

Welcome to BiNA

The Biological Network Analyzer (BiNA) is a workbench for visualizing and analyzing biological networks. Various biological networks can be displayed, edited and analyzed.

BiNA 2.4.1.1 updated release

2013-12-16

This updated release fixed a small bug, which causes the process dialog to not disappear.

BiNA 2.4.1 released

2013-12-06

This release is a maintenance release, containing only few new features.

New Features

- KEGG Visualization: Improved layouts by using the partial layouter. Support for some metabolic overview maps.
- Regulatory Visualization: Feature for loading connected pathways from the context menu of a pathway.
- We changed the default layout style for regulatory visualizations, such that every pathway has its own layout, not the parental one. This is for the up-coming feature of the KEGG regulatory style of the next release.
- ...

Major Improvements

- Drastical speed-up for rendering of large networks due to some implementation improvements.

Bug Fixes

- BugFix: Major problem with the process dialog, which sometime caused BiNA to be dead-locked.
- BugFix: Closing large visualization could take several minutes, this has been reduced to < 1 second.
- BugFix: Opening an argument was not able anymore.
- BugFix: Serialization problem of visualization in KEGG style.
- ... many more.

Fixed problems with latest Java 7 update 45

2013-10-24

The latest update of Java 7 (update 45) raised the security base line. Therefore, all Java users are forced to update to this version. This version also introduced new security policies for Java Webstart, which were not compatible with the Webstart version of BiNA 2.4.0. Note, the download version was not affected.

BiNA 2.4.0 released

2013-08-14

This BiNA release has many improvements but also changes the license of BiNA to 3-clause BSD to solve license incompatibilities between the LGPL and the yFiles for Java license. For more information have a look at our [license](#) [1] page.

New Features

- Analysis: An new example analysis algorithm for determine the betweenness centrality of the network is provided.
- Analysis: The plane representation which is created for analysis algorithms is now configurable.
- Visualization: A new exploration view mode.
- ...

Major Improvements

- KEGG layouts have been drastically improved.

Bug Fixes

- Timeseries data is shown correctly.
- A number of GUI bugs have been solved.
- A huge number of smaller bugs have been fixed.

BiNA 2.3.1 released

2012-09-11

New Features and Changes

- Support for searching of pathways containing things from a series shon in the *Analysis Data Explorer* view. We support different scoring methods including enrichment score.
- Id translation for id lists of serieses using UniProt ID mapping service.
- Improved speed for data base access.

Fixed Bugs

- Log entries in the early startup are now written to the log file.
- Fixed problem with n.a. data for visibility mapping point.

BiNA 2.3.0 released

2012-08-17

New Features and Changes

We improved a lot of things under the hood, but the most important ones for you are:

- If BiNA is already running and you start it again with a different file to open, the existing instance will open the requested files. This works also for the Webstart version.
- Data mapping now supports multiple values per id. This features the visualization of multiple time-series from one series per node.
- Improved mapping legends and image exporter now support exporting of mapping legends.
- Added some new functions for playing around with serieses (e.g., global scaling)
- Improved SwissProt sub-cellular compartment locator by parsing GO terms.
- Improved side-compound handling for metabolic visualization style by combining with alias functionality.
- New File->*Open URL...* menu.
- New *File->Recent* menu containg recently opened/saved files.
- Importing/exporting of SIF format supports now inline labeling of complexes/families.
- Support for Windows shortcuts in bundle folder.

Fixed Bugs

- There are a large number of BugFixes, which are noted in the mercurial commit messages. We also removed a number of memory leaks, coming from not disposed swing dialogs.

BiNA 2.2.1 released

2012-05-28

- Faster rendering of networks.
- Some smaller fixes.

BiNA 2.2.0 released

2012-05-11

- New: Support for accessing a Rserve server.
- New: Improvement of installation/update wizard.
- New: Swissprot protein location can be directly used for assigning cellular components in layered background model.
- Improved native access to R via JRI.
- A large number of smaller fixes.

Source URL: <http://www.bina.unipax.info/home>

Links

[1] <http://www.bina.unipax.info/license>