an exact match to the query will be returned. In the case of large networks or broad queries the search results may be capped to ensure the performance of the system. The limit of displaying search results can be configured

via the Admin view (see [Admin manual - Configuration](#)).

Direct link to the elements in the display area is possible, as the search query can be provided within the web address of the displayed project. An address constructed as follows:

```
your.webserver.address/?search='search query'
```

is a link executing the search for a given **search query** in the default project of your MINERVA instance. For example, an address

```
your.webserver.address/?search=reaction:xyz123
```

will directly point to an interaction with id **xyz123**. Referring to a given project on your MINERVA instance requires additionally to pass the project identifier in the address, as shown below. Identifiers of projects are accessible using the Admin view.

```
your.webserver.address/?id='project id'&search='search query'
```

Drug (targets)

The Drug scope works as follows. **Drug** subtab under the the **Search** tab allows to look for known drugs or their brand names and display their targets in the map. Targets will be marked by pins in the display area. Please, note that they have specific shape, different than the results of other search scopes.

- **Search** field: type your search query here, separating multiple drug names or their brand names with a semicolon ';'. DrugBank www.drugbank.ca and ChEMBL www.ebi.ac.uk/chembl/ will be queried for known targets to be displayed in the map.
- Drug description, synonyms and all known targets will be displayed in the left panel.

Chemical (targets)

The Chemical scope works as follows. **Chemical** subtab under the the **Search** tab allows to look for known chemicals or their synonyms and display their targets in the map. Targets will be marked by pins in the display area. Please, note that they have specific shape, different than the results of other search scopes.

- **Search** field: type your search query here, separating multiple chemical names or their synonyms with a semicolon ';'. Clinical Toxicogenomic Database ctdbase.org will be queried for known targets to be displayed in the map.
- Drug description, synonyms and all known targets will be displayed in the left panel.

microRNA (targets)

The MiRNA scope works as follows. **miRNA** subtab under the the **Search** tab allows to look for miRNAs and display their targets in the map. Targets will be marked by pins in the display area. Please, note that they have specific shape, different than the results of other search scopes.

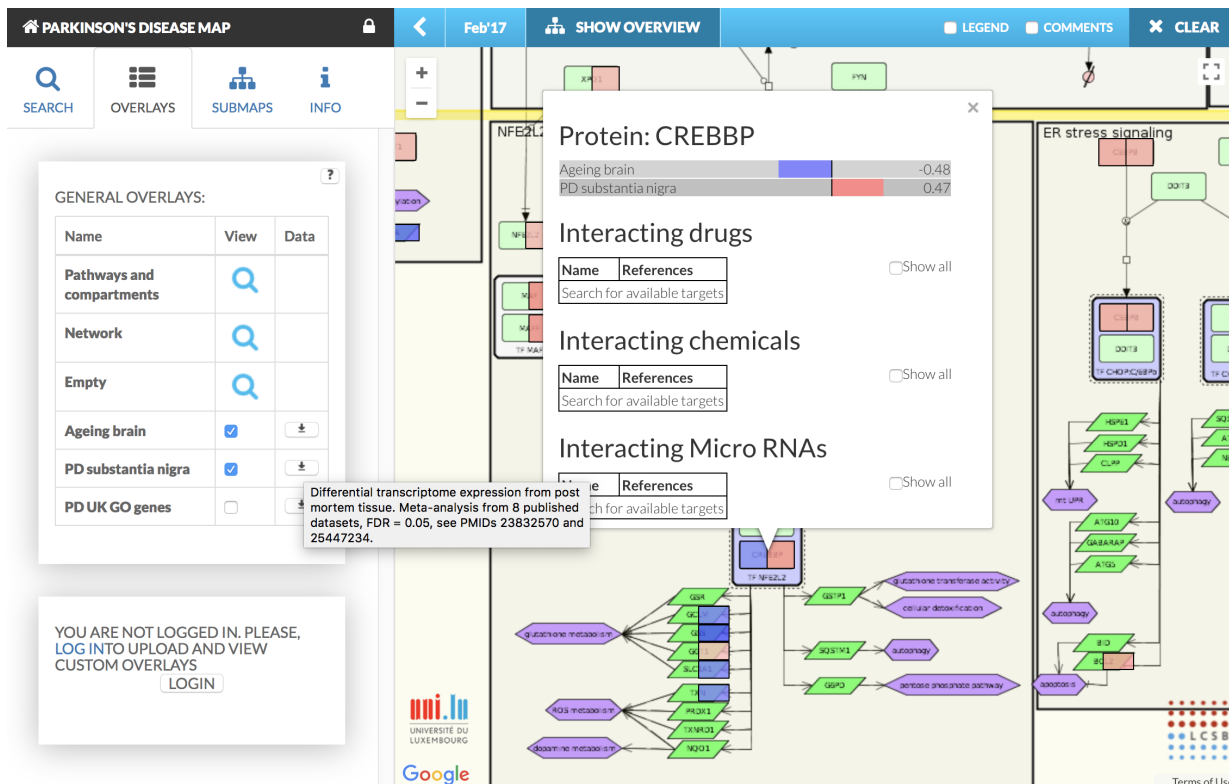
- **Search** field: type your search query here, separating multiple miRNAs with a semicolon ';'. miRTarBase mirtarbase.mbc.nctu.edu.tw will be queried for known targets to be displayed in the map. Use only mature sequence IDs according to www.mirbase.org (e.g., hsa-miR-125a-3p)
- known targets will be displayed in the left panel.

Overlays tab

Overlays tab allows to display or generate custom coloring of elements and interactions in the map. It is composed of two sections - general overlays and custom overlays (see figure below).

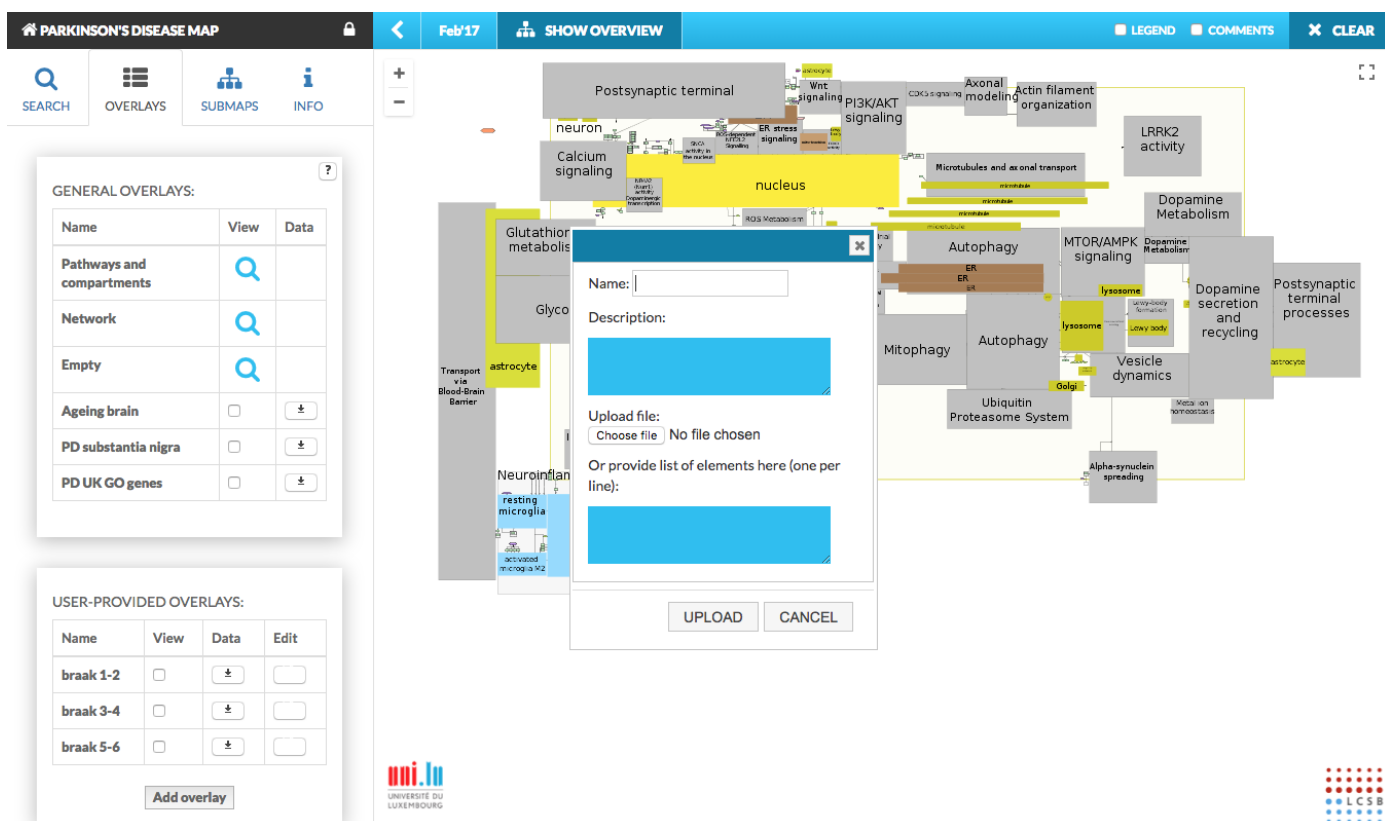
- **View** column allows to
 - Change to viewing mode (click the **magnifying glass** icon) allowing to switch between
 - **Pathways and compartments** (hierarchically masked content)
 - **Network** (only colored network structure shown)
 - **Empty** (only network structure, no coloring, recommended for data display)
 - Display multiple overlays (tick chosen tickboxes)
- **Data** column contains buttons, where applicable, allowing to download the dataset used to generate the overlay. Mouseover over the button displays a short description of the dataset, if provided on upload

