

MINERVA Home

User manual

Admin manual

Examples

MINERVA configuration: Administrator's manual

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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 **ADMIN** button in the bottom 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 user having administrator rights to at least one of them can log via **ADMIN** link. After successful login (see below), you will have access to the administrator panel to manage your MINERVA instance.

Authorization complete

Use main menu to start managing.

Comments

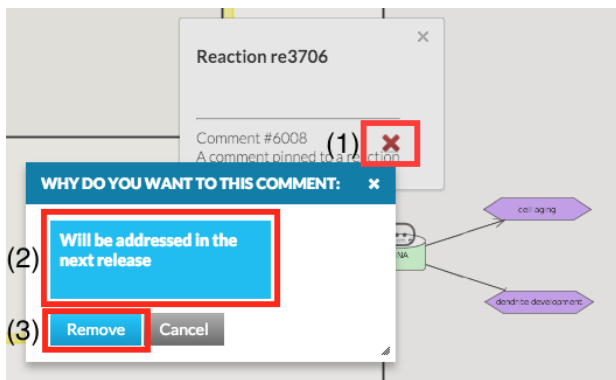
This panel allows you to manage comments provided by users of your maps (see [Section User manual - Comments](#)). The panel to the right (**Projects**) allows you to switch between different maps. Current active map will be highlighted. For the current active map, comments will be displayed in the panel to the left. The field **Title** is a hyperlink to a given comment in the map.

Id	Title	Author	Email	Content	Removed	Pinned
6007	LMNA	Marek	marek.ostaszewski@uni.lu	A comment pinned to LMNA	NO	YES
6008	Reaction re3706	Marek	marek.ostaszewski@uni.lu	A comment pinned to a reaction	NO	YES
6009	LMNA	Marek	marek.ostaszewski@uni.lu	An unpinned comment to LMNA	NO	NO

Projects

- [PARKINSON'S DISEASE MAP \(ndmap oct15 v2\)](#)
- [PARKINSON'S DISEASE MAP \(ndmap oct15\)](#)
- [UNKNOWN DISEASE MAP \(ndmap oct15 22\)](#)

Users logged in as administrators have a possibility to remove a comment, as for them an additional button is visible on the comment pop-up (see below, 1). You can provide a comment associated with the removed comment (see below, 2) and press the **Remove** button (see below, 3).



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

<div><div></div><div>Id</div><div></div></div>	<div><div></div><div>Title</div><div></div></div>	<div><div></div><div>Author</div><div></div></div>	<div><div></div><div>Email</div><div></div></div>	<div><div></div><div>Content</div><div></div></div>	<div><div></div><div>Removed</div><div></div></div>	<div><div></div><div>Pinned</div><div></div></div>
6007	LMNA	Marek	marek.ostaszewski@uni.lu	A comment pinned to LMNA	NO	YES
6009	LMNA	Marek	marek.ostaszewski@uni.lu	An unpinned comment to LMNA	NO	NO
6008	Reaction re3706	Marek	marek.ostaszewski@uni.lu	A comment pinned to a reaction	YES (Will be addressed in the next release)	YES

Map manager

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.

PARKINSON'S DISEASE MAP

COMMENTS | **MAP MANAGER** | USER MANAGER | SERVICE STATUS | CONFIGURATION | MIRIAM

PROJECTS

(1) **+ ADD PROJECT**

Projectid ▾	Name ▾	Status ▾	
empty	Empty DISEASE MAP	Ok (100%)	(2) 🔍
TF3001		Ok (100%) ⚠️	🔍
pdmmap_oct15_v2	PARKINSON'S DISEASE MAP	Ok (100%) ⚠️	🔍
pdmmap_oct15	PARKINSON'S DISEASE MAP	Ok (100%) ⚠️	🔍
pdmmap_oct15_23_2	PARKINSON'S DISEASE MAP	Ok (100%) ⚠️	(3)

Add project

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

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
- 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; currently in development and unused
 - *File type*: type of the uploaded file; recognized automatically.
- Additional layouts: this section describes uploaded additional layouts (element and interaction colorings) to be generated and accessible for all users of the project via **Layouts** 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: this section describes data mining candidates uploaded for the project. Ignore it if you submit a single file.
 - *Filename*: name of one of data mining files
 - *Name*: name of the resource visible in the project
 - *Source*: (optional) weblink to the source of the data mining set
 - *Type*: currently in development and unused
- 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.

