Procedure for preparation of ACSN modular map in NaviCell format

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1. Essential tools

CellDesigner4.2 or 4.3, Gimp and Cytoscape 2.8.
Ensure that the latest version of BiNoM is installed in the Cytoscape.
Download the latest experimental version of BiNoM from the website (http://binom.curie.fr); in the Cytoscape folder 'plugins' replace the 'binom.jar' by newly downloaded version of 'binom.jar'. (currently use jar file' binom-3.jar')

2. Preparation of master map

Important NOTE:
It is recommended to verify systematically that all steps of maps preparation in NaviCell format were performed correctly. Use checklist table for master and module maps('Maps_to_NaviCell_CheckList.docx').

2.1. Map dimensions and characteristics (CellDesigner)

2.1.1 Map dimensions

Adjust to multiplication of 256 (*Component, Model information*)

2.1.2 Map name

Include map name in Model information (*Component, Model information*). Map name is as the name of the map file (e.g. 'dnarepair').
For map name, see the table 'Maps and modules titles and tags' in the 'ACSN database paper preparation' Google doc.

2.1.3 Map title

Include map title in the in the first line of Model notes (*Component, Model notes*). This title will appear on the upper panel in the NaviCell representation of the map (e.g. DNA repair map).
For map title, see the table 'Maps and modules titles and tags' in the 'ACSN database paper preparation' Google doc.

2.1.4 Map annotation

Include the annotation text of the map (*Component, Model notes*) from the second line of model notes (10-20 lines of text about the map with PMIDs). This annotation will appear in the callout and the annotation post in the NaviCell representation of the map.

2.1.5 Map modules marks

Introduce layers for each module of the map; name layers by module name (e.g. NER).
In corresponding layers, draw small square (*using the 'Layer square' function*) in the place where module marker should be dropped in the NaviCell representation (preferably upper-left corner of the module). Distribute location of marker homogeneously on the map.
For modules names, see the table 'Maps and modules titles and tags' in the 'ACSN database paper preparation' Google doc.

2.1.6 Compartments name

Assign names for all compartments (avoid name 'default'). For common compartment use the names existing in other maps of ACSN.
For compartments name, see the table 'Common rules for map entities naming' in the 'ACSN database paper preparation' Google doc.

2.1.7 Entities and modules names

Check that all entities, complexes and modules are named according to the NaviCell annotation rules.
See the requirement for NaviCell entities and complexes naming in http://navicell.curie.fr/doc/NaviCellMapperAdminGuide.pdf

2.1.8 Map layout

Apply default colour and size of entities (if possible), make layers invisible. Generate final layout before proceeding to modules background colouring and zoom levels generations.

2.1.9 Map file name

The map file is named according to NaviCell standard (e.g. dnarepair_master) and saved in the src folder as described in the section 'Pre-defined folder structure for generating the map files' in the NaviCell guide.

See the requirement for NaviCell source folder structure in
http://navicell.curie.fr/doc/NaviCellMapperAdminGuide.pdf

2.1.10 Map check-up in BiNoM

Perform map check-up for obvious inconsistencies using BiNoM plugin *(BiNoM I/O, 'check CellDesigner file'*)

Important NOTE:
CheckCellDesigner file function checks for 3 recurrent problems in CellDesigner files:
1a) Attachment of reactions to included species
1b) Species without aliases in CellDesigner file
1c) Inconsistency in the heterodimer association reactions.

2.2. Map entities annotation

2.2.1 Manual application of NaviCell entities annotation format

The NaviCell format for entities and reactions annotation can be done manually in CellDesigner using the template described in the section 'NaviCell entities annotation format in CellDesigner' in the NaviCell guide.