Overlays are also visible in the popup menu, with the value and the sign marked on the horizontal color bars (see figure below).



In the figure above:

- **General overlays** are overlays accessible for every user viewing the content
- **User-provided overlays** menu becomes available upon login (see below).



User-provided overlays part contains the following elements (above):

- **List** of uploaded overlays containing
 - **View** column with buttons enabling switching between User-provided overlays
 - **Data** column with buttons allowing the user to download the dataset used to generate the overlay. The users have access only to their respective datasets.
 - **Edit** column with buttons allowing the user to provide description to the uploaded datasets
- **Add overlay** button invoking the dialog window with the following components
 - **Name** field for the new overlay
 - **Description**: description of the dataset
 - **Choose file** button to select a file with overlay data

- **List of elements** field - instead of providing an overlay file, the user can provide a list of named elements to highlight in the map (e.g. list of genes)
- **Upload** button to generate the user-defined

Upload user-provided overlay data

Format

For examples of basic and advanced data upload, see [Examples - user-provided overlay data upload by registered users](#). Description of the format follows below.

Basic format The basic format of file containing the uploaded data is two-column, tab-separated text file, with the columns **Name** and **Value**.

- **Name** column contains the names of elements to be colored
- **Value** column contains the values normalized to [-1,1] range.

Basic format will match names of the elements provided in the **Name** column among the names of elements in a given network and for the matching ones will assign them colors: blue for negative values, red for positive values, with the saturation proportional to the value. The color range for the data upload is customizable in the admin panel.

Advanced format The advanced format allows for by identifier matching, custom color assignment and coloring of interactions. Advanced format foresees two parts of the uploaded dataset - header and body.

Header lines have to start with '#'. It can contain the following elements:

- **Version** **# VERSION=xyz** - a version of this custom overlay
- **Name** **# NAME=xyz** - a name that will be automatically assigned upon upload
- **Description** **# DESCRIPTION=xyz** - a description that will be automatically assigned upon upload

Body is a table with a following set of allowed columns:

- **Name, Value** - same as in basic overlay
- **Compartment** - name of a compartment in which coloring should take place
- **Chebi** - ChEBI identifiers of elements to be colored
- **Entrez gene** - Entrez identifiers of elements to be colored
- **Gene ontology** - Gene Ontology identifiers of elements to be colored
- **Ensembl** - Ensembl identifiers of elements to be colored
- **Hgnc symbol** - HGNC symbols of elements to be colored
- **Uniprot** - Uniprot identifiers of elements to be colored
- **ReactionIdentifier** - ID of interaction to be colored (interactions coloring only)
- **LineWidth** - linewidth of the colored interaction (interactions coloring only)
- **Color** - color of the colored element.

The dataset for upload may be integrated and sparse, i.e. a document may contain all columns at once, and, where irrelevant, their content may be left blank. In other words, you can color interactions and elements in the same dataset, leaving blank fields in **ReactionIdentifier** and **LineWidth** for elements, and leaving blank fields in **Name** for interactions.

Procedure

After choosing the dataset to upload, pressing **Upload** button will invoke a comment, initiate generation and reduce the amount of available custom overlays (see below, left).

You will be notified by email when your overlay is ready. The email will also contain the list of elements in your dataset not found in the map.

Important reminder:

- The number of available overlays is configured in the Admin view (see [Admin manual - User manager](#))
- The number of available overlays is common for all projects hosted on your MINERVA instance. If a user is registered in a number of projects and uploads custom datasets in all of them, the global number of available custom overlays will be reduced with each uploaded overlay.

Submaps tab

The **Submaps** tab summarizes all the submap networks uploaded together and linked to the main network of this project hosted by your MINERVA instance. See [Admin manual - Source file](#) to learn how to upload the submaps together with the main file.

The **Submaps** tab contains the **Name** column, and the column with the buttons invoking corresponding submaps. The submaps show as a pop-up window on top of the main map, and are synchronized with respect to search queries and displaying mapped experimental data. This means that search results and search target bubbles will be visible in the main map and the displayed submaps. Similarly, coloring for overlays are mirrored in the submaps (see figures below).

- **Name** - name of the element
- **Compartment** - compartment containing the element
- **Component** - CellDesigner specific, TextArea covering the element, see also Section 4.1.4. Content curation
- **Type** - SBGN type of the element
- **Id** - identifier in the system
- **Parent complex** - complex element containing this element
- **Submodel** - name of the subnetwork containing this element
- **Annotations** - filters the annotations of elements in the downloaded file; by default all annotation types are considered
- **Included/excluded compartments** - filters the elements by compartments they are in; by default all compartments are considered as “included”, none as “excluded”.
- Network export tab allows to narrow down and download the interactions in the hosted networks. Importantly, the exported network file is not a fixed-column table. As interactions are in fact hyperedges, each line may contain different number of reactants, products and identifiers. Available filters include:
 - **Nodes** - filters the nodes of exported interactions by the SBGN-compliant type
 - **Annotations** - filters the annotations of elements and interactions in the downloaded file; by default all annotation types are considered
 - **Included/excluded compartments** - filters the elements by compartments they are in; by default all compartments are considered as “included”, none as “excluded”.
- Graphics export tab allows to download graphics of the map in the SVG format.

User data

It allows a registered user to type in their login and password, or to request for an account from the administrators of this MINERVA instance. Platform administrators can register new users (see **Section 3.4 User manager**) and configure **Request an account** functionality (see [Admin manual - Configuration](#))

After login, this panel displays information about the user. After the successful login the user gains the possibility to upload custom overlays (see **Section Overlays**).