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:

Biocompendium

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

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

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

Configure automatic verification

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

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

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

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.

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.

PARKINSON'S DISEASE MAP

COMMENTS **MAP MANAGER** USER MANAGER SERVICE STATUS CONFIGURATION MIRIAM LOGOUT

PROJECTS

(1) **+ ADD PROJECT**

Projectid ▾	Name ▾	Status ▾
empty	Empty DISEASE MAP	Ok (100%) (2)
TF3001		Ok (100%) ⚠️
pdmapp oct15 v2	PARKINSON'S DISEASE MAP	Ok (100%) ⚠️
pdmapp oct15	PARKINSON'S DISEASE MAP	Ok (100%) ⚠️
pdmapp oct15_23_2	PARKINSON'S DISEASE MAP	Ok (100%) ⚠️ (3)

Clicking on the magnifying glass icon in the last column with the project parameters (see above, 2) will invoke a dialog window to modify the configuration of a generated project (see below)

General is the first configuration tab, allowing edition of basic information about the project. Using **Remove** button you can permanently

delete the current active project.

PROJECT DETAIL ✕

GENERALLAYOUTSDATAMININGUSERS

ProjectId:	pdmap_oct15
Name:	PARKINSON'S DISEASE MAP
Version:	Oct'15
Description:	
Notify email:	marek.ostaszewski@uni.lu

Save Remove Cancel

Layouts tab allows you to examine and manage layouts (custom colorings of elements and interactions) in the current project (see below). Layouts accessible for all users are marked as N/A in the **Owner** column. Below, you can examine layouts generated by other users. If you have appropriate privileges (see **Section User manager**), you can remove generated layouts by pressing a respective button in the **Remove** column.

Removed layouts cannot be restored.

PROJECT DETAIL ✕

GENERALLAYOUTSDATAMININGUSERS

(1 of 1) 1

Name	Directory	Description	Owner	Data	Remove
Pathways and compartments	aff23e1160208519c3c4c824c10		N/A		
Normal	aff23e1160208519c3c4c824c10		N/A		
Ageing brain	aff23e1160208519c3c4c824c10	Differential transcriptome expression from post-mortem brain samples	N/A		
PD substantia nigra	aff23e1160208519c3c4c824c10	Differential transcriptome expression from post-mortem substantia nigra	N/A		
SN proteomics	aff23e1160208519c3c4c824c10		Stephan Gebel		
SN RNA	aff23e1160208519c3c4c824c10		Stephan Gebel		

(1 of 1) 1

Add layout

Data mining tab allows you to examine and manage data mining files uploaded for the project (see below). Using buttons in the **Data** column you can download respective datasets.

PROJECT DETAIL ✕

GENERALLAYOUTSDATAMININGUSERS

Name	Description	Source	Type	Data
Interacting candidates (text mining)	Candidates suggested by text mining of PD related literature.		Text mining	
Interacting candidates (PathExpand)	Candidates suggested by the PathExpand analysis of the PD map.	http://www.pathexpand.net	Structure analysis	

Users tab provides a project-level overview of access and management rights of users registered on the platform (see below). First two columns (**Drug targeting advanced view** and **Edit suggested connections**) concern functionalities under development, they are currently not supported. Remaining columns (**Manage comments**, **Manage layouts** and **View project**) correspond to respective user privileges are discussed in detail in **Section User manager**.

