
pypath Documentation

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CONTENTS:

1	Installation	3
1.1	Linux	3
1.1.1	igraph C library, cairo and pycairo	3
1.1.2	Directly from git	3
1.1.3	With pip	3
1.1.4	Build source distribution	3
1.2	Mac OS X	3
1.2.1	Troubleshooting	4
1.3	Microsoft Windows	4
1.3.1	With Anaconda	4
1.3.2	With other Python distributions	5
1.3.3	Known issues	5
2	Reference	7
2.1	annot module	7
2.2	bel module	8
2.3	complex module	8
2.4	intera module	9
2.5	intercell module	9
2.6	main module	9
2.7	ptm module	56
3	Webservice	57
3.1	Mouse and rat	57
3.2	Examples	57
4	Release history	59
4.1	0.1.0	59
4.2	0.2.0	59
4.3	0.3.0	59
4.4	0.4.0	59
4.5	0.5.0	59
4.6	0.7.74	60
4.7	Upcoming	60
5	Features	61
5.1	ID conversion	61
5.2	Pathways	61
5.3	Structural features	61
5.4	Sequences	61

5.5	Tissue expression	62
5.6	Functional annotations	62
5.7	Drug compounds	62
5.8	Technical	62
6	OmniPath in R	63
	Python Module Index	65
	Index	67

pypath is a Python package built around igraph to work with molecular network representations e.g. protein, miRNA and drug compound interaction networks.

note `pypath` supports both Python 2.7 and Python 3.6+. In the beginning, `pypath` has been developed only for Python 2.7. Then the code have been adjusted to Py3 however we can not guarantee no incompatibilities remained. If you find any method does not work please submit an issue on github. For few years I develop and test `pypath` in Python 3. Therefore this is the better supported Python variant.

documentation <http://saezlab.github.io/pypath>

issues <https://github.com/saezlab/pypath/issues>

INSTALLATION

1.1 Linux

In almost any up-to-date Linux distribution the dependencies of **pypath** are built-in, or provided by the distributors. You only need to install a couple of things in your package manager (cairo, py(2)cairo, igraph, python(2)-igraph, graphviz, pygraphviz), and after install **pypath** by *pip* (see below). If any module still missing, you can install them the usual way by *pip* or your package manager.

1.1.1 igraph C library, cairo and pycairo

python(2)-igraph is a Python interface to use the igraph C library. The C library must be installed. The same goes for *cairo*, *py(2)cairo* and *graphviz*.

1.1.2 Directly from git

```
pip install git+https://github.com/saezlab/pypath.git
```

1.1.3 With pip

Download the package from /dist, and install with pip:

```
pip install pypath-x.y.z.tar.gz
```

1.1.4 Build source distribution

Clone the git repo, and run setup.py:

```
python setup.py sdist
```

1.2 Mac OS X

On OS X installation is not straightforward primarily because cairo needs to be compiled from source. We provide 2 scripts here: the **mac-install-brew.sh** installs everything with HomeBrew, and **mac-install-conda.sh** installs from Anaconda distribution. With these scripts installation of igraph, cairo and graphviz goes smoothly most of the time, and options are available for omitting the 2 latter. To know more see the description in the script header. There is a

third script **mac-install-source.sh** which compiles everything from source and presumes only Python 2.7 and Xcode installed. We do not recommend this as it is time consuming and troubleshooting requires expertise.

1.2.1 Troubleshooting

- no module named ... when you try to load a module in Python. Did the installation of the module run without error? Try to run again the specific part from the mac install shell script to see if any error comes up. Is the path where the module has been installed in your `$PYTHONPATH`? Try `echo $PYTHONPATH` to see the current paths. Add your local install directories if those are not there, e.g. `export PYTHONPATH="/Users/me/local/python2.7/site-packages:$PYTHONPATH"`. If it works afterwards, don't forget to append these export path statements to your `~/.bash_profile`, so these will be set every time you launch a new shell.
- `pkgconfig` not found. Check if the `$PKG_CONFIG_PATH` variable is set correctly, and pointing on a directory where `pkgconfig` really can be found.
- Error while trying to install `py(2)cairo` by `pip`. `py(2)cairo` could not be installed by `pip`, but only by `waf`. Please set the `$PKG_CONFIG_PATH` before. See **mac-install-source.sh** on how to install with `waf`.
- Error at `pygraphviz` build: `graphviz/cgraph.h` file not found. This is because the directory of `graphviz` detected wrong by `pkgconfig`. See **mac-install-source.sh** how to set include dirs and library dirs by `--global-option` parameters.
- Can not install `bioservices`, because installation of `jurko-suds` fails. Ok, this fails because `pip` is not able to install the recent version of `setuptools`, because a very old version present in the system path. The development version of `jurko-suds` does not require `setuptools`, so you can install it directly from git as it is done in **mac-install-source.sh**.
- In **Anaconda**, `pypath` can be imported, but the modules and classes are missing. Apparently Anaconda has some built-in stuff called `pypath`. This has nothing to do with this module. Please be aware that Anaconda installs a completely separated Python distribution, and does not detect modules in the main Python installation. You need to install all modules within Anaconda's directory. **mac-install-conda.sh** does exactly this. If you still experience issues, please contact us.

1.3 Microsoft Windows

Not many people have used `pypath` on Microsoft computers so far. Please share your experiences and contact us if you encounter any issue. We appreciate your feedback, and it would be nice to have better support for other computer systems.

1.3.1 With Anaconda

The same workflow like you see in `mac-install-conda.sh` should work for Anaconda on Windows. The only problem you certainly will encounter is that not all the channels have packages for all platforms. If certain channel provides no package for Windows, or for your Python version, you just need to find an other one. For this, do a search:

```
anaconda search -t conda <package name>
```

For example, if you search for `pycairo`, you will find out that `vgauther` provides it for `osx-64`, but only for Python 3.4, while `richlewis` provides also for Python 3.5. And for `win-64` platform, there is the channel of `KristanAmstrong`. Go along all the commands in `mac-install-conda.sh`, and modify the channel if necessary, until all packages install successfully.

1.3.2 With other Python distributions

Here the basic principles are the same as everywhere: first try to install all external dependencies, after *pip* install should work. On Windows certain packages can not be installed by compiled from source by *pip*, instead the easiest to install them precompiled. These are in our case *fisher*, *lxml*, *numpy* (*mkl version*), *pycairo*, *igraph*, *pygraphviz*, *scipy* and *statsmodels*. The precompiled packages are available here: <http://www.lfd.uci.edu/~gohlke/pythonlibs/>. We tested the setup with Python 3.4.3 and Python 2.7.11. The former should just work fine, while with the latter we have issues to be resolved.

1.3.3 Known issues

- “No module *fabirc* available.” – or *pysftp* missing: this is not

important, only certain data download methods rely on these modules, but likely you won’t call those at all. * Progress indicator floods terminal: sorry about that, will be fixed soon. * Encoding related exceptions in Python2: these might occur at some points in the module, please send the traceback if you encounter one, and we will fix as soon as possible.

Special thanks to Jorge Ferreira for testing pypath on Windows!

REFERENCE

2.1 annot module

```
class pypath.annot.Adhesome (**kwargs)

class pypath.annot.AnnotationBase (name, ncbi_tax_id=9606, input_method=None, input_args=None, **kwargs)

    all_uniprots ()
        All UniProt IDs annotated in this resource.

    get_subset (method=None, **kwargs)
        Retrieves a subset by filtering based on kwargs. Each argument should be a name and a value or set of values. Elements having the provided values in the annotation will be returned. Returns a set of UniProt IDs.

    load_uniprots ()
        Retrieves a set of all UniProt IDs to have a base set of the entire proteome.

    reload ()
        Reloads the object from the module level.

class pypath.annot.CellPhoneDB (**kwargs)

class pypath.annot.CellPhoneDBComplex (**kwargs)

class pypath.annot.CellSurfaceProteinAtlas (ncbi_tax_id=9606, **kwargs)

class pypath.annot.Corum (annot_attr, **kwargs)

class pypath.annot.CorumFuncat (**kwargs)

class pypath.annot.CorumGO (**kwargs)

class pypath.annot.Exocarta (ncbi_tax_id=9606, **kwargs)

class pypath.annot.GOIntercell (categories=None, go_annot=None, ncbi_tax_id=9606)

class pypath.annot.GuideToPharmacology (load_sources=False, **kwargs)

class pypath.annot.Hgnc (**kwargs)

class pypath.annot.HpmrComplex (**kwargs)

class pypath.annot.HumanPlasmaMembraneReceptome (**kwargs)

class pypath.annot.Integrins (**kwargs)

class pypath.annot.Kirouac2010 (load_sources=False, **kwargs)
```

```
class pypath.annot.LigandReceptor (name, ligand_col=None, recep-
                                tor_col=None, ligand_id_type=None, recep-
                                tor_id_type=None, record_processor_method=None,
                                record_extra_fields=None, record_defaults=None, ex-
                                tra_fields_methods=None, **kwargs)
```

```
class pypath.annot.Locate (ncbi_tax_id=9606, literature=True, external=True, predictions=False)
```

```
class pypath.annot.Matrisome (ncbi_tax_id=9606, **kwargs)
```

```
class pypath.annot.Matrixdb (ncbi_tax_id=9606)
```

```
class pypath.annot.Membranome (**kwargs)
```

```
class pypath.annot.Opm (ncbi_tax_id=9606, **kwargs)
```

```
class pypath.annot.Ramilowski2015 (load_sources=False, **kwargs)
```

```
class pypath.annot.Surfaceome (**kwargs)
```

```
class pypath.annot.Topdb (ncbi_tax_id=9606, **kwargs)
```

```
class pypath.annot.Vesiclepedia (ncbi_tax_id=9606, **kwargs)
```

```
class pypath.annot.Zhong2015 (**kwargs)
```

```
pypath.annot.get_db (keep_annotators=True)
```

Retrieves the current database instance and initializes it if does not exist yet.

```
pypath.annot.init_db (keep_annotators=True)
```

Initializes or reloads the annotation database. The database will be assigned to the `db` attribute of this module.

2.2 bel module

2.3 complex module

```
class pypath.complex.AbstractComplexResource (name, ncbi_tax_id=9606, in-
                                put_method=None, input_args=None,
                                **kwargs)
```

A resource which provides information about molecular complexes.

```
class pypath.complex.CellPhoneDB (**kwargs)
```

```
class pypath.complex.Compleat (input_args=None, **kwargs)
```

```
class pypath.complex.ComplexAggregator (resources=None)
```

```
class pypath.complex.ComplexPortal (input_args=None, **kwargs)
```

```
class pypath.complex.Corum (input_args=None, **kwargs)
```

```
class pypath.complex.GuideToPharmacology (input_args=None, **kwargs)
```

```
class pypath.complex.Havugimana (input_args=None, **kwargs)
```

```
class pypath.complex.Hpmr (input_args=None, **kwargs)
```

```
class pypath.complex.Humap (input_args=None, **kwargs)
```

```
class pypath.complex.Pdb (input_args=None, **kwargs)
```

```
class pypath.complex.Signor (input_args=None, **kwargs)
```

```
pypath.complex.get_db()
```

Retrieves the current database instance and initializes it if does not exist yet.

```
pypath.complex.init_db()
```

Initializes or reloads the complex database. The database will be assigned to the `db` attribute of this module.

2.4 intera module

This module provides classes to represent and handle structural details of protein interactions i.e. residues, post-translational modifications, short motifs, domains, domain-motifs and domain-motif interactions, binding interfaces.

2.5 intercell module

```
class pypath.intercell.IntercellRole (source, role)
```

role

Alias for field number 1

source

Alias for field number 0

2.6 main module

```
class pypath.main.PyPath (ncbi_tax_id=None, copy=None, name='unnamed', cache_dir=None,
                          outdir='results', loglevel=0, loops=False)
```

Main network object.

Parameters

- **ncbi_tax_id** (*int*) – Optional, 9606 (Homo sapiens) by default. NCBI Taxonomic identifier of the organism from which the data will be downloaded.
- **default_name_type** (*dict*) – Optional, {'protein': 'uniprot', 'mirna': 'mirbase', 'drug': 'chembl', 'lncrna': 'lncrna-genesymbol'} by default. Contains the default identifier types to which the downloaded data will be converted. If others are used, user may need to provide the format definitions for the conversion tables.
- **copy** (*pypath.main.PyPath*) – Optional, None by default. Other *pypath.main.PyPath* instance from which the data will be copied.
- **mysql** (*tuple*) – Optional, (None, 'mapping') by default. Contains the MySQL parameters used by the *pypath.mapping* module to load the ID conversion tables.
- **chembl_mysql** (*tuple*) – Optional, (None, 'chembl') by default. Contains the MySQL parameters used by the *pypath.mapping* module to load the ChEMBL ID conversion tables.
- **name** (*str*) – Optional, 'unnamed' by default. Session or project name (custom).
- **outdir** (*str*) – Optional, 'results' by default. Output directory where to store all output files.

- **loglevel** (*int*) – Optional, 0 by default. Sets the level of the logger. The higher the level the more messages will be written to the log.
- **loops** (*bool*) – Optional, `False` by default. Determines if self-loop edges are allowed in the graph.