Information bar

Information bar is the topmost part of the user view, containing the **Show overview** button, **Comment** and **Legend** checkboxes and **Clear button**. The **Clear** button clears all search results currently shown in the display area. The remaining functionalities are detailed below.

Show overview

This button invokes a static image associated with the displayed content. It may be a graphics facilitating the understanding of the underlying network, or any other visual cue that the content curator decided to present. The initial image displayed with the **Show overview** button can be linked to:

- another static image to be displayed next
- a defined area in the displayed content
- a set of elements or interactions.

Detailed information on how to configure **Show overview** images display is provided in [Admin manual - Source file](#).

Comments

If this checkbox is checked, the comments provided by users with **Pinned** option set to **Yes** will become visible in the display area (see also **Section Add comment**).

Legend

If this checkbox is checked, the legend describing element and interaction types will be displayed.

[R3lab homepage](#)

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MINERVA configuration: Administrator's manual

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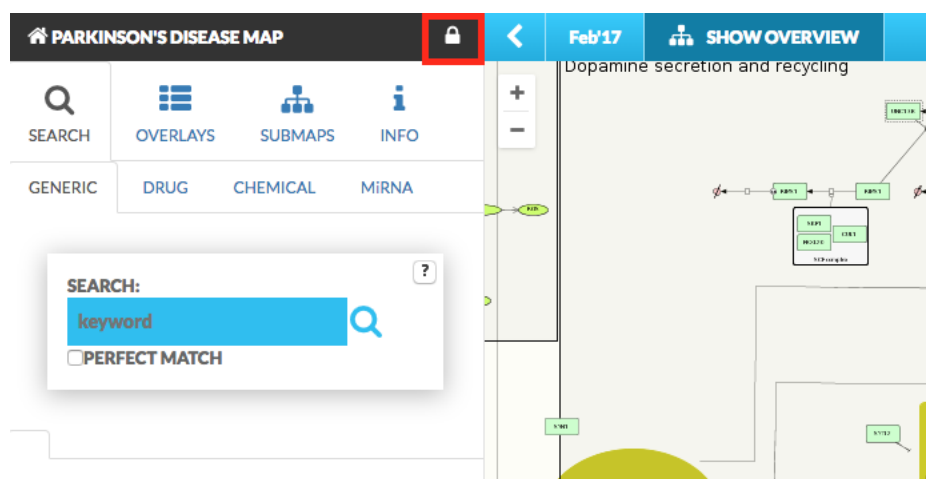
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Administrator view


Administrator view refers to the set of functionalities for web-based management of the content and configuration of your MINERVA instance.

Login

Administrator view is accessible via the button with the **lock icon** in the upper left corner of the user view (see below). See also [User manual - Main view](#)).



Many projects (maps, networks) can be hosted in parallel on a single MINERVA instance (see [User manual - Accessing the project](#)), and a

 PARKINSON'S DISEASE MAP

COMMENTS

MAP MANAGER

USER MANAGER


SERVICE STATUS

CONFIGURATION


MIRIAM

MANUAL


LOGOUT

 Authorization complete

Use main menu to start managing.

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MINERVA version 11.0.8;
build 07/02/2018 10:53;
git: 2d738b4b240eba8eb79d6eeb605e8d5a8500ae27

 LCSB

The removed comment will no longer be visible among the pinned comments, and its status will be updated in the **Comments** panel (see below).

This panel allows you to add new projects and manage existing ones. In the top left corner, the name of current active project is displayed. The panel allows you to (1) add new projects (2) edit them and (3) examine messages generated during the upload of the project.

PROJECTS

ADD PROJECT (1)

ProjectId	Name	Disease	Organism	Status	
empty		N/A	N/A	Ok (100%)	(2)
pdmap		D010300	Taxonomy (9606)	Ok (100%)	
pdmap_mar16	PARKINSON'S DISEASE MAP	D010300	Taxonomy (9606)	Ok (100%)	
pdmap_jun16	PARKINSON'S DISEASE MAP	D010300	Taxonomy (9606)	Ok (100%)	
pdmap_oct16	PARKINSON'S DISEASE MAP	D010300	Taxonomy (9606)	Ok (100%)	
pdmap_feb17	PARKINSON'S DISEASE MAP	D010300	Taxonomy (9606)	Ok (100%) (3)	

This view gives information about: - Disease: the disease associated with the project, the code has to be a valid MeSH identifier, e.g.D010300. This is needed for chemical target search, see [Section User manual - chemical target](#). - Organism: the taxonomy id of the species, for which the map is primarily developed, e.g. 9606.

Detailed map management

The magnifying glass symbol in the last column of the map manager gives access to the management dialogue (see below).

PROJECT DETAIL

GENERAL OVERLAYS DATA MINING USERS

ProjectId:

pdmap_feb17

Name:

PARKINSON'S DISEASE MAP

Disease:

D010300

Organism:

9606

Version:

Feb'17

Description:

The PD map is a manually curated

Notify email:

marek.ostaszewski@uni.lu

Save

Remove

Cancel

- **Save** button saves all introduced changes
- **Remove** button removes this map

There are four tabs available: - **General** - allows to edit information about this map, including disease and species - **Overlays** - allows to manage overlays for this map, both general and user-provided - **Data mining** - obsolete, will be removed in the upcoming version of MINERVA - **Users** - allows to manage users' rights to access and manage this map

Manage overlays tab

This tab allows you to edit the details about the overlays and their ownership. You see here overlays that have been: 1. uploaded with the project (see [Section Add project](#)) - **Important!** overlays named **Pathways and compartments**, **Network** and **Empty** allow for different ways of displaying the map's content, and they don't have any data associated with them. 2. uploaded by the users (see [Section Upload user-provided overlay data](#)) 3. uploaded by the administrators (see this section, below)

In this tab, besides **Name** and **Description**, the following columns are available: - **Directory** - an internal reference for storage at the MINERVA webserver - **Owner** - the user having the access right to a given overlay. Dropdown menu allows to choose from existing users. - **Important!** Choosing the owner to be 'N/A' (top of the list) makes this overlay a **General overlay**, publicly visible for all users - **Data** - action buttons allowing to download the associated dataset of a particular overlay - **Update** - action buttons to save any changes in the configuration of a particular overlay - **Remove** - action buttons to remove a particular overlay

GENERAL OVERLAYS DATA MINING USERS						
(1 of 9) 1 2 3 4 5 6 7 8 9 >> >						
Name	Directory	Description	Owner	Data	Update	Remove
Pathways and compartments	5d734979682bb18de6e3fc32fc8		N/A			
Network	5d734979682bb18de6e3fc32fc8		N/A			
Ageing brain	5d734979682bb18de6e3fc32fc8	Differential transcriptome expression from post mortem tissue. Source: Allen Brain Atlas datasets	N/A			
PD substantia nigra	5d734979682bb18de6e3fc32fc8	Differential transcriptome expression from post mortem tissue. Meta-analysis from 8 published	N/A			
s.nigra	5d734979682bb18de6e3fc32fc8	Riley et al., PMID: 25170892	Stephan Gebel			
striatum	5d734979682bb18de6e3fc32fc8	Riley et al., PMID: 25170892	Stephan Gebel			
(1 of 9) 1 2 3 4 5 6 7 8 9 >> >						
Add overlay						

Manage users tab

This tab contains a table of all users of the system (including the administrators) and allows to assign them rights to this particular map. It contains the following columns of checkboxes: - **Manage comments** - **Manage overlays** - **View project** Ticking a checkbox in a respective column for a given user assigns this privilege to them. Each change needs to be saved with the **Update privileges** button.

User privileges are discussed in detail in [Section User manager](#))

Important! Columns 'Drug targeting advanced view' and 'Edit suggested connections' are obsolete.

Add project

The **Add project** button invokes a menu allowing you to upload your project and start its generation in the MINERVA platform.