PROJECT DETAIL

GENERAL

LAYOUTS

DATA MINING

USERS

(1 of 3)

1

2

3

>>

>>>

User	Drug targeting advanced view	Edit suggested connections	Manage comments	Manage layouts	View project
Gawron Piotr (gawi)	<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
(anonymous)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>
Ostaszewski Marek (marek)	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>
Gebel Stephan (stephan)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input checked="" type="checkbox"/>

(1 of 3)

1

2

3

>>

>>>

Update privileges

Examine warnings

PARKINSON'S DISEASE MAP					
COMMENTS	MAP MANAGER	USER MANAGER	SERVICE STATUS	CONFIGURATION	MIRIAM
LOGOUT					
PROJECTS					
(1) ADD PROJECT					
Projectid	Name	Status			
empty	Empty DISEASE MAP	Ok (100%)	(2)	<input checked="" type="checkbox"/>	<input type="checkbox"/>
TF3001		Ok (100%)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
pdmap_oct15_v2	PARKINSON'S DISEASE MAP	Ok (100%)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
pdmap_oct15	PARKINSON'S DISEASE MAP	Ok (100%)	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>
pdmap_oct15_23_2	PARKINSON'S DISEASE MAP	Ok (100%)	(3)	<input checked="" type="checkbox"/>	<input type="checkbox"/>

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	
1 2 3 4 5 6 7 8 9 10 >> >>>	
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.
Download	

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).

PARKINSON'S DISEASE MAP

[COMMENTS](#)
[MAP MANAGER](#)
[USER MANAGER](#)
[SERVICE STATUS](#)
[CONFIGURATION](#)
[MIRIAM](#)
[LOGOUT](#)

USERS

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

(1)

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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. For a detailed explanation, see below.

USER DETAIL

×

Id:

Login:

Password:

Name:

Surname:

Email:

Privileges:

Add project	<input type="checkbox"/>
Custom layouts	0
Manage configuration	<input type="checkbox"/>
Map management	<input type="checkbox"/>
User management	<input type="checkbox"/>

Project:

PD map nested bioview all
pdmap_oct15
SNCA
TF0605

Access:

No records found.

Save

Remove

Cancel

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 panel is shown in the figure below.

USER DETAIL

×

Id:

Login:

Password:

Name:

Surname:

Email:

Privileges:

Add project	<input checked="" type="checkbox"/>
Custom layouts	10
Manage configuration	<input checked="" type="checkbox"/>
Map management	<input checked="" type="checkbox"/>
User management	<input checked="" type="checkbox"/>

Project:

PD map nested bioview all	<input checked="" type="checkbox"/>	Drug targeting advanced view
pdmap_oct15	<input checked="" type="checkbox"/>	Edit suggested connections
SNCA	<input checked="" type="checkbox"/>	Manage comments
TF0605	<input checked="" type="checkbox"/>	Manage layouts
PD_141212_3	<input checked="" type="checkbox"/>	View project

Save

Remove

Cancel


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 layouts 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 layouts of all users for this specific project
- **View project** checkbox, if checked, grants the user right to view this specific project
- **Drug targeting advanced view** and **Edit suggested connections** are functionalities under development and are not supported at the moment
- **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.


 **PARKINSON'S DISEASE MAP**

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





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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 (see below, 1) displays the table of global parameters, which can be edited set using and **Save** button (see below, 2).

CONFIGURATION

SYSTEM VERSION: 6 UNSTABLE DEVEL VERSION

Svn build version: **659**

Build date: **23/10/2015 10:32**

PrimeFaces version: **4.0**

CHANGELOG:

Type ↕	Description ↕
functionality	Uploaded datasets are available for download
functionality	Entrez annotator
functionality	Ensembl annotator
functionality	Valid/required annotations and used annotations saved in user profile
functionality	Export to pdf/png/jpg/svg
functionality	New web interface

SYSTEM PARAMETERS:

Id ↕	Title ↕	Value ↕
No records found.		