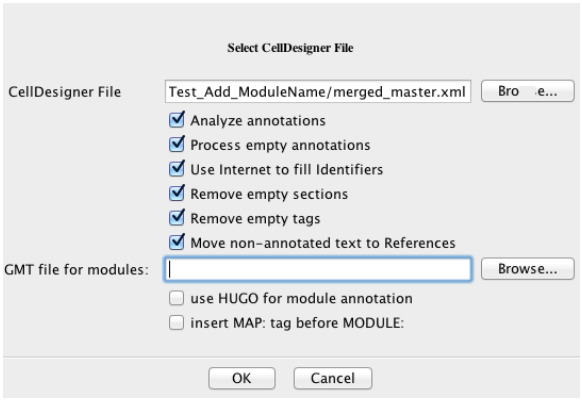
See the requirement for NaviCell annotation sections and content in
http://navicell.curie.fr/doc/NaviCellMapperAdminGuide.pdf

2.2.2 Application of NaviCell entities annotation format using BiNoM

Important NOTE:
If the full NaviCell annotation format with sections is not applied during map construction, the NaviCell annotation format can be introduced while map processing.
In this case ensure that minimal essential information for entities annotations is included:
(1). HUGO (for protein, gene, RNA and asRNA) or ChEBI (for ions, small molecules and drugs) names are used as entity name or if entity name is a synonym* (e.g. p53*), HUGO of CheBI name is included in the entity annotation.
(2). List of module names whether the entity participates is included in annotation (MODULE:NER).
(3). References cited as PMID:NUMBER (e.g. PMID:5275894) and followed by free text, if needed.
The processing of annotations and application of NaviCell sectioning format is done in BiNoM using the minimal essential information (1)-(3).

- **Apply NaviCell annotation format**

If the minimal essential requirements for entities map annotations were fulfilled, apply NaviCell annotation format using BiNoM plugin *(BiNoM I/O, 'Extract CellDesigner notes')*
Use this setting:



File 'mapname_notes.txt' with list of map entities annotations in NaviCell format is generated in the same folder.

- **Manually check/correct the annotation file**

See the requirement for NaviCell annotation format in http://navicell.curie.fr/doc/NaviCellMapperAdminGuide.pdf

- Correct sectioning and content of sections

-Presence of official identifiers

-Modules naming consistency

- **Optional: Add module tag into the entities' annotation**

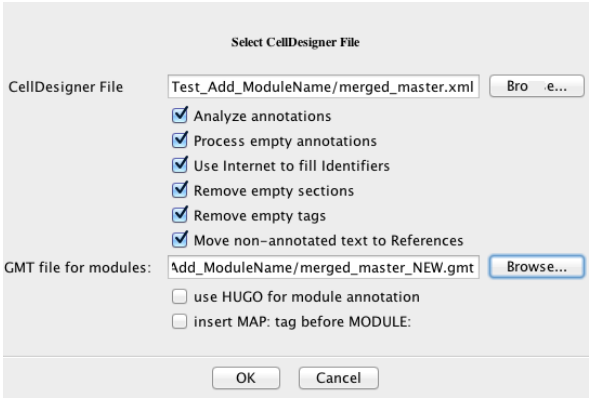
If modification or assignment of new module tags into the entities annotations is essential, the manual assignment of module tags to the annotations can be replaced by semi-automated procedure. The gmt file containing map content grouped per modules should be generated and used for module tags assignment into the annotation while application of NaviCell annotation format using BiNoM plugin.

See Appendix 3 for procedure of new gmt file generation. Note that this gmt contains entities names. It may also contain complexes names, if needed.

In this case, assign new module tags in the annotations of entities of master map from the gmt file.

-Apply NaviCell annotation format using BiNoM plugin *(BiNoM I/O, 'Extract CellDesigner notes').*

-Use this setting for generation the annotations file:

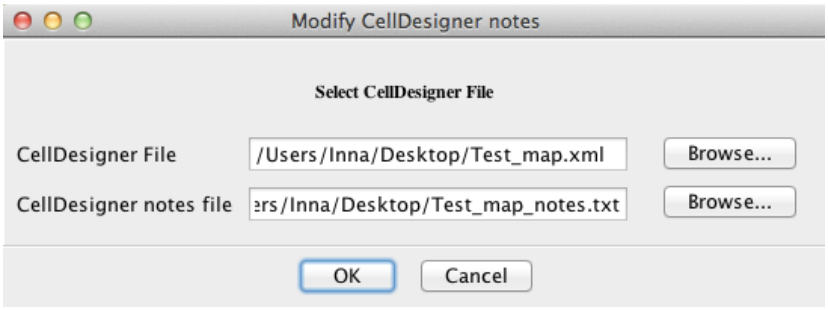


Module tags are added into annotations of entities. File 'mapname_notes.txt' with list of map entities annotations is generated in the same folder.