PARKINSON'S DISEASE MAP

COMMENTS MAP MANAG **ADD PROJECT**

+ ADD PROJECT

ProjectId \downarrow

empty	
pdmap	
pdmap_mar16	PARI
pdmap_jun16	PARI
pdmap_oct16	PARI
PD_170202_2	PARI
pdmap_feb17	PARI

File:

ProjectId:

Project name:

Project Disease:

Organism:

Complex:

Filename	Name	Root model	Mapping file	Model type	File type
No records found.					

Additional overlays:

Filename	Name	Description
No records found.		

Data mining:

Filename	Name	Description	Source	Type
No records found.				

Overview images:

Filename
No records found.

Version:

Annotate model automatically: ☒ Advanced

Verify manual annotations: ☒ Advanced

Cache data: ☒

Auto margin: ☒

Display as SBGN: ☒

Default network overlay: ☒

Semantic zooming: ☒

MINERVA version 11.0.8;
build 07/02/2018 10:53;
git: 2d738b4b240eba8eb79d6eeb605e8d5a8500ae27

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LCSB

Fields of the Add project window

- **File** - Choose button: invokes a file upload dialog. For a quick start, CellDesigner files are accepted directly. Available options and configurations of the source file are discussed in [Section Source file](#).
- **ProjectId**: a working name of the uploaded project on the MINERVA platform
- **Project name**: the name of the uploaded project displayed in the top left corner of the Admin and User panels; your official name of the project
- **Project disease**: the disease associated with the project, the code has to be a valid MeSH identifier, e.g.D010300. This is needed for chemical target search, see [Section User manual - chemical target](#).
- **Project organism**: the taxonomy id of the species, for which the map is primarily developed, e.g. 9606.
- **Complex**: this section describes how main map and uploaded submaps (if any) are related. For more details on how to upload predefined layouts, data mining datasets, images with biological overview and submaps associated with the main map, [Source file](#). Ignore it if you submit a single file.
 - *Filename*: name of one of multiple files
 - *Name*: name of the main map, or a submap, in the project
 - *Root model*: a column of checkboxes; only one position must be checked, corresponding to the main map in the project
 - *Mapping file*: a column of checkboxes; only one position must be checked, corresponding to the mapping file describing relationships between the main map and the submap(s)
 - *Model type*: whether the submap is a pathway, or a list of downstream targets; this name will appear in the Submaps tab.
 - *File type*: type of the uploaded file; recognized automatically.
- **Additional overlays**: this section describes uploaded additional overlays (element and interaction colorings) to be generated and accessible for all users of the project via **Overlays** tab in the **User panel**. Ignore it if you submit a single file.
 - *Filename*: name of one of custom layout files
 - *Name*: name of the layout visible in the project
 - *Description*: the text to appear after mouseover on the name of the layout.
- **Data mining**: **Obsolete**. Will be removed in the upcoming release.

- **Overview images:** this section describes the uploaded overview images and their configuration file. It is a column of filenames. Ignore it if you submit a single file.
- **Version:** a text field displayed next to the name of your project in the **User panel**.
- **Annotate model automatically:** if this checkbox is checked, elements of the uploaded map will be automatically annotated using built in annotators. Behavior of the annotators can be configured by clicking the **Advanced** button (see [Section Configure automatic annotation](#)).
- **Verify manual annotations:** if this checkbox is checked, elements and interactions of the uploaded map will be scanned for existing annotations; if present these existing annotations will be validated against a set of rules. Verification rules can be configured by clicking the **Advanced** button (see [Section Configure automatic verification](#)).
- **Cache data:** if this checkbox is checked, all hyperlinks in the project resolved by MIRIAM repository (e.g. cross-links to external bioinformatic databases) are resolved and cached.
- **Auto margin:** if this checkbox is checked, upon generation of the graphics, empty spaces surrounding elements and interactions will be cropped.
- **Display SBGN:** if this checkbox is checked, the uploaded model will be displayed in SBGN format, instead of default CellDesigner format.
- **Default network overlay:** if this checkbox is checked, the default view of the map will be **Network** (see **Overlays** tab), without masking of the contents by the compartments and pathways on the higher zoom levels.
- **Semantic zoom:** if this checkbox is checked, detailed semantic zoom is created for the map.

Configure automatic annotation

The **Advanced** button, next to the **Annotate model automatically** checkbox under **Add project** button, invokes a dedicated configuration window (see below).

ANNOTATORS DETAIL

Object Annotators

▼ Element

Compartment (1)

▼ Species

Gene (5)

Unknown

▼ Chemical (2)

Ion (2)

SimpleMolecule (2)

ComplexSpecies (1)

AntisenseRna

Phenotype (1)

▼ Protein (5)

IonChannelProtein (5)

TruncatedProtein (5)

GenericProtein (5)

ReceptorProtein (5)

Degraded

Drug

Rna (5)

▼ Reaction (1)

DissociationReaction (1)

Protein annotators:

Available

Biocompendium

Uniprot

Entrez Gene

Ensembl

→

→

←

←

In use

HGNC

Clicking on each element type (**Object annotators**) in the left panel, an annotator can be assigned in the right panel that will attempt to automatically retrieve information from external bioinformatic databases for each relevant element, and annotate them. There are a number of annotators available, utilizing either the name, or existing identifier of an object. These are:

HGNC

HGNC identifier, if present, or, if absent, name of an element will be used to retrieve additional information, including full name, symbols, description and identifiers: RefSeq, ENSEMBL and Entrez Gene identifier

Uniprot:

Uniprot identifier, if present, will be used to retrieve additional information, including HGNC symbol and identifier, and Entrez Gene identifier

Entrez Gene

Entrez Gene identifier, if present, will be used to retrieve additional information, including full name, synonyms, description, HGNC symbol and identifier, and ENSEMBL identifier

ENSEMBL:

ENSEMBL identifier, if present, will be used to retrieve additional information, including symbol, full name, synonyms, HGNC symbol and identifier, and Entrez Gene identifier

ChEBI:

Uniprot identifier, if present, will be used to retrieve additional information, including synonyms, parents and children in the ChEBI ontology tree

Gene Ontology

Gene Ontology identifier, if present, will be used to retrieve additional information, including full GO definition for this identifier.

Biocompendium

Warning! this annotation service is unstable due to maintenance

name of an element will be used to retrieve additional information, including: full name, symbols, description and identifiers: RefSeq, ENSEMBL, Entrez Gene identifier, HGNC symbol, KEGG, Reactome, Pubmed and others

Configure automatic verification

The **Advanced** button, next to the **Verify manual annotations** checkbox under **Add project** button, invokes a dedicated configuration window (see below).

MIRIAM VALIDATION DETAIL

Classes

▼ Element

Compartment

▼ Species

Gene

Unknown

▼ Chemical

Ion

SimpleMolecule

ComplexSpecies

AntisenseRna

Phenotype

▼ Protein

IonChannelProtein

TruncatedProtein

GenericProtein

ReceptorProtein

Degraded

Drug

Rna

▼ Reaction

DissociationReaction

Protein

Annotations to be considered as valid:

Available

Enzyme Nomenclature

Ensembl

Entrez Gene

Gene Ontology

HGNC

HGNC Symbol

HMDB

InterPro

Kegg Compound

Kegg Genes

Valid

PubMed

Require annotations

One of these miriam should be required:

Available

Enzyme Nomenclature

Ensembl

Entrez Gene

Gene Ontology

HGNC

HGNC Symbol

HMDB

InterPro

Kegg Compound

Required

Clicking on each element or interaction type (**Classes**) in the left panel:

top right panels

a list of valid MIRIAM identifiers can be assigned. All elements or interactions in the uploaded model, annotated with an identifier outside of the ****Valid**** list will be flagged as warnings

bottom right panels

a list of mandatory MIRIAM identifiers can be assigned. If checkbox ****Require annotations**** is checked, all elements or interactions in the uploaded model, annotated without at least one identifier marked as ****Required**** list will be flagged as warnings.