Variables

- **adjlist** (*list*) – List of [set] containing the adjacency of each node. See [PyPath.update_adjlist\(\)](#) method for more information.
- **chembl** (*pypath.chembl.Chembl*) – Contains the ChEMBL data. See [pypath.chembl](#) module documentation for more information.
- **chembl_mysql** (*tuple*) – Contains the MySQL parameters used by the [pypath.mapping](#) module to load the ChEMBL ID conversion tables.
- **data** (*dict*) – Stores the loaded interaction and attribute table. See [PyPath.read_data_file\(\)](#) method for more information.
- **db_dict** (*dict*) – Dictionary of dictionaries. Outer-level keys are 'nodes' and 'edges', corresponding values are [dict] whose keys are the database sources with values of type [set] containing the edge/node indexes for which that database provided some information.
- **dgraph** (*igraph.Graph*) – Directed network graph object.
- **disclaimer** (*str*) – Disclaimer text.
- **dlabDct** (*dict*) – Maps the directed graph node labels [str] (keys) to their indices [int] (values).
- **dnodDct** (*dict*) – Maps the directed graph node names [str] (keys) to their indices [int] (values).
- **dnodInd** (*set*) – Stores the directed graph node names [str].
- **dnodLab** (*dict*) – Maps the directed graph node indices [int] (keys) to their labels [str] (values).
- **dnodNam** (*dict*) – Maps the directed graph node indices [int] (keys) to their names [str] (values).
- **edgeAttrs** (*dict*) – Stores the edge attribute names [str] as keys and their corresponding types (e.g.: set, list, str, ...) as values.
- **exp** (*pandas.DataFrame*) – Stores the expression data for the nodes (if loaded).
- **exp_prod** (*pandas.DataFrame*) – Stores the edge expression data (as the product of the normalized expression between the pair of nodes by default). For more details see [pypath.main.PyPath.edges_expression\(\)](#).
- **exp_samples** (*set*) – Contains a list of tissues as downloaded by ProteomicsDB. See [PyPath.get_proteomicsdb\(\)](#) for more information.
- **failed_edges** (*list*) – List of lists containing information about the failed edges. Each failed edge sublist contains (in this order): [tuple] with the node IDs, [str] names of nodes A and B, [int] IDs of nodes A and B and [int] IDs of the edges in both directions.
- **go** (*dict*) – Contains the organism(s) NCBI taxonomy ID as key [int] and [pypath.go.GOAnnotation](#) object as value, which contains the GO annotations for the nodes in the graph. See [pypath.go.GOAnnotation](#) for more information.
- **graph** (*igraph.Graph*) – Undirected network graph object.

- **gsea** (*pypath.gsea.GSEA*) – Contains the loaded gene-sets from MSigDB. See *pypath.gsea.GSEA* for more information.
- **has_cats** (*set*) – Contains the categories (e.g.: resource types) [str] loaded in the current network. Possible categories are: 'm' for PTM/enzyme-substrate resources, 'p' for pathway/activity flow resources, 'i' for undirected/PPI resources, 'r' for process description/reaction resources and 't' for transcription resources.
- **htp** (*dict*) – Contains information about high-throughput data of the network for different thresholds [int] (keys). Values are [dict] containing the number of references ('rnum') [int], number of edges ('enum') [int], number of sources ('snum') [int] and list of PMIDs of the most common references above the given threshold ('htrefs') [set].
- **labDct** (*dict*) – Maps the undirected graph node labels [str] (keys) to their indices [int] (values).
- **lists** (*dict*) – Contains specific lists of nodes (values) for different categories [str] (keys). These can to be loaded from a file or a resource. Some methods include *pypath.main.PyPath.receptor_list()* ('rec'), *pypath.main.PyPath.druggability_list()* ('dgb'), *pypath.main.PyPath.kinases_list()* ('kin'), *pypath.main.PyPath.tfs_list()* ('tf'), *pypath.main.PyPath.disease_genes_list()* ('dis'), *pypath.main.PyPath.signaling_proteins_list()* ('sig'), *pypath.main.PyPath.proteome_list()* ('proteome') and *pypath.main.PyPath.cancer_drivers_list()* ('cdv').
- **loglevel** (*str*) – The level of the logger.
- **loops** (*bool*) – Whether if self-loop edges are allowed in the graph.
- **mapper** (*pypath.mapping.Mapper*) – *pypath.mapper.Mapper* object for ID conversion and other ID-related operations across resources.
- **mutation_samples** (*list*) – DEPRECATED
- **mysql_conf** (*tuple*) – Contains the MySQL parameters used by the *pypath.mapping* module to load the ID conversion tables.
- **name** (*str*) – Session or project name (custom).
- **ncbi_tax_id** (*int*) – NCBI Taxonomic identifier of the organism from which the data will be downloaded.
- **negatives** (*dict*) – Contains a list of negative interactions according to a given source (e.g.: Negatome database). See *pypath.main.PyPath.apply_negative()* for more information.
- **nodDct** (*dict*) – Maps the undirected graph node names [str] (keys) to their indices [int] (values).
- **nodInd** (*set*) – Stores the undirected graph node names [str].
- **nodLab** (*dict*) – Maps the undirected graph node indices [int] (keys) to their labels [str] (values).
- **nodNam** (*dict*) – Maps the directed graph node indices [int] (keys) to their names [str] (values).
- **outdir** (*str*) – Output directory where to store all output files.
- **palette** (*list*) – Contains a list of hexadecimal [str] of colors. Used for plotting purposes.

- **pathway_types** (*list*) – Contains the names of all the loaded pathway resources [str].
- **pathways** (*dict*) – Contains the list of pathways (values) for each resource (keys) loaded in the network.
- **plots** (*dict*) – DEPRECATED (?)
- **proteomicsdb** (*pypath.proteomicsdb.ProteomicsDB*) – Contains a *pypath.proteomicsdb.ProteomicsDB* instance, see the class documentation for more information.
- **raw_data** (*list*) – Contains a list of loaded edges [dict] from a data file. See *PyPath.read_data_file()* for more information.
- **seq** (*dict*) – (?)
- **session** (*str*) – Session ID, a five random alphanumeric characters.
- **session_name** (*str*) – Session name and ID (e.g. 'unnamed-abc12').
- **sourceNetEdges** (*igraph.Graph*) – (?)
- **sourceNetNodes** (*igraph.Graph*) – (?)
- **sources** (*list*) – List containing the names of the loaded resources [str].
- **u_pfam** (*dict*) – Dictionary of dictionaries, contains the mapping of UniProt IDs to their respective protein families and other information.
- **uniprot_mapped** (*list*) – DEPRECATED (?)
- **unmapped** (*list*) – Contains the names of unmapped items [str]. See *pypath.main.PyPath.map_item()* for more information.
- **vertexAttrs** (*dict*) – Stores the node attribute names [str] as keys and their corresponding types (e.g.: set, list, str, ...) as values.

acsn_effects (*graph=None*)

add_genesets (*genesets*)

add_grouped_eattr (*edge, attr, group, value*)

Merges (or creates) a given edge attribute as [dict] of [list] values.

Parameters

- **edge** (*int*) – Edge index where the given attribute value is to be merged or created.
- **attr** (*str*) – The name of the attribute. If such attribute does not exist in the network edges, it will be created on all edges (as an empty [dict], *value* will only be assigned to the given *edge* and *group*).
- **group** (*str*) – The key of the attribute dictionary where *value* is to be assigned.
- **value** (*list*) – The value of the attribute to be assigned/merged.

add_grouped_set_eattr (*edge, attr, group, value*)

Merges (or creates) a given edge attribute as [dict] of [set] values.

Parameters

- **edge** (*int*) – Edge index where the given attribute value is to be merged or created.
- **attr** (*str*) – The name of the attribute. If such attribute does not exist in the network edges, it will be created on all edges (as an empty [dict], *value* will only be assigned to the given *edge* and *group*).

- **group** (*str*) – The key of the attribute dictionary where *value* is to be assigned.
- **value** (*set*) – The value of the attribute to be assigned/merged.

add_list_eattr (*edge, attr, value*)

Merges (or creates) a given edge attribute as [list].

Parameters

- **edge** (*int*) – Edge index where the given attribute value is to be merged or created.
- **attr** (*str*) – The name of the attribute. If such attribute does not exist in the network edges, it will be created on all edges (as an empty [list], *value* will only be assigned to the given *edge*).
- **value** (*list*) – The value of the attribute to be assigned/merged.

add_set_eattr (*edge, attr, value*)

Merges (or creates) a given edge attribute as [set].

Parameters

- **edge** (*int*) – Edge index where the given attribute value is to be merged or created.
- **attr** (*str*) – The name of the attribute. If such attribute does not exist in the network edges, it will be created on all edges (as an empty [set], *value* will only be assigned to the given *edge*).
- **value** (*set*) – The value of the attribute to be assigned/merged.

add_update_edge (*id_a, id_b, source, is_directed, refs, stim, inh, taxon_a, taxon_b, typ, extra_attrs={}, add=False*)

Updates the attributes of one edge in the (undirected) network. Optionally it creates a new edge and sets the attributes, but it is not efficient as *igraph* needs to reindex edges after this operation, so better to create new edges in batches.

Parameters

- **id_a** (*str*) – Name of the source node of the edge to be added/updated.
- **id_b** (*str*) – Name of the source node of the edge to be added/updated.
- **source** (*set*) – Or [list], contains the names [str] of the resources supporting that edge.
- **is_directed** (*bool*) – Whether if the edge is directed or not.
- **refs** (*set*) – Or [list], contains the instances of the references *pypath.refs*. Reference for that edge.
- **stim** (*bool*) – Whether the edge is stimulatory or not.
- **inh** (*bool*) – Whether the edge is inhibitory or not.
- **taxon_a** (*int*) – NCBI Taxonomic identifier of the source molecule.
- **taxon_b** (*int*) – NCBI Taxonomic identifier of the target molecule.
- **typ** (*str*) – The type of interaction (e.g.: 'PPI')
- **extra_attrs** (*dict*) – Optional, {} by default. Contains any extra attributes for the edge to be updated.
- **add** (*bool*) – Optional, False by default. If set to True and the edge is not in the network, it will be created. Otherwise, in such case it will raise an error message.

add_update_vertex (*default_attrs*, *original_name*, *original_name_type*, *extra_attrs*={}, *add*=False)

Updates the attributes of one node in the (undirected) network. Optionally it creates a new node and sets the attributes, but it is not efficient as `igraph` needs to reindex vertices after this operation, so better to create new nodes in batches.

Parameters

- **default_attrs** (*dict*) – The attribute dictionary of the node to be updated/created.
- **original_name** (*str*) – Original node name (e.g.: UniProt ID).
- **original_name_type** (*str*) – The original node name type (e.g.: for the previous example, this would be 'uniprot').
- **extra_attrs** (*dict*) – Optional, {} by default. Contains any extra attributes for the node to be updated.
- **add** (*bool*) – Optional, False by default. If set to True and the node is not in the network, it will be created. Otherwise, in such case it will raise an error message.

affects (*identifier*)

all_between (*id_a*, *id_b*)

Checks for any edges (in any direction) between the provided nodes.

Parameters

- **id_a** (*str*) – The name of the source node.
- **id_b** (*str*) – The name of the target node.

Returns (*dict*) – Contains information on the directionality of the requested edge. Keys are 'ab' and 'ba', denoting the straight/reverse directionalities respectively. Values are [list] whose elements are the edge ID or None according to the existence of that edge in the following categories: undirected, straight and reverse (in that order).

all_neighbours (*indices*=False)

Looks for the first neighbours of all the nodes and creates an attribute ('neighbours') on each one of them containing a list of their UniProt IDs.

Parameters **indices** (*bool*) – Optional, False by default. Whether to list the neighbour nodes indices or their UniProt IDs.

apply_list (*name*, *node_or_edge*='node')

Creates vertex or edge attribute based on a list.

Parameters

- **name** (*str*) – The name of the list to be added as attribute. Must have been previously loaded with `pypath.main.PyPath.load_list()` or other methods. See description of `pypath.main.PyPath.lists` attribute for more information.
- **node_or_edge** (*str*) – Optional, 'node' by default. Whether the attribute list is to be added to the nodes or to the edges.

apply_negative (*settings*)

Loads a negative interaction source (e.g.: Negatome) into the current network.

Parameters **settings** (`pypath.input_formats.ReadSettings`) – `pypath.input_formats.ReadSettings` instance containing the detailed definition of the input format to the downloaded file. For instance `pypath.data_formats.negative['negatome']`

attach_network (*edge_list=False, regulator=False*)

Adds edges to the network from *edge_list* obtained from file or other input method. If none is passed, checks for such data in `pypath.main.PyPath.raw_data`.

Parameters

- **edge_list** (*str*) – Optional, `False` by default. The source name of the list of edges to be added. This must have been loaded previously (e.g.: with `pypath.main.PyPath.read_data_file()`). If none is passed, loads the data directly from `pypath.main.PyPath.raw_data`.
- **regulator** (*bool*) – Optional, `False` by default. If set to `True`, non previously existing nodes, will not be added (and hence, the edges involved).

basic_stats (*latex=False, caption="", latex_hdr=True, fontsize=8, font='HelveticaNeueLTStd-LtCn', fname=None, header_format='%s', row_order=None, by_category=True, use_cats=['p', 'm', 'i', 'r'], urls=True, annots=False*)

Returns basic numbers about the network resources, e.g. edge and node counts.

latex Return table in a LaTeX document. This can be compiled by PDFLaTeX: latex stats.tex

basic_stats_intergroup (*groupA, groupB, header=None*)

cancer_drivers_list (*intogen_file=None*)

Loads the list of cancer drivers. Contains information from COSMIC (needs user log in credentials) and IntOGen (if provided) and adds the attribute to the undirected network nodes.

Parameters **intogen_file** (*str*) – Optional, `None` by default. Path to the data file. Can also be [function] that provides the data. In general, anything accepted by `pypath.input_formats.ReadSettings.input`.

cancer_gene_census_list ()

Loads the list of cancer driver proteins from the COSMIC Cancer Gene Census.

clean_graph (*organisms_allowed=None*)

Removes multiple edges, unknown molecules and those from wrong taxon. Multiple edges will be combined by `pypath.main.PyPath.combine_attr()` method. Loops will be deleted unless the attribute `pypath.main.PyPath.loops` is set to `True`.

Parameters **organisms_allowed** (*set*) – NCBI Taxonomy identifiers [int] of the organisms allowed in the network.

collapse_by_name (*graph=None*)

Collapses nodes with the same name by copying and merging all edges and attributes. Operates directly on the provided network object.

Parameters **graph** (*igraph.Graph*) – Optional, `None` by default. The network for which the nodes are to be collapsed. If none is provided, takes `pypath.main.PyPath.graph` (undirected network) by default.

combine_attr (*lst, num_method=<built-in function max>*)

Combines multiple attributes into one. This method attempts to find out which is the best way to combine attributes.

- If there is only one value or one of them is `None`, then returns the one available.
- Lists: concatenates unique values of lists.
- Numbers: returns the greater by default or calls *num_method* if given.
- Sets: returns the union.
- Dictionaries: calls `pypath.common.merge_dicts()`.