-Open the File 'mapname_notes.txt' in text editor and verify that annotations are NaviCell-formatted correctly and module tags are properly assigned.

- **Replace annotations in the master map**

-Replace annotations of entities in the master map with newly generated annotations using 'mapname_notes.txt' file *(BiNoM I/O, 'Modify CellDesigner notes')*

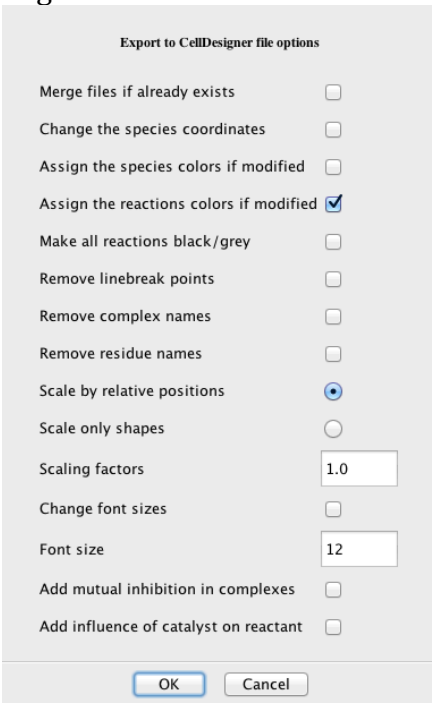


File 'mapname_notes.xml' with modified entities annotations is generated in the same folder.

2.3. Preparation of NaviCell master map layout (BiNoM, CellDesigner and GIMP)

2.3.1 Colour reaction edges and map background

- **Apply colours on map edges** while importing map to BiNoM and exporting to CellDesigner (*BiNoM I/O, 'Import CellDesigner document from file'; BiNoM I/O, 'Export current network to CellDesigner'*)
  Use this setting to change edges colors:



The edges colors are assigned while map import/export.

- **Generate map image** in png format (in CellDesigner)

- **Make reaction edges semi-transparent** (in BiNoM, using scripts)
  See Appendix 6 for procedure describing together making reaction edges semi-transparent and preparation of zoom levels.

- **Draw semi-transparent colored background per modules in GIMP**
  See Appendix 7 for procedure describing how to create images with background for each zoom level
  See example of DNArepair map colored in Gimp in the associated folder, 'dnarepair_zooms_master_GIMP_work'

2.3.2 Create zoom levels

Four zoom levels for ACSN master maps:

1. **Detailed: zoom-3** (no change)
2. **Hidden details: zoom-2** (no reactions ID, no complexes names, no modifications names)
3. **Pruned: zoom-1** (now-compression of hidden level; in future-canonical pathways representation view)
4. **Top level: zoom-0** (use semi-transparent background image without map image with names of modules and 1-3 major players of each module='capitals'), additional decorations can be added to the top level view image.

See Appendix 6 for procedure describing together making reaction edges semi-transparent and preparation of zoom levels.

Important NOTE:
Number of zooms in unlimited. For big maps additional zoom levels are recommended, create by image compression of some of above zooms.

3. Preparation of module map

Important NOTE:
1. Module map is a sub-set of master map. The content of the module map should not be modified. The content is always derived from the master map. The layout of module map can be modified and optimised to achieve the best visual representation of the module.
2. Module map can be prepared using various approaches depending on module definition and map structure. See Appendix 4 for procedure of module map extraction in Cytoscape using module tags or entities localization. The final layout of the module map is adjusted manually.
3. See update of old module map from modified master maps in Appendix 5. The layout of the module map is mainly preserved and adjusted manually if needed.

3. 1. Map dimensions and characteristics (CellDesigner)

3.1.1 Map dimensions

Adjust optimal size of module map and assign dimensions of multiplication of 256 (minimal map size 1500 pixels) (*Component, Model information*)

3.1.2 Map name

Include map name in Model information (*Component, Model information*). Map name is as the name of the map file (e.g. 'apoptosis_CASPASES').
For module map name, see the table 'Maps and modules titles and tags' in the 'ACSN database paper preparation' Google doc.