Submit button: project generation

Clicking **Submit** button at the bottom of the **Add project** dialog window will start generation of the project. The window will refresh automatically, showing status changes during the process. Any warnings raised during the process will cause an **exclamation mark** icon to appear next to the project status. The list of warnings is extended gradually, and you need to wait for the project completion to see the full list. You will receive an email notification after the generation is complete.

It may happen that the project generation will result in a failure. An icon will be displayed, and a mouseover on it will display the reason for failure. Moreover, you will receive an email message detailing the error you have received.

Examine warnings

PROJECTS

ADD PROJECT

(1)

ProjectId	Name	Disease	Organism	Status	
empty		N/A	N/A	Ok (100%)	
pdmap		D010300	Taxonomy (9606)	Ok (100%)	
pdmap_mar16	PARKINSON'S DISEASE MAP	D010300	Taxonomy (9606)	Ok (100%)	
pdmap_jun16	PARKINSON'S DISEASE MAP	D010300	Taxonomy (9606)	Ok (100%)	
pdmap_oct16	PARKINSON'S DISEASE MAP	D010300	Taxonomy (9606)	Ok (100%)	
pdmap_feb17	PARKINSON'S DISEASE MAP	D010300	Taxonomy (9606)	Ok (100%)	

(2)

(3)

Clicking on the **exclamation mark** icon (if present) next to the project status description (see above, 3) will display the list of warnings raised during the generation of this project (see below).

WARNINGS

No	Content
1	[GenericProtein s8104] Cannot find information for element.
2	[GenericProtein s3252] HGNC annotation problem
3	[Rna s10418] Cannot find information for element.
4	[GenericProtein s4226] Cannot find information for element.
5	[GenericProtein s4647] Cannot find information for element.
6	[GenericProtein s5401] Cannot find information for element.
7	[GenericProtein s2930] Cannot find information for element.
8	[GenericProtein s8563] Cannot find information for element.
9	[GenericProtein s4241] Cannot find information for element.
10	[GenericProtein s4227] Cannot find information for element.
11	[GenericProtein s10290] Cannot find information for element.
12	[GenericProtein s10277] Cannot find information for element.
13	[GenericProtein s8353] Cannot find information for element.
14	[Rna s8635] Cannot find information for element.
15	[GenericProtein s10273] Cannot find information for element.
16	[GenericProtein s8671] Cannot find information for element.
17	[GenericProtein s3232] Cannot find information for element.
18	[GenericProtein s3245] Cannot find information for element.
19	[Rna s10227] Cannot find information for element.
20	[GenericProtein s8558] Cannot find information for element.

The list can also be downloaded as a tab-delimited text file. Types and identifiers of the elements and interactions are listed in the left column (**No**), while the nature of an error is provided in the right column. The table below lists possible errors and their explanations:

Warning type	Explanation
Warnings generated by automatic annotation	
[Annotator] annotation problem	[Annotator] (e.g. HGNC) could not retrieve correct information for this element or interaction. The probable reason is wrong manual annotation, or name, of this element or interaction

Cannot find information for element.	None of the assigned annotators were able to retrieve information for this element or interaction. The probable reason is wrong manual annotation, or name, of this element or interaction
Chemical name cannot be found in chebi: [name]	ChEBI annotator could not annotate the element or interaction correctly by name, as [name] is not a ChEBI-recognized name. The annotation by manually provided identifier may still be successful.
Former symbols list different than default [list]. Ignoring	Existing annotation of an element (list of symbols) is different than the [list] retrieved by one of the assigned annotators.
New full name different than default [full name]. Ignoring.	Existing annotation of an element (full name) is different than the [full name] retrieved by one of the assigned annotators.
New symbol different than default [symbol]. Ignoring.	Existing annotation of an element (symbol) is different than the [symbol] retrieved by one of the assigned annotators.
Synonyms list different than default [list]. Ignoring.	Existing annotation of an element (list of synonyms) is different than the [list] retrieved by one of the assigned annotators.
Warnings generated by verification of manual annotation	
contains invalid annotations: [annotation]	Configuration in **Validate manual annotations** did not foresee [annotation] as allowed for this element or interaction.
misses one of the following annotations:[list].	Configuration in **Validate manual annotations** required one of [list] of annotations for this element or interaction, but none was found.
misses annotations.	No annotation exists for this element or interaction.
Unknown miriam uri: [MIRIAM type]	An element or interaction was annotated with [MIRIAM type] - this type of identifier is currently not handled.

User manager

This panel allows you to manage users registered for a given instance of MINERVA platform (see below).

COMMENTS

MAP MANAGER

USER MANAGER

SERVICE STATUS

CONFIGURATION

MIRIAM

MANUAL

LOGOUT

USERS

Id	Name	Surname	Email	Login	
3				anonymous	
4193	Marek	Ostaszewski	marek.ostaszewski@uni.lu	marek	(2)
4194	Stephan	Gebel	stephan.gebel@uni.lu	stephan	

(1)

MINERVA version 11.0.8;
build 07/02/2018 10:53;
git: 2d738b4b240eba8eb79d6eeb605e8d5a8500ae27

Registered users have access to additional functionalities besides accessing the visual content generated by the platform. Clicking on the **New user** button (above, 1) invokes the window allowing to set login, password and personal details of a new user. The window allows to set privileges of the new user.

Clicking on the magnifying glass icon (**User manager** figure above, 2) invokes a panel, allowing to configure privileges of a respective user. The panel is identical to the **New user** window, with the exception of Id and login, which are assigned and not editable.

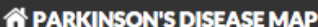
The **User detail** window allows to configure the following parameters for a given registered user:

- **Password** of the user
- **Name, Surname** and **Email** details.
- **Global privileges** concern all projects on your MINERVA instance
 - **Add project** checkbox, if checked, grants the user access right to the **Add project** button and permits the user to add new projects.
 - **Custom layouts** field defines how many overlays can be created by a given user across all projects they have access to on your instance of MINERVA platform

- **Manage configuration** checkbox, if checked, grants the user access right to access **Configuration** tab and permits them to manage the global configuration of your instance of MINERVA platform.
- **Map management** checkbox, if checked, grants the user right to access **Map manager** tab and manage existing projects
- **User management** checkbox, if checked, grants the user right to access the **User manager** tab and permits the user to manage users on your instance of MINERVA platform.
- **Project-specific privileges** concern only the project, for which they are configured
 - **Manage comments** checkbox, if checked, grants the user right to the **Comments** tab, and allows them to manage comments for this specific project
 - **Manage layouts** checkbox, if checked, grants the user right to manage overlays of all users for this specific project
 - **View project** checkbox, if checked, grants the user right to view this specific project. **Important** for non-administrator users only this box should be selected.
 - **Drug targeting advanced view** and **Edit suggested connections** are obsolete functionalities
- **Remove** button removes this registered user from your instance of MINERVA platform

Service status


Service status tab lists all external services and databases cross-linked by MINERVA platform. The left column contains service name hyperlinked to the original website. The right column contains the status of the service. Clicking on **Service status** tab invokes a checkup of the services and an update of their status. The checkup may also be invoked by the **Refresh** button at the bottom of the window. The figure below illustrates the **Service status** tab.