- **Direction**: calls their special `pypath.main.Direction.merge()` method.

Works on more than 2 attributes recursively.

Parameters

- **lst** (*list*) – List of one or two attribute values.
- **num_method** (*function*) – Optional, `max` by default. Method to merge numeric attributes.

communities (*method*, ***kwargs*)

complex_comembership_network (*graph=None*, *resources=None*)

complexes (*methods=['3dcomplexes', 'havugimana', 'corum', 'complexportal', 'compleat']*)

complexes_in_network (*csource='corum', graph=None*)

compounds_from_chembl (*chembl_mysql=None, nodes=None, crit=None, andor='or',
assay_types=['B', 'F'], relationship_types=['D', 'H'],
multi_query=False, **kwargs*)

Loads compound data from ChEMBL to the network.

Parameters

- **chembl_mysql** (*tuple*) – Optional, `None` by default. Contains the MySQL parameters used by the `pypath.mapping` module to load the ChEMBL ID conversion tables. If none is passed, takes the current instance `pypath.main.PyPath.chembl_mysql` attribute.
- **nodes** (*list*) – Optional, `None` by default. List of node indices for which the information is to be loaded. If none is provided calls the method `pypath.main.PyPath.get_sub()` with the provided *crit* parameter.
- **crit** (*dict*) – Optional, `None` by default. Defines the critical attributes to generate a subnetwork to extract the nodes in case *nodes* is not provided. Keys are 'edge' and 'node' and values are [dict] containing the critical attribute names [str] and values are [set] containing those attributes of the nodes/edges that are to be kept in the subnetwork. If none is provided, takes the whole network.
- **andor** (*str*) – Optional, 'or' by default. Determines the search mode for the subnetwork generation (if *nodes=None*). See `pypath.main.PyPath.search_attr_or()` and `pypath.main.PyPath.search_attr_and()` for more details.
- **assay_types** (*list*) – Optional, ['B', 'F'] by default. Types of assay to query. Options are: 'A' (ADME), 'B' (Binding), 'F' (Functional), 'P' (Physicochemical), 'T' (Toxicity) and/or 'U' (Unassigned).
- **relationship_types** (*list*) – Optional, ['D', 'H'] by default. Assay relationship types to query. Possible values are: 'D' (Direct protein target assigned), 'H' (Homologous protein target assigned), 'M' (Molecular target other than protein assigned), 'N' (Non-molecular target assigned), 'S' (Subcellular target assigned) and/or 'U' (Default value, target has yet to be curated).
- **multi_query** (*bool*) – Optional, `False` by default. Not used.
- ****kwargs** – Additional keyword arguments for `pypath.chembl.Chembl.compounds_targets()`.

consistency ()

copy (*other*)

Copies another `pypath.main.PyPath` instance into the current one.

Parameters **other** (`pypath.main.PyPath`) – The instance to be copied from.

copy_edges (*sources*, *target*, *move=False*, *graph=None*)

Copies edges from *sources* node(s) to another one (*target*), keeping attributes and directions.

Parameters

- **sources** (*list*) – Contains the vertex index(es) [int] of the node(s) to be copied or moved.
- **target** (*int*) – Vertex index where edges and attributes are to be copied to.
- **move** (*bool*) – Optional, `False` by default. Whether to perform copy or move (remove or keep the source edges).
- **graph** (*igraph.Graph*) – Optional, `None` by default. The network graph object from which the nodes are to be merged. If none is passed, takes the undirected network graph.

count_sol ()

Counts the number of nodes with zero degree.

Returns (*int*) – The number of nodes with zero degree.

coverage (*lst*)

Computes the coverage (range [0, 1]) of a list of nodes against the current (undirected) network.

Parameters **lst** (*set*) – Can also be [list] (will be converted to [set]) or [str]. In the latter case it will retrieve the list with that name (if such list exists in `pypath.main.PyPath.lists`).

cspa_list ()

Loads a list of cell surface proteins from the Cell Surface Protein Atlas as a list. This resource is available for human and mouse. The list name is `cspa`.

curation_effort (*sum_by_source=False*)

Returns the total number of reference-interactions pairs.

@sum_by_source [bool] If True, counts the reference-interaction pairs by sources, and returns the sum of these values.

curation_stats (*by_category=True*)

curation_tab (*fname='curation_stats.tex'*, *by_category=True*, *use_cats=['p', 'm', 'i', 'r']*, *header_size='normalsize'*, ***kwargs*)

curators_work ()

Computes and prints an estimation of how many years of curation took to achieve the amount of information on the network.

databases_similarity (*index='simpson'*)

Computes the similarity across databases according to a given index metric. Computes the similarity across the loaded resources (listed in `pypath.main.PyPath.sources` in terms of nodes and edges separately.

Parameters **index** (*str*) – Optional, 'simpson' by default. The type of index metric to use to compute the similarity. Options are 'simpson', 'sorensen' and 'jaccard'.

Returns (*dict*) – Nested dictionaries (three levels). First-level keys are 'nodes' and 'edges', then second and third levels correspond to sources names which map to the similarity index between those sources [float].

degree_dist (*prefix*, *g=None*, *group=None*)

Computes the degree distribution over all nodes of the network. If *group* is provided, also across nodes of that group(s).

Parameters

- **prefix** (*str*) – Prefix for the file name(s).
- **g** (*igraph.Graph*) – Optional, *None* by default. The network over which to compute the degree distribution. If *none* is passed, takes the undirected network of the current instance.
- **group** (*list*) – Optional, *None* by default. Additional group(s) name(s) [*str*] of node attributes to subset the network and compute its degree distribution.

degree_dists ()

Computes the degree distribution for all the different network sources. This is, for each source, the subnetwork comprising all interactions coming from it is extracted and the degree distribution information is computed and saved into a file. A file is created for each resource under the name 'pwnet-<session_id>-degdist-<resource>'. Files are stored in `pypath.main.PyPath.outdir` ('results' by default).

delete_by_organism (*organisms_allowed=None*)

Removes the proteins of all organisms which are not given in *tax*.

Parameters **organisms_allowed** (*list*, *set*) – List of NCBI Taxonomy IDs [*int*] of the organism(s) that are to be kept.

delete_by_source (*source*, *vertexAttrsToDel=None*, *edgeAttrsToDel=None*)

Deletes nodes and edges from the network according to a provided source name. Optionally can also remove the given list of attributes from nodes and/or edges.

Parameters

- **source** (*str*) – Name of the source from which the nodes and edges have to be removed.
- **vertexAttrsToDel** (*list*) – Optional, *None* by default. Contains the names [*str*] of the attributes to be removed from the nodes.
- **edgeAttrsToDel** (*list*) – Optional, *None* by default. Contains the names [*str*] of the attributes to be removed from the edges.

delete_unknown (*organisms_allowed=None*, *entity_type='protein'*, *default_name_type=None*)

Removes those items which are not in the list of all default IDs of the organisms. By default, it means to remove all protein nodes not having a human UniProt ID.

Parameters

- **typ** (*str*) – Optional, 'protein' by default. Determines the molecule type. These can be 'protein', 'drug', 'lncrna', 'mirna' or any other type defined in `pypath.main.PyPath.default_name_type`.
- **default_name_type** (*str*) – Optional, *None* by default. The default name type for the given molecular species. If *none* is specified takes it from `pypath.main.PyPath.default_name_type` (e.g.: for 'protein', default is 'uniprot').
- **organisms_allowed** (*set*) – NCBI Taxonomy identifiers [*int*] of the organisms allowed in the network.

delete_unmapped ()

Checks the network for any existing unmapped node and removes it.

dgenesymbol (*genesymbol*)

Returns `igraph.Vertex()` object if the GeneSymbol can be found in the default directed network, otherwise `None`.

@genesymbol [str] GeneSymbol.

dgenesymbols (*genesymbols*)

dgs (*genesymbol*)

Returns `igraph.Vertex()` object if the GeneSymbol can be found in the default directed network, otherwise `None`.

@genesymbol [str] GeneSymbol.

dgss (*genesymbols*)

disease_genes_list (*dataset='curated'*)

Loads the list of all disease related genes from DisGeNet. This resource is human only.

dneighbors (*identifier, mode='ALL'*)

dp (*identifier*)

Same as `PyPath.get_node`, just for the directed graph. Returns `igraph.Vertex()` object if the identifier is a valid vertex index in the default directed graph, or a UniProt ID or GeneSymbol which can be found in the default directed network, otherwise `None`.

@identifier [int, str] Vertex index (int) or GeneSymbol (str) or UniProt ID (str) or `igraph.Vertex` object.

dproteins (*identifiers*)

dps (*identifiers*)

druggability_list ()

Loads the list of druggable proteins from DgiDB. This resource is human only. The list name is `dgb`.

duniprot (*uniprot*)

Same as `PyPath.uniprot()`, just for directed graph. Returns `igraph.Vertex()` object if the UniProt can be found in the default directed network, otherwise `None`.

@uniprot [str] UniProt ID.

duniprots (*uniprots*)

Returns list of `igraph.Vertex()` object for a list of UniProt IDs omitting those could not be found in the default directed graph.

dup (*uniprot*)

Same as `PyPath.uniprot()`, just for directed graph. Returns `igraph.Vertex()` object if the UniProt can be found in the default directed network, otherwise `None`.

@uniprot [str] UniProt ID.

dups (*uniprots*)

Returns list of `igraph.Vertex()` object for a list of UniProt IDs omitting those could not be found in the default directed graph.

dv (*identifier*)

Same as `PyPath.get_node`, just for the directed graph. Returns `igraph.Vertex()` object if the identifier is a valid vertex index in the default directed graph, or a UniProt ID or GeneSymbol which can be found in the default directed network, otherwise `None`.

@identifier [int, str] Vertex index (int) or GeneSymbol (str) or UniProt ID (str) or `igraph.Vertex` object.

dvs (*identifiers*)

edge_exists (*id_a*, *id_b*)

Returns a tuple of vertex indices if edge doesn't exist, otherwise, the edge ID. Not sensitive to direction.

Parameters

- **id_a** (*str*) – Name of the source node.
- **id_b** (*str*) – Name of the target node.

Returns (*int*) – The edge index, if exists such edge. Otherwise, [tuple] of [int] corresponding to the node IDs.

edge_loc (*graph=None*, *topn=2*)

edge_names (*e*)

Returns the node names of a given edge.

Parameters **e** (*int*) – The edge index.

Returns (*tuple*) – Contains the source and target node names of the edge [str].

edges_3d (*methods=['dataio.get_instruct', 'dataio.get_i3d']*)

edges_between (*group1*, *group2*, *directed=True*, *strict=False*)

Selects edges between two groups of vertex IDs. Returns set of edge IDs.

Parameters

- **group1**, **group2** (*set*) – List, set or tuple of vertex IDs.
- **directed** (*bool*) – Only edges with direction *group1* -> *group2* selected.
- **strict** (*bool*) – Edges with no direction information still selected even if *directed* is *False*.

edges_expression (*func=<function PyPath.<lambda>>*)

Executes function *func* for each pairs of connected proteins in the network, for every expression dataset. By default, *func* simply gives the product the (normalized) expression values.

func [callable] Function to handle 2 vectors (pandas.Series() objects), should return one vector of the same length.

edges_in_complexes (*csources=['corum']*, *graph=None*)

Creates edge attributes *complexes* and *in_complex*. These are both dicts where the keys are complex resources. The values in *complexes* are the list of complex names both the source and the target vertices belong to. The values *in_complex* are boolean values whether there is at least one complex in the given resources both the source and the target vertex of the edge belong to.

@csources [list] List of complex resources. Should be already loaded.

@graph [igraph.Graph()] The graph object to do the calculations on.

edges_ptms ()

edgeseq_inverse (*edges*)

Returns the sequence of all edge indexes that are not in the argument *edges*.

Parameters **edges** (*set*) – Sequence of edge indices [int] that will not be returned.

Returns (*list*) – Contains all edge indices [int] of the undirected network except the ones on *edges* argument.

export_dot (*nodes=None, edges=None, directed=True, labels='genesymbol', edges_filter=<function PyPath.<lambda>>, nodes_filter=<function PyPath.<lambda>>, edge_sources=None, dir_sources=None, graph=None, return_object=False, save_dot=None, save_graphics=None, prog='neato', format=None, hide=False, font=None, auto_edges=False, hide_nodes=[], defaults={}, **kwargs*)

Builds a pygraphviz.AGraph() object with filtering the edges and vertices along arbitrary criteria. Returns the Agraph object if requested, or exports the dot file, or saves the graphics.

@nodes : list List of vertex ids to be included. @edges : list List of edge ids to be included. @directed : bool Create a directed or undirected graph. @labels : str Name type to be used as id/label in the dot format. @edges_filter : function Function to filter edges, accepting igraph.Edge as argument. @nodes_filter : function Function to filter vertices, accepting igraph.Vertex as argument. @edge_sources : list Sources to be included. @dir_sources : list Direction and effect sources to be included. @graph : igraph.Graph The graph object to export. @return_object : bool Whether to return the pygraphviz.AGraph object. @save_dot : str Filename to export the dot file to. @save_graphics : str Filename to export the graphics, the extension defines the format. @prog : str The graphviz layout algorithm to use. @format : str The graphics format passed to pygraphviz.AGraph().draw(). @hide : bool Hide filtered edges instead of omit them. @hide_nodes : list Nodes to hide. List of vertex ids. @auto_edges : str Automatic, built-in style for edges. 'DIRECTIONS' or 'RESOURCE_CATEGORIES' are supported. @font : str Font to use for labels. For using more than one fonts refer to graphviz attributes with constant values or define callbacks or mapping dictionaries. @defaults : dict Default values for graphviz attributes, labeled with the entity, e.g. {'edge_penwidth': 0.2}. @**kwargs : constant, callable or dict Graphviz attributes, labeled by the target entity. E.g. edge_penwidth, 'vertex_shape' or graph_label. If the value is constant, this value will be used. If the value is dict, and has _name as key, for every instance of the given entity, the value of the attribute defined by _name will be looked up in the dict, and the corresponding value will be given to the graphviz attribute. If the key _name is missing from the dict, igraph vertex and edge indices will be looked up among the keys. If the value is callable, it will be called with the current instance of the entity and the returned value will be used for the graphviz attribute. E.g. edge_arrowhead(edge) or vertex_fillcolor(vertex) Example:

```
import pypath from pypath import data_formats net = pypath.PyPath() net.init_network(pfile =
'cache/default.pickle') #net.init_network({'arn': data_formats.omnipath['arn']}) tgf = [v.index
for v in net.graph.vs if 'TGF' in v['slk_pathways']] dot = net.export_dot(nodes = tgf,
save_graphics = 'tgf_slk.pdf', prog = 'dot',
```

```
main_title = 'TGF-beta pathway', return_object = True, label_font = 'HelveticaNeueLT-
Std Med Cn', edge_sources = ['Signalink3'], dir_sources = ['Signalink3'], hide =
True)
```

export_edgelist (*fname, graph=None, names=['name'], edge_attributes=[], sep='\t'*)

Write edge list to text file with attributes

Parameters

- **fname** – the name of the file or a stream to read from.
- **graph** – the igraph object containing the network
- **names** – list with the vertex attribute names to be printed for source and target vertices
- **edge_attributes** – list with the edge attribute names to be printed
- **sep** – string used to separate columns

export_graphml (*outfile=None, graph=None, name='main'*)

Saves the network in a .graphml file.