3.1.3 Map title

Include map title in the in the first line of Model notes (*Component, Model notes*) in the first line of model notes (e.g. 'MAP:APOPTOSIS/MODULE:CASPASES'). This title will appear on the upper panel in the NaviCell representation of the module map.
For module map title, see the table 'Maps and modules titles and tags' in the 'ACSN database paper preparation' Google doc.

3.1.4 Map annotation

Include the annotation text of the map (*Component, Model notes*) from the second line of model notes (text about the module with PMIDS, 50-70 words). This annotation will appear in the callout and the annotation post in the NaviCell representation of the module map.

3.1.5 Compartments name

Check assignment of corresponding compartment names from the master map. When module maps are derived from the master map, layers corresponding to the module are preserved. Remove layers in the module maps.

3.1.6 Map layout

Generate optimal module map layout that can be different from the representation on the master map.

3.1.7 Map file name

The map file is named according to NaviCell standard (e.g. dnarepair_BER) and saved in the src folder as described in the section 'Pre-defined folder structure for generating the map files' in the NaviCell guide.

See the requirement for NaviCell source folder structure in http://navicell.curie.fr/doc/NaviCellMapperAdminGuide.pdf

3.1.8 Map check-up in BiNoM

Perform map check-up for obvious inconsistencies using BiNoM plugin *(BiNoM I/O, 'check CellDesigner file'*).

Important NOTE:
CheckCellDesigner file function checks for 3 recurrent problems in CellDesigner files:
1a) Attachment of reactions to included species
1b) Species without aliases in CellDesigner file
1c) Inconsistency in the heterodimer association reactions.

3.2. Preparation of NaviCell module map layout (BiNoM, CellDesigner and GIMP)

3.2.1 Colour reaction edges and map background

- Check that edges of the map are colored (normally preserved if module map is derived from master map with colored edges). Otherwise color the edges as described in Section 2.3.1.

3.2.2 Create zoom levels

- Generate map image in png format in CellDesigner
- Create zoom levels by image compression in GIMP (sequential two fold reduction of image size)

See Appendix 6 for procedure describing together making reaction edges semi-transparent and preparation of zoom levels.

Important NOTE:
Number of zooms in unlimited. For very small modules 2 zoom levels are recommended.

4. Preparation of NaviCell source folder

Create folder with master map and modules for NaviCell source.
See associated example of map folder for NaviCell source 'dnarepair' and the section 'Pre-defined folder structure for generating the map files' in the NaviCell guide.

- Create config file

```
base: dnarepair_
title: DNA repair map
name: dnarepair
showDefaultCompartmentName: true
```

'base' is the file name; 'title' is as in *'Model information'*, 'name' is as in '*Model notes' (see paragraph 4.2.1)*

- Place and name correctly xmls of master map and module maps

See the table 'Maps and modules titles and tags' in the 'ACSN database paper preparation' Google doc

- Place and name correctly zoom levels pngs of master map and module maps (for master map zoom levels created using script and decorated in Gimp, for module maps from the folder where zoom leves where generated using scripts, **as described in Appendix 6**)

See the table 'Maps and modules titles and tags' in the 'ACSN database paper preparation' Google doc