COMMENTS
MAP MANAGER
USER MANAGER
SERVICE STATUS
CONFIGURATION
MIRIAM
LOGOUT

SERVICE STATUS

Name ↕	status ↕
DrugBank	OK
ChEMBL	OK
ChEBI	OK
Europe PubMed Central	OK
MIRIAM Registry	OK
Biocompendium	OK
Ensembl	OK
Entrez Gene	OK
Gene Ontology	OK
HGNC	OK
Uniprot	OK




MINERVA version 659; build 23/10/2015 10:32


Configuration

Configuration tab provides a summary of the current version of your MINERVA instance. Moreover, it allows privileged users to configure global parameters of the MINERVA instance. Clicking **Refresh** button (bottom left) displays the table of global parameters, which can be edited set using and **Save** button (bottom right).

Global MINERVA configuration parameters are:

- **E-mail address**: e-mail address used for sending notifications about the activity of your MINERVA instance - project uploads, comments, etc.
- **E-mail server login, E-mail server password, IMAP server** and **SMTP server**: configuration of your mail server for notification sending
- **Default project id**: the project that will be displayed by default under the root address of the platform (your.url/MapView/))
- **Logo icon**: the filename of your logo icon, displayed in the bottom-right corner of the visualized content
- **Logo link**(after click): the website to which you will be redirected after clicking on the logo
- **Max distance for clicking on element (px)**: the content visualized by MINERVA platform is interactive, and clicked elements or

interactions are recognized by the vicinity of the click event. This parameter controls, how close to an element or interaction, in pixels, you need to click to select them

- **Email used for requesting an account**: the **Login** tab in the user interface features a **Request for an account** button; clicking the button will auto-generate an message to the e-mail, or list of e-mails separated by a semicolon, provided in this field
- **Max number of results in search box**: it may happen that a **Search** query returns a large amount of results. This parameter allows to tune the performance of your MINERVA instance by setting the cap for the number of displayed results
- **Google Analytics** tracking ID used for statistics: MINERVA platform offers integration with Google Analytics to track user activity of your MINERVA instance by providing an appropriate Google Analytics ID in this field
- **Logo description**: the popup text that will be displayed upon mouseover on your logo
- **Domain allowed to connect via x-frame technology**: the address of a website allowed to embed this instance of MINERVA via x-frame technology
- **Path to store big files**: location in the directory structure of this MINERVA instance to store big files
- **Legend 1-4 image file**: location in the directory structure of this MINERVA instance for displayed legend images
- **User manual file**: location in the directory structure of this MINERVA instance for the user manual file
- **Overlay color for negative/positive values**: configuration of overlay display - what colors should be used for positive and negative values. Values close to zero have the lowest color saturation, values close to -1/1 have the lowest color saturation (see Section [User manual - Upload user-provided overlay data](#))
- **Overlay color when no values are defined**: configuration of overlay display - what color to use for coloring named elements (see Section [User manual - Upload user-provided overlay data](#))

MIRIAM

The **MIRIAM** panel lists all MIRIAM-supported resources (<http://www.ebi.ac.uk/miriam/main/mdb?section=intro>) currently handled by MINERVA platform. In particular:

- **Annotation type**: column lists the names of the resources, hyperlinked to the original website
- **Miriam identifier**: column lists corresponding MIRIAM identifiers, hyperlinked to their definition in the MIRIAM registry
- **Valid for elements**: column provides information, for which records this identifier is configured as **valid** (see Section [Configure automatic verification](#))
- **Valid uri** column provides information on the correct format of corresponding MIRIAM identifier

Source file

The source file is uploaded to establish a project on your MINERVA instance. It is a SBGN-compliant file in the .xml format. Two modes of upload can be discussed - basic and advanced. In the basic mode, a single SBGN file (.zip compressed files are also accepted) is uploaded via the **Add project** button (see [Section Add project](#)). This way the SBGN-compliant network is uploaded, without additional files.

Advanced upload mode assumes that a zip-compressed directory will be submitted as an input, with the following structure:

- main map: file in a SBGN-compliant format (CellDesigner or pure SBGN)
- images: directory with files (see Appendix [Images](#))
- layouts: directory with overlay files (see Appendix [Overlays](#))
- submaps: directory with submap files (see Appendix [Submaps](#))

For an example, see [Examples - Advanced file upload](#). Detailed description of each section of the source file follows below.

Images

The **images** subdirectory contains static image files in .png format that will be displayed after pressing the **Show overview** button (see [User manual - Show overview](#)). Besides the images, the directory also has to contain a text, tab-separated file named **coords.txt**, describing links between the images and the associated network(s). The **coords.txt** file is a table with the following structure:

- **FILE** - linked image file
- **POLYGON** - a sequence of points in the linked image file forming a polygon, which will be treated as an active area for the link. The points should be **x,y** pairs separated by a spacebar, representing absolute coordinates of the pixels in the corresponding image. They should be provided in a single line
- **LINK_TYPE** - the type of link to the image, has to be one of the types specified below; link type determines the usage of the remaining fields.
 - **IMAGE** - links to another image of the uploaded set
 - **MODEL** - link to the main map, or one of the submaps
 - **SEARCH** - link to the results of a search query
- **LINK_TARGET** - determined by the field **LINK_TYPE**
 - if **IMAGE** - filename, must be one of the uploaded image files in the **images** directory
 - if **MODEL** - filename of the uploaded main map, or one of the submaps
 - if **SEARCH** - query to be executed and linked (see [Section User manual - Search](#))
- **MODEL_COORDINATES** - if the field **LINK_TYPE** is **MODEL**, this field should contain absolute coordinates of the point in the target map, in the format **x,y**; otherwise it should be left empty
- **MODEL_ZOOM_LEVEL** - if the field **LINK_TYPE** is **MODEL** and absolute coordinates are given, this field should contain a number corresponding to the zoom levels in the display area; otherwise it should be left empty. The the furthest zoom out has number 1, each zoom in increases the zoom number by one. Smaller maps will have less zoom levels than big ones. Try uploading the map without **images** first,

and assess the coordinates and zoom levels for the version with **images**

- **COMMENT** - a field for supplementary information, not used for configuration.

Example of a **coords.txt** file:

FILE	POLYGON	LINK_TYPE	LINK_TARGET	MODEL_COORDINATES	MODEL_ZOOM_LEVEL	COMMENT
image.A.png	51,218 107,218 107,252 51,252	MODEL	PD_151023_1.xml	7488,11986	5	A link from image.A file to a point in the display area with zoom level 5
image.B.png	15,187 73,187 73,52 15,52	IMAGE	image.A.png			A link from image.B file to invoke image.A
image.C.png	30,8 10,8 10,7 30,7	SEARCH	reaction:c1,reaction:c2			A link from image.C to results of a search query pointing to interactions **c1** and **c2**

Overlays

The **layouts** subdirectory contains files with custom colorings of the uploaded content that will be accessible to all the users. The format is identical to the format of files uploaded by registered users. See [Section Upload custom data - format](#) for details on file format.

Submaps

The **submaps** subdirectory contains SBGN files that will be displayed in the **Submaps** tab in the functional area of the User view (see [Section User view - Submaps](#)). Additionally to the submap files, one additional file, a **submap mapping file**, can be added to the directory. This file describes connections between the submaps and the main map itself. See below for the exact structure of the **submap mapping file**.