Parameters

- **outfile** (*str*) – Optional, None by default. Name/path of the output file. If none is passed, 'results/netrowk-<session_id>.graphml' is used.

- **graph** (*igraph.Graph*) – Optional, *None* by default. The network object to be saved. If none is passed, takes the undirected network of the current instance.
- **name** (*str*) – Optional, 'main' by default. The graph name for the output file.

export_ptms_tab (*outfile=None*)

Exports a tab file containing the PTM interaction information loaded in the network.

Parameters **outfile** (*str*) – Optional, *None* by default. The output file name/path to store the PTM information. If none is provided, the default is 'results/network-<session_id>.tab'.

Returns (*list*) – Contains the edge indices [int] of all PTM interactions.

export_sif (*outfile=None*)

Exports the network interactions in .sif format (Simple Interaction Format).

Parameters **outfile** (*str*) – Optional, *None* by default. Name/path of the output file. If none is passed, 'results/network-<session_id>.sif' is used.

export_struct_tab (*outfile=None*)

Exports a tab file containing the domain interaction information and PTM regulation loaded in the network.

Parameters **outfile** (*str*) – Optional, *None* by default. The output file name/path to store the PTM information. If none is provided, the default is 'results/network-<session_id>.tab'.

Returns (*list*) – Contains the edge indices [int] of all PTM interactions.

export_tab (*outfile=None*, *extra_node_attrs={}*, *extra_edge_attrs={}*, *unique_pairs=True*, ***kwargs*)

Exports the network in a tabular format. By default UniProt IDs, Gene Symbols, source databases, literature references, directionality and sign information and interaction type are included.

Parameters

- **outfile** (*str*) – Optional, *None* by default. Name/path of the output file. If none is passed, 'results/network-<session_id>.tab' is used.
- **extra_node_attrs** (*dict*) – Optional, {} by default. Additional node attributes to be included in the exported table. Keys are column names used in the header while values are names of vertex attributes. In the header '_A' and '_B' suffixes will be appended to the column names so the values can be assigned to A and B side interaction partners.
- **extra_edge_attrs** (*dict*) – Optional, {} by default. Additional edge attributes to be included in the exported table. Keys are column names used in the header while values are names of edge attributes.
- **unique_pairs** (*bool*) – Optional, *True* by default. If set to *True* each line corresponds to a unique pair of molecules, all directionality and sign information are covered in other columns. If *False*, order of 'A' and 'B' IDs corresponds to the direction while sign covered in further columns.
- **kwargs** (****) – Additional keyword arguments passed to `pypath.export.Export`.

filters (*line*, *positive_filters=[]*, *negative_filters=[]*)

find_all_paths (*start*, *end*, *attr=None*, *mode='OUT'*, *maxlen=2*, *graph=None*, *silent=False*, *update_adjlist=True*)

Finds all paths up to length *maxlen* between groups of vertices. This function is needed only because `igraph's get_all_shortest_paths()` finds only the shortest, not any path up to a defined length.

start [int or list] Indices of the starting node(s) of the paths.

end [int or list] Indices of the target node(s) of the paths.

attr [str] Name of the vertex attribute to identify the vertices by. Necessary if **start** and **end** are not igraph vertex ids but for example vertex names or labels.

mode ['IN', 'OUT', 'ALL'] Passed to `igraph.Graph.neighbors()`

maxlen [int] Maximum length of paths in steps, i.e. if **maxlen** = 3, then the longest path may consist of 3 edges and 4 nodes.

graph [igraph.Graph object] The graph you want to find paths in. `self.graph` by default.

find_all_paths2 (*graph, start, end, mode='OUT', maxlen=2, psize=100, update_adjlist=True*)

find_complex (*search*)

Finds complexes by their non standard names. E.g. to find DNA polymerases you can use the search term *DNA pol* which will be tested against complex names in CORUM.

first_neighbours (*node, indices=False*)

Looks for the first neighbours of a given node and returns a list of their UniProt IDs.

Parameters

- **node** (*str*) – The UniProt ID of the node of interest. Can also be the index of such node [int].
- **indices** (*bool*) – Optional, `False` by default. Whether to return the neighbour nodes indices or their UniProt IDs.

Returns (*list*) – The list containing the first neighbours of the queried node.

fisher_enrichment (*lst, attr, ref='proteome'*)

Computes an enrichment analysis using Fisher's exact test. The contingency table is built as follows: First row contains the number of nodes in the *ref* list (such list is considered to be loaded in `pypath.main.PyPath.lists`) and the number of nodes in the current (undirected) network. Second row contains the number of nodes in *lst* list (also considered to be already loaded) and the number of nodes in the network with a non-empty attribute *attr*. Uses `scipy.stats.fisher_exact()`, see the documentation of the corresponding package for more information.

Parameters

- **lst** (*str*) – Name of the list in `pypath.main.PyPath.lists` whose number of elements will be the first element in the second row of the contingency table.
- **attr** (*str*) – The node attribute name for which the number of nodes in the network with such attribute will be the second element of the second row of the contingency table.
- **ref** (*str*) – Optional, 'proteome' by default. The name of the list in `pypath.main.PyPath.lists` whose number of elements will be the first element of the first row of the contingency table.

Returns

- (*float*) – Prior odds ratio.
- (*float*) – P-value or probability of obtaining a distribution as extreme as the observed, assuming that the null hypothesis is true.

geneset_enrichment (*proteins, all_proteins=None, geneset_ids=None, alpha=0.05, correction_method='hommel'*)

Does not work at the moment because `cfisher` module should be replaced with `scipy`.

genesymbol (*genesymbol*)

Returns `igraph.Vertex()` object if the GeneSymbol can be found in the default undirected network, otherwise `None`.

@genesymbol [str] GeneSymbol.

genesymbol_labels (*graph=None, remap_all=False*)

Creates vertex attribute 'label' and fills up with the corresponding GeneSymbols of all proteins where the GeneSymbol can be looked up based on the default name of the protein vertex (UniProt ID by default). If the attribute 'label' has been already initialized, updates this attribute or recreates if *remap_all* is set to True.

Parameters

- **graph** (*igraph.Graph*) – Optional, None by default. The network graph object where the GeneSymbol labels are to be set/updated. If none is passed, takes the current network undirected graph by default (`pypath.main.PyPath.graph`).
- **remap_all** (*bool*) – Optional, False by default. Whether to map anew the GeneSymbol labels if those were already initialized.

genesymbols (*genesymbols*)

get_attrs (*line, spec, lnum*)

get_directed (*graph=False, conv_edges=False, mutual=False, ret=False*)

Converts a copy of *graph* undirected *igraph.Graph* object to a directed one. By default it converts the current network instance in `pypath.main.PyPath.graph` and places the copy of the directed instance in `pypath.main.PyPath.dgraph`.

Parameters

- **graph** (*igraph.Graph*) – Optional, None by default. Undirected graph object. If none is passed, takes the current undirected network instance and saves the directed network under the attribute `pypath.main.PyPath.dgraph`. Otherwise, the directed graph will be returned instead.
- **conv_edges** (*bool*) – Optional, False by default. Whether to convert undirected edges (those without explicit direction information) to an arbitrary direction edge or a pair of opposite edges. Otherwise those will be deleted.
- **mutual** (*bool*) – Optional, False by default. If *conv_edges* is True, whether to convert the undirected edges to a single, arbitrary directed edge, or a pair of opposite directed edges.
- **ret** (*bool*) – Optional, False by default. Whether to return the directed graph instance, or not. If a *graph* is provided, its directed version will be returned anyway.

Returns (*igraph.Graph*) – If *graph* is passed or *ret* is True, returns the copy of the directed graph. otherwise returns None.

get_dirs_signs ()

get_edge (*source, target, directed=True*)

Returns *igraph.Edge* object if an edge exist between the 2 proteins, otherwise None.

Parameters

- **source** (*int, str*) – Vertex index or UniProt ID or GeneSymbol or *igraph.Vertex* object.
- **target** (*int, str*) – Vertex index or UniProt ID or GeneSymbol or *igraph.Vertex* object.
- **directed** (*bool*) – To be passed to *igraph.Graph.get_eid*()

get_edges (*sources, targets, directed=True*)

Returns a generator with all edges between source and target vertices.

Parameters

- **sources** (*iterable*) – Source vertex IDs, names, labels, or any iterable yielding `igraph.Vertex` objects.
- **targets** (*iterable*) – Target vertex IDs, names, labels, or any iterable yielding `igraph.Vertex` objects.
- **directed** (*bool*) – Passed to `igraph.get_eid()`.

get_function (*fun*)

get_giant (*replace=False, graph=None*)

Returns the giant component of the *graph*, or replaces the `igraph.Graph` instance with only the giant component if specified.

Parameters

- **replace** (*bool*) – Optional, `False` by default. Specifies whether to replace the `igraph.Graph` instance. This can be either the undirected network of the current `pypath.main.PyPath` instance (default) or the one passed under the keyword argument *graph*.
- **graph** (*igraph.Graph*) – Optional, `None` by default. The graph object from which the giant component is to be computed. If none is specified, takes the undirected network of the current `pypath.main.PyPath` instance.

Returns (*igraph.Graph*) – If `replace=False`, returns a copy of the giant component graph.

get_go (*organism=None*)

Returns the `GOAnnotation` object for the organism requested (or the default one).

get_max (*attrList*)

get_network (*crit, andor='or', graph=None*)

Retrieves a subnetwork according to a set of user-defined attributes. Basically applies `pypath.main.PyPath.get_sub()` on a given *graph*.

Parameters

- **crit** (*dict*) – Defines the critical attributes to generate the subnetwork. Keys are 'edge' and 'node' and values are [dict] containing the critical attribute names [str] and values are [set] containing those attributes of the nodes/edges that are to be kept.
- **andor** (*str*) – Optional, 'or' by default. Determines the search mode. See `pypath.main.PyPath.search_attr_or()` and `pypath.main.PyPath.search_attr_and()` for more details.
- **graph** (*igraph.Graph*) – Optional, `None` by default. The graph object where to extract the subnetwork. If none is passed, takes the current network (undirected) graph (`pypath.main.PyPath.graph`).

Returns (*igraph.Graph*) – The subgraph obtained from filtering according to the attributes defined in *crit*.

get_node (*identifier*)

Returns `igraph.Vertex()` object if the identifier is a valid vertex index in the default undirected graph, or a UniProt ID or GeneSymbol which can be found in the default undirected network, otherwise `None`.

@**identifier** [int, str] Vertex index (int) or GeneSymbol (str) or UniProt ID (str) or `igraph.Vertex` object.

get_node_d (*identifier*)

Same as `PyPath.get_node`, just for the directed graph. Returns `igraph.Vertex()` object if the

identifier is a valid vertex index in the default directed graph, or a UniProt ID or GeneSymbol which can be found in the default directed network, otherwise `None`.

@identifier [int, str] Vertex index (int) or GeneSymbol (str) or UniProt ID (str) or `igraph.Vertex` object.

get_node_pair (*id_a*, *id_b*, *directed=False*)

Retrieves the node IDs from a pair of node names.

Parameters

- **id_a** (*str*) – Name of the source node.
- **id_b** (*str*) – Name of the target node.
- **directed** (*bool*) – Optional, `False` by default. Whether to return the node indices from the directed or undirected graph.

Returns (*tuple*) – The pair of node IDs of the selected graph. If not found, returns `False`.

get_nodes (*identifiers*)

get_nodes_d (*identifiers*)

get_pathways (*source*)

get_proteomicsdb (*user*, *passwd*, *tissues=None*, *pickle=None*)

get_sub (*crit*, *andor='or'*, *graph=None*)

Selects the nodes from *graph* (and edges to be removed) according to a set of user-defined attributes.

Parameters

- **crit** (*dict*) – Defines the critical attributes to generate the subnetwork. Keys are 'edge' and 'node' and values are [dict] containing the critical attribute names [str] and values are [set] containing those attributes of the nodes/edges that are to be kept.
- **andor** (*str*) – Optional, 'or' by default. Determines the search mode. See `pypath.main.PyPath.search_attr_or()` and `pypath.main.PyPath.search_attr_and()` for more details.
- **graph** (*igraph.Graph*) – Optional, `None` by default. The graph object where to extract the subnetwork. If none is passed, takes the current network (undirected) graph (`pypath.main.PyPath.graph`).

Returns (*dict*) – Keys are 'nodes' and 'edges' whose values are [list] of elements (as indexes [int]). Nodes are those to be kept and edges to be removed on the extracted subnetwork.

get_taxon (*tax_dict*, *fields*)

go_annotate_graph (*aspects=('C', 'F', 'P')*)

Annotates protein nodes with GO terms. In the `go` vertex attribute each node is annotated by a dict of sets where keys are one letter codes of GO aspects and values are sets of GO accessions.

go_enrichment (*proteins=None*, *aspect='P'*, *alpha=0.05*, *correction_method='hommel'*, *all_proteins=None*)

Does not work at the moment because `cfisher` module should be replaced with `scipy`.

gs (*genesymbol*)

Returns `igraph.Vertex()` object if the GeneSymbol can be found in the default undirected network, otherwise `None`.