5. Appendixes

Appendix 1: Example of gmt file with map content grouped per modules

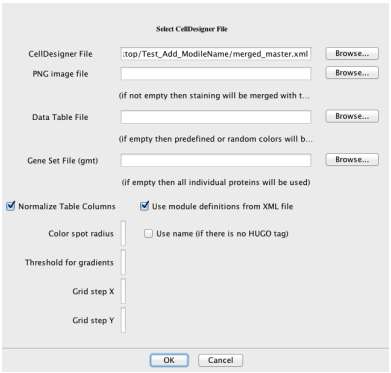
Example of gmt file created in text editor, in text format (name.gmt)

```
DDR	na	APBB1	ATM	BARD1	BAZ1B	BCL2	BRCA1	BRCC3	CK2_alpha_'*
CK2_alpha_*	CK_beta_*	Caspase2*	DFFB	DNA-PK*	ENDOG	EYA*	EYA1
EYA3	FAM175A	H2A*	H2AFX	IGFBP3	JNK*	TIP60*	Ku70*	LRDD	MDC1	MRE11*
NBS1*	PCAF*	PP2A*	PPARGC1A	PPIA	PPM1D	RAD50	RNF168	RNF8	SIRT1
SMARCA5	STK11	STRADA	TP53BP1	UBE2N	UIMC1	USP3	active~Caspases*
cleaved~AIFM1*	cleaved~ATM*	cleaved~Caspase2*	cleaved~Caspase3*
cleaved~DNA-PK*	gDNA2	rIGFBP3	rRNA	phDNA~fragmentation	phDNA~damage
phDNA~integrity	s4501	s3751	s3707	s4510	s4041

Autophagy	na	H2A*	H2AFX	IGFBP3	JNK*	TIP60*	Ku70*	LRDD	MDC1
MRE11*	NBS1*	PCAF*	PP2A*	PPARGC1A	PPIA	PPM1D	RAD50	RNF168	RNF8
SIRT1	SMARCA5	STK11	STRADA	TP53BP1	UBE2N	UIMC1	USP3	active~Caspases*
cleaved~AIFM1*	cleaved~ATM*
```

Appendix 2: Extraction of gmt file from map

Extract from map gmt file with map content grouped per modules (BiNoM I/O, 'Stain CellDesigner Map'). This action uses module tags assigned for entities in the annotations.
Use this setting:



Appendix 3: Manual construction of master map gmt file from module maps gmt files

If the master map and the module maps were updated/modified, it may happen that new/modified set of module tags should be added to some map entities. To avoid manual

module tag assignment into the annotations of entities, extraction of module maps content and systematic module tag sets assignment for map entities can be used.
To achieve it, new master map gmt file should be combined from the lists module maps content, namely module maps gmt files. The new combined gmt file containing lists of content for all modules will be used to replace the old module tags in the master map annotations by the new module tags.

Gmt file from each one of new/updated module maps should be generated. Gmt files from all module maps are merged together to create the gmt for master map.

-Extract names of entities and complexes in the module and create gmt file

- Create gmt file of content for extraction of entities and complexes names (*BiNoM I/O, 'Color CellDesigner proteins', select the sub-map)*
- Open gmt file of content in Excel, select first column and transverse column to raw, insert two new columns on the left. In the first column type *MODULE_NAME*, in the second column type *na*
  (Alternatively: create txt tile in text editor, make 'plain text', separation by tab. In front of the entities and complexes list type: MODULE_NAME, tab, na, tab; add complexes species IDs as described below)
- Open module map in Cytoscape (*BiNoM I/O, 'Import CellDesigner document from file')*
- Optional: Adding complexes to the list of entities in gmt file.
  Select complexes species IDs (in Cytoscape select all map; data panel; select attributes (CELLDESIGNER_NODE_TYPE; CELLDESIGNER_SPECIES), order per CELLDESIGNER_NODE_TYPE; select CELLDESIGNER_SPECIES for complexes (species ID), paste to the list of components in the gmt file (in Excel or in text editor)
- Save as txt file
- Change extension *.txt* to *.gmt*

For generation of global gmt file with master map content grouped per modules, repeat the above procedure for all modules of the map. Add into the gmt file module names followed by lists of module's components. See example of gmt file in the Appendix 1.

Appendix 4: Extraction of module maps from the master map

Extraction of module fmaps rom master map by module tags in the annotations

- Open master map in Cytoscape (*BiNoM I/O, 'Import CellDesigner document from file')*
- Select Module attribute that corresponds to the module name (*BiNoM Utilities, 'Select nodes by substring in attributes').* In the dialogue chose: *'Attribute name', 'MODULE' and 'Substring', 'Name of the module that has in the update process', OK*
  Important note: this action selects the corresponding entities. Do not click on the map, the selection will disappear!!
- Select first neighbourhood (*Select, Nodes, First neighbours of selected nodes*)
- Create a new map from selected nodes (*File, new, network, from selected nodes all edges*)
  Optional: Select again first neighbourhood and thus create the new network. It is possible that there are nodes and edges that potentially can be included into the module map.
- Export new module map to CellDesigner (*BiNoM I/O, 'Export current network to CellDesigner'*), associate with (*select the original map from which the new network was derived*), name the module file, in the dialog use default setting
- The final layout of the module map should be manually adjusted in CellDesigner

For modules names, see the table 'Maps and modules titles and tags' in the 'ACSN database paper preparation' Google doc.