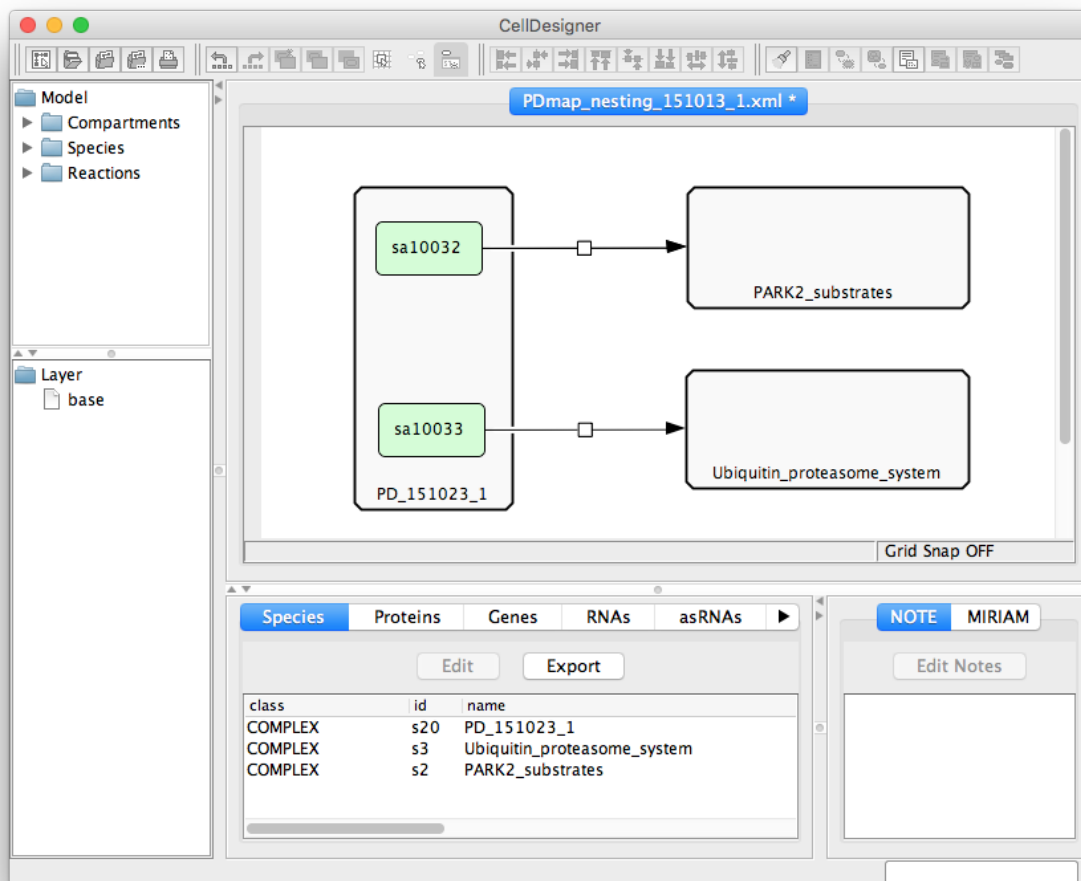
Submap mapping file

Submap mapping file is a CellDesigner file, in which relations between the uploaded maps is represented graphically. Two types of components and one type of interaction is considered when parsing this file:

- **Complex** should be named as a map file (the main map, or a submap), but without the .xml extension
- **Protein** should be named as an **alias of referred element in the source file** (the main map, or a submap). Please, note that a species alias is not the same as a species identifier! (see remark below)
- **State transition** reaction describes relations between components of the map.

Remark to alias vs identifier: CellDesigner has a single species identifier for all copies of a certain element (e.g. protein) in a file. Different instances of the same element have a distinct species alias. It is the species alias that is used to link specific map elements with submaps.

A screenshot below demonstrates an exemplary **submap mapping file**.



[R3lab homepage](#)

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MINERVA configuration: Examples

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 - [Automatic annotation](#)
 - [Automatic verification](#)
 - [Procedural semantic zoom](#)
- [Custom data upload by registered users](#)
 - [Basic format](#)
 - [Advanced format](#)
 - [By-identifier coloring](#)
 - [Custom colors and interaction coloring](#)
 - [Remarks](#)
- [Advanced file upload](#)

CellDesigner file upload and annotation

This section provides examples of usage of automatic annotators, automatic verifiers and construction of procedural semantic zoom.

This is [Example File 1](#), containing a CellDesigner file. The file is quite simple, and has the following properties:

- Annotations
 - Gene component (SNCA) is not annotated
 - RNA component (SNCA) is annotated with Entrez Gene id (NCBI Gene in CellDesigner MIRIAM tab)
 - one protein component (SNCA) is annotated with UniProt ID, while the other (PARK2) is not annotated
 - Phenotype component (UPS) is annotated with Gene Ontology
 - one interaction **re3** is annotated with PubMed id, while others are not
- Compartments and visual layers
 - **Translation** and **Degradation** visual layers are drawn on top of the diagram
 - **cell** and **nucleus** compartments are drawn

Automatic annotation

See [Admin manual - Configure automatic annotation](#) for details on annotators.

1. Upload the **Example File 1** to your MINERVA instance using [Add project button](#)
2. Configure automatic annotations by:
 1. checking the checkbox **Annotate model automatically**
 2. pressing the **Advanced** button; set the following:
 1. for **Element > Species > Gene**, set HGNC annotator
 2. for **Element > Species > Phenotype**, set Gene Ontology annotator
 3. for **Element > Species > Rna**, set Entrez annotator
 4. for **Element > Species > Protein > GenericProtein**, set Uniprot annotator
3. Press **Submit**

Examine the generated content. Please note that:

- Annotations between SNCA DNA, RNA and Protein are different, because different annotators used different information sources to obtain the information on the elements
- Even though SNCA DNA had no CellDesigner annotation, it was correctly annotated by name by HGNC annotator
- Uniprot annotator works only by identifier, so it was unable to provide annotations for PARK2
- Gene Ontology annotator retrieved a definition of the annotated Phenotype

Automatic verification

See Section [Configure automatic verification](#) for details on annotators.

NOTE: Your MINERVA instance remembers the settings from the previous run, so keep annotation settings as above.

1. Upload the **Example File 1** to your MINERVA instance again. Make sure to either remove previously uploaded example, or to name the uploaded project differently (use [Add project button](#) button)
2. Configure automatic verification by:
 1. checking the checkbox **Verify manual annotations**
 2. pressing the **Advanced** button; set the following:
 1. for **Element > Species > Gene**
 - set HGNC, HGNC symbol and Entrez Gene as *Valid*
 - check *Require annotations* checkbox and as *Required* set HGNC, HGNC symbol and Entrez Gene
 2. for **Element > Species > Phenotype**, set Gene Ontology annotator
 - set Gene Ontology as *Valid*
 - check *Require annotations* checkbox and as *Required* set Gene Ontology
 3. for **Element > Species > Rna**
 - set HGNC, HGNC symbol and Entrez Gene as *Valid*
 - check *Require annotations* checkbox and as *Required* set HGNC, HGNC symbol and Entrez Gene
 4. for **Element > Species > Protein > GenericProtein**
 - set Uniprot as *Valid*
 - check *Require annotations* checkbox and as *Required* set Uniprot
 5. for **Reaction > StateTransitionReaction**
 - set Pubmed as *Valid*
 - check *Require annotations* checkbox and as *Required* set Pubmed
 6. for **Reaction > TranslationReaction**
 - set Pubmed as *Valid*
 - uncheck *Require annotations* checkbox
 7. for **Reaction > TranscriptionReaction**
 - set Pubmed as *Valid*
 - uncheck *Require annotations* checkbox
 8. Make sure no items in upper hierarchy levels (e.g. Element, Species or Protein for GenericProtein) have different sets of verification rules
3. Press **Submit**

Upon upload, an exclamation mark icon will appear next to the project. After clicking, the popup window will look like this:

WARNINGS ×

No	Content
1	[Gene s2] contains invalid annotations: Ensembl(ENSG00000145335),
2	[Gene s2] contains invalid annotations: RefSeq(NM_000345),
3	[Rna s3] contains invalid annotations: Ensembl(ENSG00000145335),
4	[GenericProtein s9] misses one of the following annotations: Uniprot,
5	[StateTransitionReaction re4] misses one of the following annotations: PubMed,

Download

Examine the generated warnings. Please note that:

- Automatic annotators provided additional annotations to Gene and RNA elements, outside of the **Valid** list, you can suppress these warnings by updating the **Valid** list
- GenericProtein element (Parkin) was indicated as missing a required annotation (Uniprot)
- **StateTransitionReaction** re4 was indicated as missing a required annotation (PubMed)
- **TranslationReaction** and **TranscriptionReaction** did not raise any warnings as no annotation was required for them

NOTE: Valid and Required settings for lower hierarchy levels are overridden by settings for upper hierarchy levels. For instance, if no PubMed annotation is required for TranslationReaction, but Reaction requires PubMed, reactions re1 and re2 raise a warning.