@genesymbol [str] GeneSymbol.

gs_affected_by (*genesymbol*)

gs_affects (*genesymbol*)

gs_edge (*source, target, directed=True*)

Returns `igraph.Edge` object if an edge exist between the 2 proteins, otherwise `None`.

@source [*str*] `GeneSymbol`

@target [*str*] `GeneSymbol`

@directed [*bool*] To be passed to `igraph.Graph.get_eid()`

gs_in_directed (*genesymbol*)

gs_in_undirected (*genesymbol*)

gs_inhibited_by (*genesymbol*)

gs_inhibits (*genesymbol*)

gs_neighborhood (*genesymbols, order=1, mode='ALL'*)

gs_neighbors (*genesymbol, mode='ALL'*)

gs_stimulated_by (*genesymbol*)

gs_stimulates (*genesymbol*)

gss (*genesymbols*)

guide2pharma ()

having_attr (*attr, graph=None, index=True, edges=True*)

Checks if edges or nodes of the network have a specific attribute and returns an iterator of the indices (or the edge/node instances) of edges/nodes having such attribute.

Parameters

- **attr** (*str*) – The name of the attribute to look for.
- **graph** (*igraph.Graph*) – Optional, `None` by default. The graph object where the edge/node attribute is to be searched. If none is passed, takes the undirected network of the current instance.
- **index** (*bool*) – Optional, `True` by default. Whether to return the iterator of the indices or the node/edge instances.
- **edges** (*bool*) – Optional, `True` by default. Whether to look for the attribute in the networks edges or nodes instead.

Returns (*generator*) – Generator object containing the edge/node indices (or instances) having the specified attribute.

having_eattr (*attr, graph=None, index=True*)

Checks if edges of the network have a specific attribute and returns an iterator of the indices (or the edge instances) of edges having such attribute.

Parameters

- **attr** (*str*) – The name of the attribute to look for.
- **graph** (*igraph.Graph*) – Optional, `None` by default. The graph object where the edge/node attribute is to be searched. If none is passed, takes the undirected network of the current instance.
- **index** (*bool*) – Optional, `True` by default. Whether to return the iterator of the indices or the node/edge instances.

Returns (*generator*) – Generator object containing the edge indices (or instances) having the specified attribute.

having_ptm (*index=True, graph=None*)

Checks if edges of the network have the 'ptm' attribute and returns an iterator of the indices (or the edge instances) of edges having such attribute.

Parameters

- **index** (*bool*) – Optional, *True* by default. Whether to return the iterator of the indices or the node/edge instances.
- **graph** (*igraph.Graph*) – Optional, *None* by default. The graph object where the edge/node attribute is to be searched. If none is passed, takes the undirected network of the current instance.

Returns (*generator*) – Generator object containing the edge indices (or instances) having the 'ptm' attribute.

having_vattr (*attr, graph=None, index=True*)

Checks if nodes of the network have a specific attribute and returns an iterator of the indices (or the node instances) of nodes having such attribute.

Parameters

- **attr** (*str*) – The name of the attribute to look for.
- **graph** (*igraph.Graph*) – Optional, *None* by default. The graph object where the edge/node attribute is to be searched. If none is passed, takes the undirected network of the current instance.
- **index** (*bool*) – Optional, *True* by default. Whether to return the iterator of the indices or the node/edge instances.

Returns (*generator*) – Generator object containing the node indices (or instances) having the specified attribute.

homology_translation (*target, source=None, only_swissprot=True, graph=None*)

Translates the current object to another organism by orthology. Proteins without known ortholog will be deleted.

Parameters **target** (*int*) – NCBI Taxonomy ID of the target organism. E.g. 10090 for mouse.

htp_stats ()

in_complex (*csources=['corum']*)

Deprecated, will be removed.

in_directed (*vertex*)

in_undirected (*vertex*)

info (*name*)

Given the name of a resource, prints out the information about that source/database. You can check the list of available resource descriptions in `yopath.descriptions.descriptions.keys()`.

Parameters **name** (*str*) – The name of the resource from which to print the information.

init_complex_attr (*graph, name*)

init_edge_attr (*attr*)

Fills all edges attribute *attr* with its default type (if such attribute value is *None*), creates [list] if in `yopath.main.PyPath.edgeAttrs` such attribute is registered as [list].

Parameters *attr* (*str*) – The attribute name to be initialized on the network edges.

init_gsea (*user*)

Initializes a `pypath.gsea.GSEA` object and shows the list of the collections in MSigDB.

init_network (*lst=None*, *exclude=[]*, *cache_files={}*, *pfile=False*, *save=False*, *reread=None*, *redownload=False*, *keep_raw=False*, ***kwargs*)

Loads the network data.

This is a lazy way to start the module, load data and build the high confidence, literature curated part of the signaling network.

Parameters

- **lst** (*dict*) – Optional, `None` by default. Specifies the data input formats for the different resources (keys) [str]. Values are `pypath.input_formats.ReadSettings` instances containing the information. By default uses the set of resources of `OmniPath`.
- **exclude** (*list*) – Optional, `[]` by default. List of resources [str] to exclude from the network.
- **cache_files** (*dict*) – Optional, `{}` by default. Contains the resource name(s) [str] (keys) and the corresponding cached file name [str]. If provided (and file exists) bypasses the download of the data for that resource and uses the cache file instead.
- **pfile** (*str*) – Optional, `False` by default. If any, provides the file name or path to a previously saved network pickle file. If `True` is passed, takes the default path from `PyPath.save_network()` ('cache/default_network.pickle').
- **save** (*bool*) – Optional, `False` by default. If set to `True`, saves the loaded network to its default location ('cache/default_network.pickle').
- **reread** (*bool*) – Optional, `False` by default. Specifies whether to reread the data files from the cache or omit them (similar to *redownload*).
- **redownload** (*bool*) – Optional, `False` by default. Specifies whether to re-download the data and ignore the cache.
- ****kwargs** – Not used.

init_vertex_attr (*attr*)

Fills all vertices attribute *attr* with its default type (if such attribute value is `None`), creates [list] if in `pypath.main.PyPath.vertexAttrs` such attribute is registered as [list].

Parameters *attr* (*str*) – The attribute name to be initialized on the network vertices.

intergroup_shortest_paths (*groupA*, *groupB*, *random=False*)

intogen_cancer_drivers_list (*intogen_file*)

Loads the list of cancer driver proteins from IntOGen data.

Parameters *intogen_file* (*str*) – Path to the data file. Can also be [function] that provides the data. In general, anything accepted by `pypath.input_formats.ReadSettings.input`.

iter_interactions ()

Iterates over edges and yields interaction records.

jaccard_edges ()

Computes the Jaccard similarity index between the sets of first neighbours of all node pairs. **NOTE:** this method can take a while to compute, e.g.: if the network has 10K nodes, the total number of possible pairs

to compute is:

$$\binom{10^4}{2} = 49995000$$

Returns (*list*) – Large list of [tuple] elements containing the node pair names [str] and their corresponding first neighbours Jaccard index [float].

jaccard_meta (*jedges, critical*)

Creates a (undirected) graph from a list of edges filtering by their Jaccard index.

Parameters

- **jedges** (*list*) – List of [tuple] containing the edges node names [str] and their Jaccard index. Basically, the output of `pypath.main.PyPath.jaccard_edges()`.
- **critical** (*float*) – Specifies the threshold of the Jaccard index from above which an edge will be included in the graph.

Returns (*igraph.Graph*) – The Undirected graph instance containing only the edges whose Jaccard similarity index is above the threshold specified by *critical*.

kegg_directions (*graph=None*)

kegg_pathways (*graph=None*)

kinase_stats ()

kinases_list ()

Loads the list of all known kinases in the proteome from kinase.com. This resource is human only.

label (*label, idx, what='vertices'*)

Creates a boolean attribute `label` True for the vertex or edge IDs in the set `idx`.

label_by_go (*label, go_terms, method='ANY'*)

Assigns a boolean vertex attribute to nodes which tells whether the node is annotated by all or any of the GO terms.

label_edges (*label, edges*)

Creates a boolean edge attribute `label` True for the edge IDs in the set `edges`.

label_vertices (*label, vertices*)

Creates a boolean vertex attribute `label` True for the vertex IDs in the set `vertices`.

laudanna_directions (*graph=None*)

laudanna_effects (*graph=None*)

static license (*self*)

Prints information about data licences.

static list_resources ()

Prints the list of resources through the standard output.

load_3dcomplexes (*graph=None*)

load_3did_ddi ()

load_3did_ddi2 (*ddi=True, interfaces=False*)

load_3did_dmi ()

load_3did_interfaces ()

load_all_pathways (*graph=None*)

load_compleat (*graph=None*)
 Loads complexes from Compleat. Loads data into vertex attribute *graph.vs['complexes']['compleat']*. This resource is human only.

load_complexportal (*graph=None*)
 Loads complexes from ComplexPortal. Loads data into vertex attribute *graph.vs['complexes']['complexportal']*. This resource is human only.

load_compypi (*graph=None*)

load_corum (*graph=None*)
 Loads complexes from CORUM database. Loads data into vertex attribute *graph.vs['complexes']['corum']*. This resource is human only.

load_dbptm (*non_matching=False, trace=False, **kwargs*)

load_ddi (*ddi*)
ddi is either a list of intera.DomainDomain objects, or a function resulting this list

load_ddis (*methods=['dataio.get_3dc_ddi', 'dataio.get_domino_ddi', 'self.load_3did_ddi2']*)

load_depod_dmi ()

load_disgenet (*dataset='curated', score=0.0, umls=False, full_data=False*)
 Assigns DisGeNet disease-gene associations to the proteins in the network. Disease annotations will be added to the *dis* vertex attribute.

Parameters

- **score** (*float*) – Confidence score from DisGeNet. Only associations above the score provided will be considered.
- **umls** (*bool*) – By default we assign a list of disease names to each protein. To use Unified Medical Language System IDs instead set this to *True*.
- **full_data** (*bool*) – By default we load only disease names. Set this to *True* if you wish to load additional annotations like number of PubMed IDs, number of SNPs and original sources.

load_dmi (*dmi*)
dmi is either a list of intera.DomainMotif objects, or a function resulting this list

load_dmis (*methods=['self.pfam_regions', 'self.load_depod_dmi', 'self.load_dbptm', 'self.load_mimp_dmi', 'self.load_pnetworks_dmi', 'self.load_domino_dmi', 'self.load_pepcyber', 'self.load_psite_reg', 'self.load_psite_phos', 'self.load_ielm', 'self.load_phosphoelm', 'self.load_elm', 'self.load_3did_dmi']*)

load_domino_dmi (*organism=None*)

load_elm ()

load_exocarta_attrs (*load_samples=False, load_refs=False*)
 Creates vertex attributes from ExoCarta data. Creates a boolean attribute *exocarts_exosomal* which tells whether a protein is in ExoCarta i.e. has been found in exosomes. Optionally creates attributes *exocarta_samples* and *exocarta_refs* listing the sample tissue and the PubMed references, respectively.

load_expression (*array=False*)
 Expression data can be loaded into vertex attributes, or into a pandas DataFrame – the latter offers faster ways to process and use these huge matrices.

load_go (*organism=None*)
 Creates a *pypath.go.GOAnnotation* object for one organism in the dict under *go* attribute.

Parameters **organism** (*int*) – NCBI Taxonomy ID of the organism.

load_havugimana (*graph=None*)

Loads complexes from Havugimana 2012. Loads data into vertex attribute *graph.vs['complexes']*['havugimana']. This resource is human only.

load_hpa (*normal=True, pathology=True, cancer=True, summarize_pathology=True, tissues=None, quality={'Approved', 'Supported'}, levels={'High': 3, 'Low': 1, 'Medium': 2, 'Not detected': 0}, graph=None, na_value=0*)

Loads Human Protein Atlas data into vertex attributes.

load_hprd_ptms (*non_matching=False, trace=False, **kwargs*)

load_ielm ()

load_interfaces ()

load_li2012_ptms (*non_matching=False, trace=False, **kwargs*)

load_ligand_receptor_network (*lig_rec_resources=True, inference_from_go=True, sources=None, keep_undirected=False, keep_rec_rec=False, keep_lig_lig=False*)

Initializes a ligand-receptor network.

load_list (*lst, name*)

Loads a custom list to the object's node data lists. See `pypath.main.PyPath.lists` attribute for more information.

Parameters

- **lst** (*list*) – The list containing the node names [str] from the given category (*name*).
- **name** (*str*) – The category or identifier for the list of nodes provided.

load_lmpid (*method*)

load_matrisome_attrs (*organism=None*)

Loads vertex attributes from MatrisomeDB 2.0. Attributes are *matrisome_class*, *matrisome_subclass* and *matrisome_notes*.

load_membranome_attrs ()

Loads attributes from Membranome, a database of single-helix transmembrane proteins.

load_mimp_dmi (*non_matching=False, trace=False, **kwargs*)

load_mutations (*attributes=None, gdsc_datadir=None, mutation_file=None*)

Mutations are listed in vertex attributes. `Mutation()` objects offers methods to identify residues and look up in `Ptm()`, `Motif()` and `Domain()` objects, to check if those residues are modified, or are in some short motif or domain.

load_negatives ()

load_old_omnipath (*kinase_substrate_extra=False, remove_htp=False, htp_threshold=1, keep_directed=False, min_refs_undirected=2*)

Loads the OmniPath network as it was before August 2016. Furthermore it gives some more options.

load_omnipath (*kinase_substrate_extra=False, remove_htp=True, htp_threshold=1, keep_directed=True, min_refs_undirected=2, old_omnipath_resources=False*)

Loads the OmniPath network.

load_pathways (*source, graph=None*)

Generic method to load pathway annotations from a resource. We don't recommend calling this method but either specific methods for a single source e.g. `kegg_pathways()` or `simor_pathways()` or call `load_all_pathways()` to load all resources.