Extraction of module maps using entities localization

- Open master map in Cytoscape (*BiNoM I/O, 'Import CellDesigner document from file')*
- Select entities or area of module, create a new network (*File; New; Network; From selected nodes, all edges*)
- Export new module to CellDesigner (*BiNoM I/O, 'Export current network to CellDesigner'*), associate with (*select the original map from which the new network was derived*), name the module file, in the dialog use default setting
- The final layout of the module should be manually adjusted in CellDesigner

For modules names, see the table 'Maps and modules titles and tags' in the 'ACSN database paper preparation' Google doc.

Appendix 5: Updating old module map from modified master map using module tags

If the master map has been modified, the old modules have to be updated with new entities and edges. To avoid re-generation of the module map and re-designing the layout *de novo*, the old module map layout can be preserved. The new objects added during the procedure of module update can be manually relocated/ embedded into the old layout of the module map.

In the case all entities of the master map have corresponding module tag:

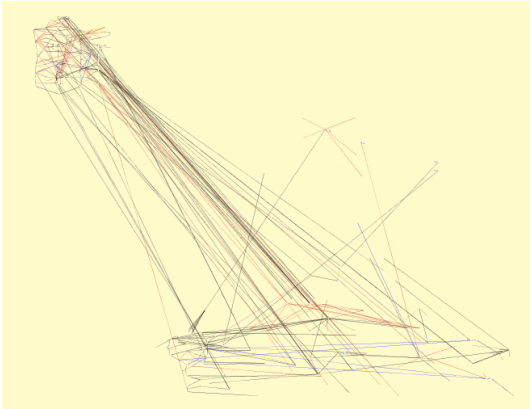
- Open master map and the old module map that has to be updated in Cytoscape (*BiNoM I/O, 'Import CellDesigner document from file')*
- On the old module map, move the module to the upper left corner away from the original location of the module on the master map (to prevent the overlap between the old module and newly added entities from the master map during the merging).
- Associate the old module map with the new master map *BiNoM I/O, 'Associate CellDesigner source', click 'change cooordinates'in the dialogues window, if appears)*
- On the master map, select Module attribute that corresponds to the module name of the module map that has to be updated (*BiNoM Utilities, 'Select nodes by substring in attributes').* In the dialogue chose: *'Attribute name', 'MODULE' and 'Substring', 'Name of the module that has in the update process', OK*
  Important note: this action selects all entities, do not click on the map, the selection will disappear!!
- Select first neighbourhood (*Select, Nodes, First neighbours of selected nodes*)
- Create a new map from selected nodes (*File, new, network, from selected nodes all edges*)
  Optional: Select again first neighbourhood and thus create the new network. It is possible that there are nodes and edges that potentially can be included into the module map.
- Associate the new network with the new master map (*BiNoM I/O, 'Associate CellDesigner source')*
- Merge the new network with the old module map
    1. Copy new network to clipboard (*Select the whole new network, BiNoM, Utilities, Clipboard, Copy selected nodes and edges to clipboard*)
    2. Insert the new network to the old module map (*Go to the old module map, BiNoM, Utilities, Clipboard, Paste nodes and edges from clipboard, click OK in the dialogue window)*
    3. Associate the resulting network with the new master map (*BiNoM I/O, 'Associate CellDesigner source')*
    4. Export the resulting network to CellDesigner , (*BiNoM I/O, 'Export current network to CellDesigner'*)
    5. Finalise parsing the network and creating final layout of the new module amp

Important note: Then layout of the old module map will be preserved. The common entities in both maps will stay at the location as in the old module map, only new entities will be at the location of the new network. Parsing of the network and relocation of entities can be done in Cytoscape or in CellDesigner.