Procedural semantic zoom

[Example File 1](#) after upload and submit will generate a view with procedurally-generated semantic zoom. Please, note that on the highest zoom out level only one compartment, **cell**, is visible. After zoom-in, two gray areas become visible, describing functional areas in the map. After another zoom-in, they are revealed and the **nucleus** compartment becomes visible. After a final zoom-in, **nucleus** becomes transparent as well. See also [Add project button](#).

Custom data upload by registered users

This section provides examples of data upload by registered users. Two subsection provide detailed examples for uploading basic and advanced formats.

Basic format

The file in basic format has two tab-separated columns **Name** and **Value** (see also [Upload custom data - format](#)):

- **Name** containing names of elements to be colored
- **Value** containing a value from [-1,1] range, to be transformed to red-green coloring, with negative values colored red, positive colored green; the saturation of the color will be defined by the absolute value.

This is [Example File 2](#), containing a custom coloring for an example map above ([Example File 1](#)).

To upload this data set, do the following:

1. Make sure you have the privileges to generate layouts in the example map
 1. Click on **Project detail** (magnifying glass icon in the rightmost column)
 2. See that by your name the **View project** checkbox is checked
2. Enter the **User view** of the example map: from the **Admin view > Map viewer**, click on the name of the uploaded project (**example_map** by default)
3. Make sure that you are logged in by checking the **Profile** tab in the left panel
4. In **Layouts > Custom layouts** tab, use **+Choose** button to select **Example File 2** and press generate
5. In **Layouts > Custom layouts** tab, use the **View** icon (magnifying glass) to examine generated view

Examine the generated coloring and the uploaded data set. Please note that:

- All SNCA elements are colored to the same color because of by-name matching
- SNCA elements are red-colored (the value in the file is -0.25), while PARK2 is green (the value in the file is 0.75)

Advanced format

Advanced format foresees two parts of the uploaded dataset - header and body (see also [Upload custom data - format](#)).

Header lines have to start with '#'. It can contain the following elements:

- **Version** **# VERSION=xyz** - a version of this custom layout
- **Name** **# NAME=xyz** - a name that will be automatically assigned upon upload
- **Description** **# DESCRIPTION=xyz** - a description that will be automatically assigned upon upload

Body is a table with a following set of columns:

- **Name, Value** - same as in basic layout
- **Compartment** - name of a compartment in which coloring should take place
- **Chebi** - ChEBI identifiers of elements to be colored
- **Entrez gene** - Entrez identifiers of elements to be colored
- **Gene ontology** - Gene Ontology identifiers of elements to be colored
- **Ensembl** - Ensembl identifiers of elements to be colored
- **Hgnc symbol** - HGNC symbols of elements to be colored
- **Uniprot** - Uniprot identifiers of elements to be colored
- **ReactionIdentifier** - ID of interaction to be colored (interactions coloring only)
- **LineWidth** - linewidth of the colored interaction (interactions coloring only)
- **Color** - color of the colored element.

By-identifier coloring

This is [Example File 3](#), containing a custom coloring for an example map above ([Example File 1](#)).

Upload this data set similarly as in [basic format upload](#).

Examine the generated coloring and the uploaded data set. Please note that:

- elements are colored by their identifiers instead of their names
- groups of SNCA elements are colored differently - nucleus elements are colored red, cell elements are colored green; this is a combination of two factors
 - by compartment constraint (red SNCA elements in **nucleus**)
 - by identifier constraint (SNCA elements in **cell** compartment only are annotated with uniprot)
- removing **compartment** column will cause an error, because due to automatic annotation SNCA elements in **cell** compartment are also annotated with **Entrez gene** identifier
- using SNCA coloring by-name overrides by-identifier coloring, the order of selection is as follows:
 - match by-name
 - match by-identifier
 - constrain by-compartment

Custom colors and interaction coloring

Advanced format foresees assigning user-defined colors to both elements and interactions.

This is [Example File 4](#), containing a custom coloring for an example map above ([Example File 1](#)).

Upload this data set similarly as in [basic format upload](#).

Examine the generated coloring and the uploaded data set. Please note that:

- **color** column replaces **value** for defining colors of interactions and elements
- **reactionIdentifier** is not affected by **compartment** constraint

Remarks

- Column names work only if an element is annotated by one of the terms above
- Column name: **Name** refers to the full name in the annotation panel; e.g., HGNC gene name for genes/proteins; ChEBI name for simple molecules or GO name for a Gene Ontology term.
- Elements needs to be written in the table as displayed in the left panel; e.g., hgnc: pure ID number; ensemble: "ENSG00000184845"; chebi: "CHEBI:18243".
- The uploaded table must be a text file
- Most columns could be used simultaneously as long as the same element is not addressed in two different columns; e.g., LRRK2 by HGNC name (=LRRK2) and Entrez gene ID (=120892) or a reaction Identifier and a pubmed target the same reaction.
- Restrictions:
 - A value or a color columns must in the uploaded text file but they mutually exclusive
 - name should only be combined with the identifiers: reaction Identifier and compartment
 - reaction identifier should only be combined with the identifiers name or pubmed
 - If the columns compartment is used the field must be filled by a compartment name derived from the content, otherwise the element will not be displayed in the content. Currently there is no possibility to choose **all compartments**.

Alternatively: you can always extract an area of interest as a CellDesigner file, open it in CellDesigner and colour it there.

Advanced file upload

This is [Example File 5](#), containing a .zip archive with the following structure:

- **example_advanced_map.xml** - CellDesigner file with the main map
- **images** - folder containing:
 - image files **overview_main.png** and **overview_sub.png**
 - **coords.txt** file containing relationships between the images and the content of the map
- **layouts** - folder containing a text file **example_upload_basic.txt**
- **submaps** - folder containing:
 - a submap CellDesigner file **example_submap.xml**
 - a mapping CellDesigner file **mapping.xml**

1. Upload the **Example File 1** to your MINERVA instance using [Add project button](#)
2. Examine the upload window, note the automatically filled positions
3. Make sure that in the **Complex** section proper checkboxes are checked for the main map and the mapping file \$. In the **Complex** section, you can set the names of uploaded submaps

Examine the generated project. Please note that:

- **Images** files
 - **Show overview** button is displayed, invoking one of the uploaded images
 - Links between the images and links directly to the map are configured
 - The link from *Active area 3* invokes a search query, highlighting two interactions
- **Layout** files: one selectable, predefined overlay in **General overlays** named **Advanced example** is available for non-registered users
- **Submap** files
 - in the **Submap** tab, the uploaded **example_submap** is visible
 - in the **Search** tab, if you look for PARK2 or SNCA, the results in both main map and the submap will be shown
 - contents of the **example_submap** are not annotated, as the **example_submap.xml** file elements are not annotated with relevant MIRIAM identifiers; even though SNCA elements are annotated in the main map, SNCA element in the submap is not annotated.
 - upon switching to a custom coloring (**Overlays** tab) contents of the **example_submap** are colored as the contents of the main map

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