Parameters

- **source** (*str*) – Name of the source, this need to match a method in the dict in *get_pathways()* method and the edge and vertex attributes with pathway annotations will be called “<source>_pathways”.
- **graph** (*igraph.Graph*) – A graph, by default the default the *graph* attribute of the current instance.

load_pdb (*graph=None*)

Loads the 3D structure information from PDB into the network. Creates the node attribute 'pdb' containing a [dict] whose keys are the PDB identifier [str] and values are [tuple] of two elements denoting the experimental method [str] (e.g.: 'X-ray', 'NMR', ...) and the resolution [float] (if applicable).

Parameters **graph** (*igraph.Graph*) – Optional, *None* by default. The network object for which the information is to be loaded. If none is passed, takes the undirected network of the current instance.

load_pepcyber ()

load_pfam (*graph=None*)

Loads the protein family information from UniProt into the network. Creates the node attribute 'pfam' containing a [list] of protein family identifier(s) [str].

Parameters **graph** (*igraph.Graph*) – Optional, *None* by default. The network object for which the information is to be loaded. If none is passed, takes the undirected network of the current instance.

load_pfam2 ()

Loads the protein family information from Pfam into the network. Creates the node attribute 'pfam' containing a [list] of [dict] whose keys are protein family identifier(s) [str] and corresponding values are [list] of [dict] containing detailed information about the protein family(ies) for regions and isoforms of the protein.

Parameters **graph** (*igraph.Graph*) – Optional, *None* by default. The network object for which the information is to be loaded. If none is passed, takes the undirected network of the current instance.

load_pfam3 ()

Loads the protein domain information from Pfam into the network. Creates the node attribute 'doms' containing a [list] of *pypath.intera.Domain* instances with information about each domain of the protein (see the corresponding class documentation for more information).

load_phospho_dmi (*source, trace=False, return_raw=False, **kwargs*)

load_phosphoelm (*trace=False, **kwargs*)

load_pisa (*graph=None*)

load_pnetworks_dmi (*trace=False, **kwargs*)

load_psite_phos (*trace=False, **kwargs*)

load_psite_reg ()

load_ptms ()

load_ptms2 (*input_methods=None, map_by_homology_from=[9606], homology_only_swissprot=True, ptm_homology_strict=False, nonhuman_direct_lookup=True, inputargs={}*)

This is a new method which will replace *load_ptms*. It uses *pypath.ptm.PtmAggregator*, a newly introduced module for combining enzyme-substrate data from multiple resources using homology translation on users demand.

Parameters

- **input_methods** (*list*) – Resources to collect enzyme-substrate interactions from. E.g. [*Signor*, *phosphoELM*]. By default it contains Signor, PhosphoSitePlus, HPRD, phosphoELM, dbPTM, PhosphoNetworks, Li2012 and MIMP.
- **map_by_homology_from** (*list*) – List of NCBI Taxonomy IDs of source taxons used for homology translation of enzyme-substrate interactions. If you have a human network and you add here [*10090*, *10116*] then mouse and rat interactions from the source databases will be translated to human.
- **homology_only_swissprot** (*bool*) – *True* by default which means only SwissProt IDs are accepted at homology translation, Trembl IDs will be dropped.
- **ptm_homology_strict** (*bool*) – For homology translation use PhosphoSite’s PTM homology table. This guarantees that only truly homologous sites will be included. Otherwise we only check if at the same numeric offset in the homologous sequence the appropriate residue can be found.
- **nonhuman_direct_lookup** (*bool*) – Fetch also directly nonhuman data from the resources wherever it’s available. PhosphoSite contains mouse enzyme-substrate interactions and it is possible to extract these directly beside translating the human ones to mouse.
- **inputargs** (*dict*) – Additional arguments passed to *PtmProcessor*. A *dict* can be supplied for each resource, e.g. {*Signor*: {...}, *PhosphoSite*: {...}, ...}. Those not used by *PtmProcessor* are forwarded to the *pypath.dataio* methods.

load_resource (*settings*, *clean=True*, *cache_files={}*, *reread=None*, *redownload=False*, *keep_raw=False*)

Loads the data from a single resource and attaches it to the network

Parameters

- **settings** (*pypath.input_formats.ReadSettings*) – *pypath.input_formats.ReadSettings* instance containing the detailed definition of the input format to the downloaded file.
- **clean** (*bool*) – Optional, *True* by default. Whether to clean the graph after importing the data or not. See *pypath.main.PyPath.clean_graph()* for more information.
- **cache_files** (*dict*) – Optional, {} by default. Contains the resource name(s) [str] (keys) and the corresponding cached file name [str]. If provided (and file exists) bypasses the download of the data for that resource and uses the cache file instead.
- **reread** (*bool*) – Optional, *False* by default. Specifies whether to reread the data files from the cache or omit them (similar to *redownload*).
- **redownload** (*bool*) – Optional, *False* by default. Specifies whether to re-download the data and ignore the cache.

load_resources (*lst=None*, *exclude=[]*, *cache_files={}*, *reread=False*, *redownload=False*, *keep_raw=False*)

Loads multiple resources, and cleans up after. Looks up ID types, and loads all ID conversion tables from UniProt if necessary. This is much faster than loading the ID conversion and the resources one by one.

Parameters

- **lst** (*dict*) – Optional, *None* by default. Specifies the data input formats for the different resources (keys) [str]. Values are *pypath.input_formats.ReadSettings* instances containing the information. By default uses the set of resources of *OmniPath*.

- **exclude** (*list*) – Optional, [] by default. List of resources [str] to exclude from the network.
- **cache_files** (*dict*) – Optional, {} by default. Contains the resource name(s) [str] (keys) and the corresponding cached file name [str]. If provided (and file exists) bypasses the download of the data for that resource and uses the cache file instead.
- **reread** (*bool*) – Optional, False by default. Specifies whether to reread the data files from the cache or omit them (similar to *redownload*).
- **redownload** (*bool*) – Optional, False by default. Specifies whether to re-download the data and ignore the cache.

load_signor_ptms (*non_matching=False, trace=False, **kwargs*)

load_surfaceome_attrs ()

Loads vertex attributes from the In Silico Human Surfaceome. Attributes are *surfaceome_score*, *surfaceome_class* and *surfaceome_subclass*.

load_tfregulons (*levels={'A', 'B'}, only_curated=False*)

Adds TF-target interactions from TF regulons to the network. TF regulons is a comprehensive resource of TF-target interactions combining multiple lines of evidences: literature curated databases, ChIP-Seq data, PWM based prediction using HOCOMOCO and JASPAR matrices and prediction from GTEx expression data by ARACNe.

For details see <https://github.com/saezlab/DoRothEA>.

Parameters

- **levels** (*set*) – Optional, {'A', 'B'} by default. Confidence levels to be loaded (from A to E) [str].
- **only_curated** (*bool*) – Optional, False by default. Whether to retrieve only the literature curated interactions or not.

load_vesiclepedia_attrs (*load_samples=False, load_refs=False, load_vesicle_type=False*)

Creates vertex attributes from Vesiclepedia data. Creates a boolean attribute *vesiclepedia_in_vesicle* which tells whether a protein is in ExoCarta i.e. has been found in exosomes. Optionally creates attributes *vesiclepedia_samples*, *vesiclepedia_refs* and *vesiclepedia_vesicles* listing the sample tissue, the PubMed references and the vesicle types, respectively.

lookup_cache (*name, cache_files, int_cache, edges_cache*)

Checks up the cache folder for the files of a given resource. First checks if *name* is on the *cache_files* dictionary. If so, loads either the interactions or edges otherwise. If not, checks *edges_cache* or *int_cache* otherwise.

Parameters

- **name** (*str*) – Name of the resource (lower-case).
- **cache_files** (*dict*) – Contains the resource name(s) [str] (keys) and the corresponding cached file name [str] (values).
- **int_cache** (*str*) – Path to the interactions cache file of the resource.
- **edges_cache** (*str*) – Path to the edges cache file of the resource.

Returns

- (*file*) – The loaded pickle file from the cache if the file contains the interactions. None otherwise.

- *(list)* – List of mapped edges if the file contains the information from the edges. [] otherwise.

loop_edges (*index=True, graph=None*)

Returns an iterator of the indices (or the edge instances) of the edges which represent a loop (whose source and target node are the same).

Parameters

- **index** (*bool*) – Optional, `True` by default. Whether to return the iterator of the indices or the edge instances.
- **graph** (*igraph.Graph*) – Optional, `None` by default. The graph object where the edge loops are to be searched. If none is passed, takes the undirected network of the current instance.

Returns (*generator*) – Generator object containing the edge indices (or instances) containing loops.

map_edge (*edge, expand_complexes=True*)

Translates the identifiers in *edge* representing an edge. Default name types are defined in `pypath.main.PyPath.default_name_type`. If the mapping is unsuccessful, the item will be added to `pypath.main.PyPath.unmapped` list.

Parameters

- **edge** (*dict*) – Item whose name is to be mapped to a default name type.
- **expand_complexes** (*bool*) – Expand complexes, i.e. create links between each member of the complex and the interacting partner.

Returns (*list*) – Contains the edge(s) [dict] with default mapped names.

map_item (*item, expand_complexes=True*)

Translates the name in *item* representing a molecule. Default name types are defined in `pypath.main.PyPath.default_name_type`. If the mapping is unsuccessful, the item will be added to `pypath.main.PyPath.unmapped` list.

Parameters

- **item** (*dict*) – Item whose name is to be mapped to a default name type.
- **expand_complexes** (*bool*) – Expand complexes, i.e. create links between each member of the complex and the interacting partner.

Returns (*list*) – The default mapped name(s) [str] of *item*.

map_list (*lst, single_list=False, expand_complexes=True*)

Maps the names from a list of edges or items (molecules).

Parameters

- **lst** (*list*) – List of items or edge dictionaries whose names have to be mapped.
- **single_list** (*bool*) – Optional, `False` by default. Determines whether the provided elements are items or edges. This is, either calls `pypath.main.PyPath.map_edge()` or `pypath.main.PyPath.map_item()` to map the item names.
- **expand_complexes** (*bool*) – Expand complexes, i.e. create links between each member of the complex and the interacting partner.

Returns (*list*) – Copy of *lst* with their elements' names mapped.

mean_reference_per_interaction ()

Computes the mean number of references per interaction of the network.

Returns (*float*) – Mean number of interactions per edge.

merge_lists (*id_a, id_b, name=None, and_or='and', delete=False, func='max'*)

Merges two lists from `pypat.main.PyPath.lists`.

Parameters

- **id_a** (*str*) – Name of the first list to be merged.
- **id_b** (*str*) – Name of the second list to be merged.
- **name** (*str*) – Optional, `None` by default. Specifies a new name for the merged list. If none is passed, name will be set to `id_a*_id_b`.
- **and_or** (*str*) – Optional, 'and' by default. The logic operation performed in the merging: 'and' performs an union, 'or' for the intersection.
- **delete** (*bool*) – Optional, `False` by default. Whether to delete the former lists or not.
- **func** (*str*) – Optional, 'max' by default. Not used.

merge_nodes (*nodes, primary=None, graph=None*)

Merges all attributes and edges of selected nodes and assigns them to the primary node (by default the one with lowest index).

Parameters

- **nodes** (*list*) – List of node indexes [int] that are to be collapsed.
- **primary** (*int*) – Optional, `None` by default. ID of the primary edge, if none is passed, the node with lowest index on *nodes* is selected.
- **graph** (*igraph.Graph*) – Optional, `None` by default. The network graph object from which the nodes are to be merged. If none is passed, takes the undirected network graph.

mimp_directions (*graph=None*)

mutated_edges (*sample*)

Compares the mutated residues and the modified residues in PTMs. Interactions are marked as mutated if the target residue in the underlying PTM is mutated.

name_edgelist (*graph=None*)

Returns an edge list, i.e. a list with tuples of vertex names.

names2vids (*names*)

From a list of node names, returns their corresponding indices.

Parameters **names** (*list*) – Contains the node names [str] for which the IDs are to be searched.

Returns (*list*) – The queried node IDs [int].

negative_report (*lst=True, outFile=None*)

Generates a report file with the negative interactions (assumed to be already loaded).

Parameters

- **lst** (*bool*) – Optional, `True` by default. Whether to return a list of edges containing the edge instances which have negative references.
- **outFile** (*str*) – Optional, `None` by default. The output file name/path. If none is passed, the default is 'results/<session_id>-negatives'

Returns (*list*) – If *lst* is set to `True`, returns a [list] is returned with the `igraph.Edge` instances that contain at least a negative reference.

neighborhood (*identifiers, order=1, mode='ALL'*)

neighbors (*identifier, mode='ALL'*)

neighbourhood_network (*center, second=False*)

network_by_go (*node_categories, network_sources=None, include=None, exclude=None, directed=False, keep_undirected=False, prefix='GO', delete=True, copy=False, vertex_attrs=True, edge_attrs=True*)

Creates or filters a network based on Gene Ontology annotations.

Parameters

- **node_categories** (*dict*) – A dict with custom category labels as keys and expressions of GO terms as values. E.g. “{ ‘extracell’: ‘GO:0005576 and not GO:0070062’, ‘plasmamem’: ‘GO:0005887’ }”.
- **network_sources** (*dict*) – A dict with anything as keys and network input format definitions (`input_formats.ReadSettings` instances) as values.
- **include** (*list*) – A list of tuples of category label pairs. By default we keep all edges connecting proteins annotated with any of the defined categories. If `include` is defined then only edges between category pairs defined here will be kept and all others deleted.
- **exclude** (*list*) – Similarly to `include`, all edges will be kept but the ones listed in `exclude` will be deleted.
- **directed** (*bool*) – If `True` `include` and `exclude` relations will be processed with directed (source, target) else direction won't be considered.
- **keep_undirected** (*bool*) – If `True` the interactions without direction information will be kept even if `directed` is `True`. Passed to `edges_between` as `strict` argument.
- **prefix** (*str*) – Prefix for all vertex and edge attributes created in this operation. E.g. if you have a category label ‘bar’ and prefix is ‘foo’ then you will have a new vertex attribute ‘foo_bar’.
- **delete** (*bool*) – Delete the vertices and edges which don't belong to any of the categories.
- **copy** (*bool*) – Return a copy of the entire `PyPath` object with the graph filtered by GO terms. By default the object is modified in place and `None` is returned.
- **vertex_attrs** (*bool*) – Create vertex attributes.
- **edge_attrs** (*bool*) – Create edge attributes.

network_filter (*p=2.0*)

This function aims to cut the number of edges in the network, without losing nodes, to make the network less connected, less hairball-like, more usable for analysis.

network_stats (*outfile=None*)

Calculates basic statistics for the whole network and each of sources (node and edge counts, average node degree, graph diameter, transitivity, adhesion and cohesion). Writes the results in a tab file. File is stored in `pypath.main.PyPath.outdir('results')` by default).