Old module map, the layout is preserved

The edges between modules can guide the parsing of the new network, new entities can be moved and embedded into the old module.

New network inserted into the old module map.



Appendix 6: Preparation of images with semi-transparent edges and zoom levels

Use folder 'zooms_preparation_scripts_ACSN' with scripts. See examples of maps prepared using this procedure.

Prepare folder per map (see folder 'zooms_preparation_scripts_ACSN', after see folder 'master'):
xml of the map
png of the map with colored edges generated in CellDesigner
7 scripts
BiNoM_all.jar

Zoom levels of master map

Step 1: Remove reactions from master map (for detailed zoom level)
Open the script 'remove_reactions.sh'; change name of the file (*e.g. dnarepair_master.xml*).
Run the scipt:
./remove_reactions.sh
This action generated xml without reactions (e.g. dnarepair_master_noreactions.xml)

Open the file in CellDesigner, generate png (e.g. dnarepair_master_noreactions.png)

Step 2: Merge level 3 zoom of master map (detailed zoom level)
Open the script 'merge_level_3.sh'; change names of the file (*e.g. png1:* dnarepair_master.png; *png2:* dnarepair_master_noreactions.png; png out: dnarepair_master-3.png).
Run the script:
./merge_level_3.sh
The generated dnarepair_master-3 is used in GIMP for creating of the image with coloured modules background (detailed zoom level, zoom 3).

Step 3: Make level 2 zoom of master map (for hidden details zoom level)
Open the script 'make_zoom2.sh'; change names of the file (*e.g. xml dnarepair_master.xml --xmlout dnarepair_master-2_noscaling.xml*)
Run the script:
./make_zoom_2.sh
The generated file is dnarepair_master-2_noscaling.xml.

Open the file in CellDesigner and generate png (dnarepair_master-2_noscaling.png)

Use this file for next step.

Step 4: Remove reactions from level 2 zoom of master map (for hidden details zoom level)
Open the script 'remove_reactions_level_2.sh; change name of the file (*e.g. ml dnarepair_master-2_noscaling.xml*).
Run the script:
./remove_reactions_level_2.sh
This action generated xml without reactions (e.g. dnarepair_master-2_noscaling_noreactions.xml)

Open the file in CellDesigner, generate png (e.g. dnarepair_master-2_noscaling_noreactions.png)

Use this file for next step.

Step 5: Merge level 2 zoom of master map (for hidden details zoom level)
Open the script 'merge_level_2.sh'; change names of the file (*e.g. png1: dnarepair_master-2.png; png2: dnarepair_master-2_noreactions.png; png out: dnarepair_master-2_merged.png*).
Run the script:
./merge_level_2.sh
The generated 'dnarepair_master-2_merged.png'' is used for next step.

Step 6: Scale down level 2 zoom of master map (hidden details zoom level)
Open the script 'scale_2_merged_to_2.sh'; change names of the file (*e.g. png1 dnarepair_master-2_merged.png --pngout dnarepair_master-2.png*).
Run the script:
./scale_2_merged_to_2.sh
The generated 'dnarepair_master-2.png'' is used in GIMP for creating of the image with coloured modules background (hidden details zoom level, zoom 2).

Step 7: Make level 1 zoom of master map (pruned zoom level)
Open the script 'scale_2_to_1.sh'; change names of the file (*dnarepair_master-2.png --pngout dnarepair_master-1.png*)
Run the script:
./scale_2_to_1.sh
The generated 'dnarepair_master-1.png' is used in GIMP for creating of the image with coloured modules background (pruned zoom level, zoom 1).

!! Note: It generated sale down from the previous zoom level. In the future this step will be replaced by pruning based on the canonical pathways content (from Reactome).

Step 8: Make level 0 zoom of master map (top level view)

Level 0, the top level view of the map is generated in Gimp from the zoom 1 image with coloured modules background without map image. The size is compressed two times from the zoom 1 image.

Zoom levels of module maps

Step 1: Remove reactions from module map
Open the script 'remove_reactions.sh'; change name of the file (*e.g. dnarepair_BER.xml*).
Name of the folded where all maps folders with zooms will be generated (e.g. zooms_preparation_scripts_ACSN)
Run the script:
./remove_reactions.sh
This action generated xml without reactions (e.g. 'dnarepair_BER_noreactions.xml')

Open the file in CellDesigner, generate png.