(1)   (2)

SYSTEM PARAMETERS:

Id ↕	Title ↕	Value ↕
2	E-mail address	
3	E-mail server login	
4	E-mail server password	
5	IMAP server	
6	SMTP server	
7	SMTP port	
1	Default Project Id	
46	Logo icon	
45	Logo link (after click)	
60	Max distance for clicking on element (px)	
104	Email used for requesting an account	
281	Max number of results in search box.	
279	Google Analytics tracking ID used for statistics	
280	Logo description	



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The list of global MINERVA configuration parameters is displayed in figure above. These 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.

MIRIAM

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

MIRIAM

SUPPORTED MIRIAM TYPES:

Annotation type ↕	Miriam identifier ↕	Valid for elements:	Valid uri:
Chemical Abstracts Service	MIR:00000237	No records found.	• urn:miriam:cas
Consensus CDS	MIR:00000375	No records found.	• urn:miriam:ccds
ChEBI	MIR:00000002	• Chemical • Drug	• urn:miriam:obo:chebi • urn:miriam:chebi
ChemSpider	MIR:00000138	No records found.	• urn:miriam:chemspider
ChEMBL	MIR:00000084	• Drug	• urn:miriam:chembl.compound
ChEMBL target	MIR:00000085	• Protein • Complex	• urn:miriam:chembl.target
DrugBank	MIR:00000102	• Drug	• urn:miriam:drugbank
DrugBank Target v4	MIR:00000528	No records found.	• urn:miriam:drugbankv4.target
Enzyme Nomenclature	MIR:00000004	• Protein • Complex	• urn:miriam:ec-code
Ensembl	MIR:00000003	No records found.	• urn:miriam:ensembl
Entrez Gene	MIR:00000069	• Protein • Gene • Rna	• urn:miriam:ncbigene • urn:miriam:entrez.gene
Gene Ontology	MIR:00000022	• Phenotype • Compartment • Complex	• urn:miriam:obo.go • urn:miriam:go
HGNC	MIR:00000080	• Protein • Gene	• urn:miriam:hgnc

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)
- data_mining: directory with files (see Appendix [Data mining files](#))
- images: directory with files (see Appendix [Images](#))
- layouts: directory with files (see Appendix [Layouts](#))
- submaps: directory with files (see Appendix [Submaps](#))

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

Data mining files

The **data_mining** subdirectory contains data used to display candidate interactions shown next to the annotations of certain elements (see [User manual - Candidate interactions](#)). The subdirectory may contain multiple files, each for a different source data. Each of the files must be a text file, follow the same format, including two parts - header and body.

Header lines have to start with '#'. It can contain the following elements: Version (# **VERSION=xyz**) - a version of this data mining file Type (# **TYPE=xyz**) - a definition of data source, either TEXT_MINING or STRUCTURE_ANALYSIS Description (# **DESCRIPTION=xyz**) - a description of the file that will be automatically assigned upon upload

Body is a tab-separated table, composed of the following columns:

- **Source** - MIRIAM identifier of an element in the hosted network
- **Target** - MIRIAM identifier of target interactor
- **Description** (optional) - description of the interaction

- **References** (optional) - article supporting this interaction

Example:

```
# VERSION=1.0
```

```
# TYPE=TEXT_MINING
```

```
# DESCRIPTION=Example data mining results.
```

Source	Target	Description	References
urn:miriam:hgnc.symbol:PARK2	urn:miriam:hgnc.symbol:KIF11	In this study, we present the first evidence that the cellular Eg5 level is down-regulated by Parkin, an E3 ubiquitin ligase well known for its role in the development of Parkinson disease.	urn:miriam:pubmed:18845538

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 series of points in the linked image file forming a ploygon, which will be treated as an active area for the link
- **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

Layouts

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 CellDesigner 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)
- **State transition** reaction describes relations between components of the map.

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