Parameters `outfile` (*str*) – Optional, `None` by default. Specifies the file name. If none is specified, this will be `'pwnet-<session_id>-stats'`.

new_edges (*edges*)

Adds new edges from any iterable of edges to the undirected graph. Basically, calls `igraph.Graph.add_edges()`.

Parameters `edges` (*list*) – Contains the edges that are to be added to the network.

new_nodes (*nodes*)

Adds new nodes from any iterable of nodes to the undirected graph. Basically, calls `igraph.Graph.add_vertices()`.

Parameters **nodes** (*list*) – Contains the nodes that are to be added to the network.

node_exists (*name*)

Checks if a node exists in the (undirected) network.

Parameters **name** (*str*) – The name of the node to be searched.

Returns (*bool*) – Whether the node exists in the network or not.

numof_directed_edges ()**numof_reference_interaction_pairs** ()

Returns the total of unique references per interaction.

Returns (*int*) – Total number of unique references per interaction.

numof_references ()

Counts the number of reference on the network.

Counts the total number of unique references in the edges of the network.

Returns (*int*) – Number of unique references in the network.

numof_undirected_edges ()**orthology_translation** (*target*, *source=None*, *only_swissprot=True*, *graph=None*)

Translates the current object to another organism by orthology. Proteins without known ortholog will be deleted.

Parameters **target** (*int*) – NCBI Taxonomy ID of the target organism. E.g. 10090 for mouse.

p (*identifier*)

Returns `igraph.Vertex()` object if the identifier is a valid vertex index in the default undirected graph, or a UniProt ID or GeneSymbol which can be found in the default undirected network, otherwise `None`.

@identifier [*int*, *str*] Vertex index (*int*) or GeneSymbol (*str*) or UniProt ID (*str*) or `igraph.Vertex` object.

pathway_attributes (*graph=None*)**pathway_members** (*pathway*, *source*)

Returns an iterator with the members of a single pathway. Apart from the pathway name you need to supply its source database too.

pathway_names (*source*, *graph=None*)

Returns the names of all pathways having at least one member in the current graph.

pathway_similarity (*outfile=None*)

Computes the Sorensen's similarity index across nodes and edges for all the available pathway sources (already loaded in the network) and saves them into table files. Files are stored in `pypath.main.PyPath.outdir` ('results' by default). See `pypath.main.PyPath.sorensen_pathways()` for more information..

Parameters **outfile** (*str*) – Optional, `None` by default. Specifies the file name prefix (suffixes will be '-nodes' and '-edges'). If none is specified, this will be 'pwnet-<session_id>-sim-pw'.

pathways_table (*filename='genes_pathways.list'*, *pw_sources=['signalink', 'signor', 'netpath', 'kegg']*, *graph=None*)

```

pfam_regions ()
phosphonetworks_directions (graph=None)
phosphopoint_directions (graph=None)
phosphorylation_directions ()
phosphorylation_signs ()
phosphosite_directions (graph=None)
prdb_tissue_expr (tissue, prdb=None, graph=None, occurrence=1, group_function=<function Py-
    Path.<lambda>>, na_value=0.0)
process_direction (line, dir_col, dir_val, dir_sep)

```

Processes the direction information of an interaction according to a data file from a source.

Parameters

- **line** (*list*) – The stripped and separated line from the resource data file containing the information of an interaction.
- **dir_col** (*int*) – The column/position number where the information about the direction is to be found (on *line*).
- **dir_val** (*list*) – Contains the terms [str] for which that interaction is to be considered directed.
- **dir_sep** (*str*) – Separator for the field in *line* containing the direction information (if any).

Returns (*bool*) – Determines whether the given interaction is directed or not.

```

process_directions (dirs, name, directed=None, stimulation=None, inhibition=None,
    graph=None, id_type=None, dirs_only=False)

```

```

process_dmi (source, **kwargs)

```

This is an universal function for loading domain-motif objects like `load_phospho_dmi()` for PTMs. TODO this will replace `load_elm`, `load_ielm`, etc

```

process_sign (signData, signDef)

```

Processes the sign of an interaction, used when processing an input file.

Parameters

- **signData** (*str*) – Data regarding the sign to be processed.
- **signDef** (*tuple*) – Contains information about how to process *signData*. This is defined in `pypath.data_formats`. First element determines the position on the direction information of each line on the data file [int], second element is either [str] or [list] and defines the terms for which an interaction is defined as stimulation, third element is similar but for the inhibition and third (optional) element determines the separator for *signData* if contains more than one element.

Returns

- (*bool*) – Determines whether the processed interaction is considered stimulation or not.
- (*bool*) – Determines whether the processed interaction is considered inhibition or not.

```

protein (identifier)

```

Same as `PyPath.get_node`, just for the directed graph. Returns `igraph.Vertex()` object if the identifier is a valid vertex index in the default directed graph, or a UniProt ID or GeneSymbol which can be found in the default directed network, otherwise `None`.

@identifier [int, str] Vertex index (int) or GeneSymbol (str) or UniProt ID (str) or `igraph.Vertex` object.

protein_edge (*source, target, directed=True*)

Returns `igraph.Edge` object if an edge exist between the 2 proteins, otherwise `None`.

Parameters

- **source** (*int, str*) – Vertex index or UniProt ID or GeneSymbol or `igraph.Vertex` object.
- **target** (*int, str*) – Vertex index or UniProt ID or GeneSymbol or `igraph.Vertex` object.
- **directed** (*bool*) – To be passed to `igraph.Graph.get_eid()`

proteins (*identifiers*)

proteome_list (*swissprot=True*)

Loads the whole proteome as a list.

Parameters **swissprot** (*bool*) – Optional, `True` by default. Determines whether to use also the information from SwissProt.

ps (*identifiers*)

random_walk_with_return (*q, graph=None, c=0.5, niter=1000*)

Random walk with return (RWR) starting from one or more query nodes. Returns affinity (probability) vector of all nodes in the graph.

param int,list q Vertex IDs of query nodes.

param igraph.Graph graph An `igraph.Graph` object.

param float c Probability of restart.

param int niter Number of iterations.

```
>>> import igraph
>>> import pypath
>>> pa = pypath.PyPath()
>>> pa.init_network({
    'signor': pypath.data_formats.pathway['signor']
})
>>> q = [
    pa.gs('EGFR').index,
    pa.gs('ATG4B').index
]
>>> rwr = pa.random_walk_with_return(q = q)
>>> palette = igraph.RainbowPalette(n = 100)
>>> colors = [palette.get(int(round(i))) for i in rwr / max(rwr) * 99]
>>> igraph.plot(pa.graph, vertex_color = colors)
```

random_walk_with_return2 (*q, c=0.5, niter=1000*)

Literally does random walks. Only for testing of the other method, to be deleted later.

read_data_file (*param, keep_raw=False, cache_files={}, reread=None, redownload=False*)

Reads interaction data file containing node and edge attributes that can be read from simple text based files and adds it to the networkdata. This function works not only with files, but with lists as well. Any other function can be written to download and preprocess data, and then give it to this function to finally attach to the network.

Parameters

- **param** (*pypath.input_formats.ReadSettings*) – *pypath.input_formats.ReadSettings* instance containing the detailed definition of the input format of the file. Instead of the file name (on the *pypath.input_formats.ReadSettings.input* attribute) you can give a custom function name, which will be executed, and the returned data will be used instead.
- **keep_raw** (*bool*) – Optional, *False* by default. Whether to keep the raw data read by this function, in order for debugging purposes, or further use.
- **cache_files** (*dict*) – Optional, *{}* by default. Contains the resource name(s) [*str*] (keys) and the corresponding cached file name [*str*]. If provided (and file exists) bypasses the download of the data for that resource and uses the cache file instead.
- **reread** (*bool*) – Optional, *False* by default. Specifies whether to reread the data files from the cache or omit them (similar to *redownload*).
- **redownload** (*bool*) – Optional, *False* by default. Specifies whether to re-download the data and ignore the cache.

read_from_cache (*cache_file*)

Reads a pickle file from the cache and returns it. It is assumed that the subfolder *cache/* is on the supplied path.

Parameters **cache_file** (*str*) – Path to the cache file that is to be loaded.

Returns (*file*) – The loaded pickle file from the cache. Type will depend on the file itself (e.g.: if the pickle was saved from a dictionary, the type will be [*dict*]).

read_list_file (*settings, **kwargs*)

Reads a list from a file and adds it to *pypath.main.PyPath.lists*.

Parameters

- **settings** (*pypath.input_formats.ReadList*) – *python.data_formats.ReadList* instance specifying the settings of the file to be read. See the class documentation for more details.
- ****kwargs** – Extra arguments passed to the file reading function. Such function name is outlined in the *python.data_formats.ReadList.input* attribute and defined in *pypath.dataio*.

receptors_list ()

Loads the Human Plasma Membrane Receptome as a list. This resource is human only. The list name is *rec*.

reference_edge_ratio ()

Computes the average number of references per edge (as in the undirected graph).

Returns (*float*) – Average number of references per edge.

reference_hist (*filename=None*)

Generates a file containing a table with information about the network's edges. First column contains the source node ID, followed by the target's ID, third column contains the number of references for that interaction and finally the number of sources. Writes the results in a tab file.

Parameters **filename** (*str*) – Optional, *None* by default. Specifies the file name and path to save the table. If none is passed, file will be saved in *pypath.main.PyPath.outdir* ('*results*' by default) with the name '*<session_id>-refs-hist*'.

reload ()

Reloads the object from the module level.

remove_http (*threshold=50, keep_directed=False*)

remove_undirected (*min_refs=None*)

run_batch (*methods, toCall=None*)

save_network (*pfile=None*)

Saves the network object.

Stores the instance into a pickle (binary) file which can be reloaded in the future.

Parameters **pfile** (*str*) – Optional, *None* by default. The path/file name where to store the pickle file. If not specified, saves the network to its default location ('cache/default_network.pickle').

save_session ()

Save the current session state into pickle dump. The file will be saved in the current working directory as 'pypath-<session_id>.pickle'.

search_attr_and (*obj, lst*)

Searches a given collection of attributes in a given object. Only returns *True*, if all elements of *lst* can be found in *obj*.

Parameters

- **obj** (*object*) – Object (dictionary-like) where to search for elements of *lst*.
- **lst** (*dict*) – Keys are the attribute names [*str*] and values the collection of elements to be searched in such attribute [*set*].

Returns (*bool*) – *True* only if *lst* is empty or all of its elements are found in *obj*. Returns *False* otherwise (as soon as one element of *lst* is not found).

search_attr_or (*obj, lst*)

Searches a given collection of attributes in a given object. As soon as one item is found, returns *True*, if none could be found then returns *False*.

Parameters

- **obj** (*object*) – Object (dictionary-like) where to search for elements of *lst*.
- **lst** (*dict*) – Keys are the attribute names [*str*] and values the collection of elements to be searched in such attribute [*set*].

Returns (*bool*) – *True* if *lst* is empty or any of its elements is found in *obj*. Returns only *False* if cannot find anything.

second_neighbours (*node, indices=False, with_first=False*)

Looks for the (first and) second neighbours of a given node and returns a list of their UniProt IDs.

Parameters

- **node** (*str*) – The UniProt ID of the node of interest. Can also be the index of such node [*int*].
- **indices** (*bool*) – Optional, *False* by default. Whether to return the neighbour nodes indices or their UniProt IDs.
- **with_first** (*bool*) – Optional, *False* by default. Whether to return also the first neighbours or not.

Returns (*list*) – The list containing the second neighbours of the queried node (including the first ones if specified).

select_by_go (*go_terms*)

Retrieves the vertex IDs of all vertices annotated with any Gene Ontology terms or their descendants, or evaluates string expression (see `select_by_go_expr`).

Parameters `go_terms` (*str*, *set*) – A single GO term, a set of GO terms or an expression with GO terms.

select_by_go_all (*go_terms*)

Selects the nodes annotated by all GO terms in `go_terms`.

Returns set of vertex IDs.

Parameters `go_terms` (*list*) – List, set or tuple of GO terms.

select_by_go_expr (*go_expr*)

Selects vertices based on an expression of Gene Ontology terms. Operator precedence not considered, please use parentheses.

Parameters `go_expr` (*str*) – An expression of Gene Ontology terms. E.g. ' (GO:0005576 and not GO:0070062) or GO:0005887 '. Parentheses and operators `and`, `or` and `not` can be used.

separate ()

Separates the undirected network according to the different sources. Basically applies `pypath.main.PyPath.get_network()` for each resource.

Returns (*dict*) – Keys are resource names [*str*] whose values are the subnetwork [*igraph.Graph*] containing the elements of that source.

separate_by_category ()

Separates the undirected network according to resource categories. Possible categories are:

- 'm': PTM/enzyme-substrate resources.
- 'p': Pathway/activity flow resources.
- 'i': Undirected/PPI resources.
- 'r': Process description/reaction resources.
- 't': Transcription resources.

Works in the same way as `pypath.main.PyPath.separate()`.

Returns (*dict*) – Keys are category names [*str*] whose values are the subnetwork [*igraph.Graph*] containing the elements of those resources corresponding to that category.

sequences (*isoforms=True*, *update=False*)

set_boolean_vattr (*attr*, *vids*, *negate=False*)

set_categories ()

Sets the category attribute on the network nodes and edges ('cat') as well the edge attribute coercing the references by category ('refs_by_cat'). The possible categories are as follows:

- 'm': PTM/enzyme-substrate resources.
- 'p': Pathway/activity flow resources.
- 'i': Undirected/PPI resources.
- 'r': Process description/reaction resources.
- 't': Transcription resources.

set_chembl_mysql (*title*, *config_file=None*)

Sets the ChEMBL MySQL configuration according to the *title* section in *config_file* ini file configuration.