Step 2: Merge level 3 zoom of module map
Open the script 'merge_level_3.sh'; change names of the file (*e.g. png1: dnarepair_BER.png; png2: dnarepair_BER_noreactions.png; png out: dnarepair_BER-3.png*).
Run the script:
./merge_level_3.sh
The generated 'dnarepair_BER-3.png' is used in NaviCell source folder for NaviCell map generation.

Step 3: Make level 2 zoom of module map
Open the script 'scale_3_to_2.sh'; change names of the file (*e.g. png1: dnarepair_BER-3.png; pngout: dnarepair_BER-2.png*)
Run the script:
./scale_3_to_2.sh
The generated 'dnarepair_BER-2.png' is used in NaviCell source folder for NaviCell map generation.

Step 4: Make level 1 zoom of module map
Open the script 'scale_2_to_1.sh'; change names of the file (*e.g. png1: dnarepair_BER-2.png; pngout: dnarepair_BER-1.png*)
Run the script:
./scale_2_to_1.sh
The generated 'dnarepair_BER-1.png' is used in NaviCell source folder for NaviCell map generation.

Step 5: Make level 0 zoom of module map
Open the script 'scale_1_to_0.sh'; change names of the file (*e.g. png1: dnarepair_BER-1.png; pngout: dnarepair_BER-0.png*)
Run the script:
./scale_1_to_0.sh
The generated 'dnarepair_BER-0.png' is used in NaviCell source folder for NaviCell map generation.

Appendix 7: Preparation of images with semi-transparent coloured modules background for each zoom level

Open the detailed zoom level image of map in Gimp *(e.g. dnarepair_master-3)*
Do not change the dimensions of the image, this size must be as in xml file
Create layer per each module for background colouring (should be the xcf file!!)
Use 25% saturation of colour for the background of modules
Assign names of modules and mega-modules (see below the fonts and sizes)
Locate names of modules avoiding overlap with the map entities
Flatten the image and save as png
NOTE!! Always save 3 files: xcf with all layers, flatten xcf, png

The generated png is used for creating the detailed zoom (zoom-3) of the map in NaviCell.

Use the xcf file from detailed zoom for preparation the file for hidden details zoom:
Open the xcf in Gimp and change the image dimensions to two times smaller
Delete the layer with detailed zoom level of the map, create enw layer and insert the hidden zoom level *(e.g. dnarepair_master-2_merged.png)*
Re-assign names of modules and mega-modules (see below the fonts and sizes)
NOTE!! When the size of the image is changed, the letters reduce too, so need to re-assign the names.
Flatten the image and save as png
NOTE!! Always save 3 files: xcf with all layers, flatten xcf, png

The generated png is used for creating the hidden details zoom (zoom-2) of the map in NaviCell.

Use the xcf file from hidden details zoom for preparation the file for canonical zoom:
Open the xcf in Gimp and change the image dimensions to two times smaller
Re-assign names of modules and mega-modules (see below the fonts and sizes)
NOTE!! When the size of the image is changed, the letters reduce too, so need to re-assign the names.
Flatten the image and save as png
NOTE!! Always save 3 files: xcf with all layers, flatten xcf, png

The generated png is used for creating the canonical zoom (zoom-1) of the map in NaviCell.

Use the xcf file from canonical zoom for preparation the file for top level zoom:
Open the xcf in Gimp and change the image dimensions to two times smaller
Delete the layer with the map, create the layer with white background
Re-assign names of modules and mega-modules (see below the fonts and sizes)

The generated png is used for creating the top-level zoom (zoom-0) of the map in NaviCell.

Use the following fonts/size/zoom in GIMP

Font is always **Serif Bold**

Font sizes

	Zoom 3			Zoom 2			Zoom 1			Zoom 0		
Map/Module	mega	normal	small	mega	normal	small	mega	normal	small	mega	normal	small
DNA repair	120	100		100	80		60	45		45	35	
PCD map	120	100	85	80	65	44	55	40	30	40	26	20