Parameters

- **title** (*str*) – Section title of the ini file.

- **config_file** (*str*) – Optional, *None* by default. Specifies the configuration file name if none is passed, `mysql_config/defaults.mysql` will be used.

set_disease_genes (*dataset='curated'*)

Creates a vertex attribute named *dis* with boolean values *True* if the protein encoded by a disease related gene according to DisGeNet.

Parameters dataset (*str*) – Which dataset to use from DisGeNet. Default is *curated*.

set_druggability ()

Creates a vertex attribute *dgb* with value *True* if the protein is druggable, otherwise *False*.

set_drugtargets (*pchembl=5.0*)

Creates a vertex attribute *dtg* with value *True* if the protein has at least one compound binding with affinity higher than *pchembl*, otherwise *False*.

Parameters pchembl (*float*) – Pchembl threshold.

set_kinases ()

Creates a vertex attribute *kin* with value *True* if the protein is a kinase, otherwise *False*.

set_plasma_membrane_proteins_cspa ()

Creates a vertex attribute *cspa* with value *True* if the protein is a plasma membrane protein according to CPSA, otherwise *False*.

set_plasma_membrane_proteins_cspa_surfaceome (*score_threshold=0.0*)

Creates a vertex attribute *surf* with value *True* if the protein is a plasma membrane protein according either to the Cell Surface Protein Atlas or the In Silico Human Surfaceome.

set_plasma_membrane_proteins_surfaceome (*score_threshold=0.0*)

Creates a vertex attribute *ishs* with value *True* if the protein is a plasma membrane protein according to the In Silico Human Surfaceome, otherwise *False*.

set_receptors ()

Creates a vertex attribute *rec* with value *True* if the protein is a receptor, otherwise *False*.

set_signaling_proteins ()

Creates a vertex attribute *kin* with value *True* if the protein is a kinase, otherwise *False*.

set_tfs (*classes=['a', 'b', 'other']*)

set_transcription_factors (*classes=['a', 'b', 'other']*)

Creates a vertex attribute *tf* with value *True* if the protein is a transcription factor, otherwise *False*.

Parameters classes (*list*) – Classes to use from TF Census. Default is *['a', 'b', 'other']*.

shortest_path_dist (*graph=None, subset=None, outfile=None, **kwargs*)

Computes the distribution of shortest paths for each pair of nodes in the network (or between group(s) of nodes if *subset* is provided). **NOTE:** this method can take a while to compute, e.g.: if the network has 10K nodes, the total number of possible pairs to compute is:

$$\binom{10^4}{2} = 49995000$$

Parameters

- **graph** (*igraph.Graph*) – Optional, *None* by default. The network object for which the shortest path distribution is to be computed. If none is passed, takes the undirected network of the current instance.
- **subset** (*tuple*) – Optional, *None* by default. Contains two lists of node indices defining two groups between which the distribution is to be computed. Can also be [list] if the

shortest paths are to be searched within the group. If none is passed, the whole network is taken by default.

- **outfile** (*str*) – Optional, *None* by default. File name/path to save the shortest path distribution. If none is passed, no file is generated.
- ****kwargs** – Additional keyword arguments passed to `igraph.Graph.get_shortest_paths()`.

Returns (*list*) – The length of the shortest paths for each pair of nodes of the network (or within/between group/s if *subset* is provided).

signaling_proteins_list()

Compiles a list of signaling proteins (as opposed to other proteins like metabolic enzymes, matrix proteins, etc), by looking up a few simple keywords in short description of GO terms.

signor_pathways (*graph=None*)

similarity_groups (*groups, index='simpson'*)

Computes the similarity index across the given *groups*.

Parameters

- **groups** (*dict*) – Contains the different group names [*str*] as keys and their corresponding elements [*set*].
- **index** (*str*) – Optional, 'simpson' by default. The type of index metric to use to compute the similarity. Options are 'simpson', 'sorensen' and 'jaccard'.

Returns (*dict*) – Dictionary of dictionaries containing the groups names [*str*] as keys (for both inner and outer dictionaries) and the index metric as inner value [*float*] between those groups.

small_plot (*graph, **kwargs*)

This method is deprecated, do not use it.

sorensen_pathways (*pwlist=None*)

Computes the Sorensen's similarity index across nodes and edges for the given list of pathway sources (all loaded pathway sources by default).

Parameters **pwlist** (*list*) – Optional, *None* by default. The list of pathway sources to be compared.

Returns (*dict*) – Nested dictionaries (three levels). First-level keys are 'nodes' and 'edges', then second and third levels correspond to <source>__<patwhay> names which map to the similarity index between those pathways [*float*].

source_diagram (*outf=None, **kwargs*)

source_network (*font='HelveticaNeueLTStd'*)

For EMBL branding, use Helvetica Neue Linotype Standard light

source_similarity (*outfile=None*)

Computes the Sorensen's similarity index across nodes and edges for all the sources available (already loaded in the network) and saves them into table files. Files are stored in `pypath.main.PyPath.outdir('results')` by default). See `pypath.main.PyPath.databases_similarity()` for more information.

Parameters **outfile** (*str*) – Optional, *None* by default. Specifies the file name prefix (suffixes will be '-nodes' and '-edges'). If none is specified, this will be 'pwnet-<session_id>-sim-src'.

source_stats ()

sources_hist()

Counts the number of sources per interaction in the graph and saves them into a file named `source_num`. File is stored in `pypath.main.PyPath.outdir('results')` by default).

sources_overlap (*diagonal=False*)**sources_venn_data** (*fname=None, return_data=False*)

Computes the overlap in number of interactions for all pairs of sources.

Parameters

- **fname** (*str*) – Optional, `None` by default. If provided, saves the results into a table file. File is stored in `pypath.main.PyPath.outdir('results')` by default).
- **return_data** (*bool*) – Optional, `False` by default. Whether to return the results as a [list].

Returns (*list*) – Only if `return_data` is set to `True`. List of lists containing the counts for each pair of resources. This is, for instance, number of interactions only in resource A, number of interactions only in resource B and number of common interactions between A and B.

straight_between (*id_a, id_b*)

Finds an edge between the provided node names.

Parameters

- **id_a** (*str*) – The name of the source node.
- **id_b** (*str*) – The name of the target node.

Returns (*int*) – The edge ID. If the edge doesn't exist, returns [list] with the node indices [int].

string_effects (*graph=None*)**sum_in_complex** (*csources=['corum'], graph=None*)

Returns the total number of edges in the network falling between two members of the same complex. Returns as a dict by complex resources. Calls `:py:func:pypath.pypath.PyPath.edges_in_complexes()` to do the calculations.

@csources [list] List of complex resources. Should be already loaded.

@graph [igraph.Graph()] The graph object to do the calculations on.

surfaceome_list (*score_threshold=0.0*)

Loads a list of cell surface proteins from the In Silico Human Surfaceome as a list. This resource is human only. The list name is `ishs`.

table_latex (*fname, header, data, sum_row=True, row_order=None, latex_hdr=True, caption="", font='HelveticaNeueLTStd-LtCn', fontsize=8, sum_label='Total', sum_cols=None, header_format='%s', by_category=True*)**tfs_list** ()

Loads the list of all known transcription factors from TF census (Vaquerizas 2009). This resource is human only.

third_source_directions (*graph=None, use_string_effects=False, use_laudanna_data=False*)

This method calls a series of methods to get additional direction & effect information from sources having no literature curated references, but giving sufficient evidence about the directionality for interactions already supported by literature evidences from other sources.

tissue_network (*tissue, graph=None*)

Returns a network which includes the proteins expressed in certain tissue according to ProteomicsDB.

Parameters

- **tissue** (*str*) – Tissue name as used in ProteomicsDB.
- **graph** (*igraph.Graph*) – A graph object, by default the *graph* attribute of the current instance.

transcription_factors ()

uniprot (*uniprot*)

Returns *igraph.Vertex*() object if the UniProt can be found in the default undirected network, otherwise None.

@uniprot [str] UniProt ID.

uniprots (*uniprots*)

Returns list of *igraph.Vertex*() object for a list of UniProt IDs omitting those could not be found in the default undirected graph.

uniq_node_list (*lst*)

Returns a given list of nodes containing only the unique elements.

Parameters *lst* (*list*) – List of nodes.

Returns (*list*) – Copy of *lst* containing only unique nodes.

uniq_ptm (*ptms*)

uniq_ptms ()

up (*uniprot*)

Returns *igraph.Vertex*() object if the UniProt can be found in the default undirected network, otherwise None.

@uniprot [str] UniProt ID.

up_affected_by (*uniprot*)

up_affects (*uniprot*)

up_edge (*source, target, directed=True*)

Returns *igraph.Edge* object if an edge exist between the 2 proteins, otherwise None.

@source [str] UniProt ID

@target [str] UniProt ID

@directed [bool] To be passed to *igraph.Graph.get_eid()*

up_in_directed (*uniprot*)

up_in_undirected (*uniprot*)

up_inhibited_by (*uniprot*)

up_inhibits (*uniprot*)

up_neighborhood (*uniprot, order=1, mode='ALL'*)

up_neighbors (*uniprot, mode='ALL'*)

up_stimulated_by (*uniprot*)

up_stimulates (*uniprot*)

update_adjlist (*graph=None, mode='ALL'*)

Creates an adjacency list in a list of sets format.

update_attrs()

Updates the node and edge attributes. Note that no data is downloaded, mainly updates the dictionaries of attributes `pypath.main.PyPath.edgeAttrs` and `pypath.main.PyPath.vertexAttrs` containing the attributes names and their corresponding types and initializes such attributes in the network nodes/edges if they weren't.

update_cats()

Makes sure that the `pypath.main.PyPath.has_cats` attribute is an up to date [set] of all categories in the current network.

update_db_dict()

update_pathway_types()

Updates the pathway types attribute (`pypath.main.PyPath.pathway_types`) according to the loaded resources of the undirected network.

update_pathways()

Makes sure that the `pypath.main.PyPath.pathways` attribute is an up to date [dict] of all pathways and their sources in the current network.

update_sources()

Makes sure that the `pypath.main.PyPath.sources` attribute is an up to date [list] of all sources in the current network.

update_vertex_sources()

Updates the all the vertex attributes 'sources' and 'references' according to their related edges (on the undirected graph).

update_vindex()

This is deprecated.

update_vname()

Fast lookup of node names and indexes, these are hold in a [list] and a [dict] as well. However, every time new nodes are added, these should be updated. This function is automatically called after all operations affecting node indices.

ups(uniprot)

Returns list of `igraph.Vertex()` object for a list of UniProt IDs omitting those could not be found in the default undirected graph.

v(identifier)

Returns `igraph.Vertex()` object if the identifier is a valid vertex index in the default undirected graph, or a UniProt ID or GeneSymbol which can be found in the default undirected network, otherwise None.

@identifier [int, str] Vertex index (int) or GeneSymbol (str) or UniProt ID (str) or `igraph.Vertex` object.

vertex_pathways()

Some resources assigns interactions some others proteins to pathways. This function copies pathway annotations from edge attributes to vertex attributes.

vsgs()

Returns a generator sequence of the node names as GeneSymbols [str] (from the undirected graph).

Returns (*generator*) – Sequence containing the node names as GeneSymbols [str].

vsup()

Returns a generator sequence of the node names as UniProt IDs [str] (from the undirected graph).

Returns (*generator*) – Sequence containing the node names as UniProt IDs [str].

wang_effects(graph=None)

write_table (*tbl*, *outfile*, *sep*='\\t', *cut*=None, *colnames*=True, *rownames*=True)

Writes a given table to a file.

Parameters

- **tbl** (*dict*) – Contains the data of the table. It is assumed that keys are the row names [str] and the values, well, values. Column names (if any) are defined with the key 'header'.
- **outfile** (*str*) – File name where to save the table. The file will be saved under the object's `pypath.main.PyPath.outdir` ('results' by default).
- **sep** (*str*) – Optional, ' ' (tab) by default. Specifies the separator for the file.
- **cut** (*int*) – Optional, None by default. Specifies the maximum number of characters for the row names.
- **colnames** (*bool*) – Optional, True by default. Specifies whether to write the column names in the file or not.
- **rownames** (*bool*) – Optional, True by default. Specifies whether to write the row names in the file or not.

class `pypath.main.Direction` (*id_a*, *id_b*)

Object storing directionality information of an edge. Also includes information about the reverse direction, mode of regulation and sources of that information.

Parameters

- **id_a** (*str*) – Name of the source node.
- **id_b** (*str*) – Name of the target node.

Variables

- **dirs** (*dict*) – Dictionary containing the presence of directionality of the given edge. Keys are *straight*, *reverse* and 'undirected' and their values denote the presence/absence [bool].
- **negative** (*dict*) – Dictionary containing the presence/absence [bool] of negative interactions for both *straight* and *reverse* directions.
- **negative_sources** (*dict*) – Contains the resource names [str] supporting a negative interaction on *straight* and *reverse* directions.
- **nodes** (*list*) – Contains the node names [str] sorted alphabetically (*id_a*, *id_b*).
- **positive** (*dict*) – Dictionary containing the presence/absence [bool] of positive interactions for both *straight* and *reverse* directions.
- **positive_sources** (*dict*) – Contains the resource names [str] supporting a positive interaction on *straight* and *reverse* directions.
- **reverse** (*tuple*) – Contains the node names [str] in reverse order e.g. (*id_b*, *id_a*).
- **sources** (*dict*) – Contains the resource names [str] of a given edge for each directionality (*straight*, *reverse* and 'undirected'). Values are sets containing the names of those resources supporting such directionality.
- **straight** (*tuple*) – Contains the node names [str] in the original order e.g. (*id_a*, *id_b*).

check_nodes (*nodes*)

Checks if *nodes* is contained in the edge.

Parameters **nodes** (*list*) – Or [tuple], contains the names of the nodes to be checked.

Returns (*bool*) – True if all elements in *nodes* are contained in the object *nodes* list.

check_param(*di*)

Checks if *di* is 'undirected' or contains the nodes of the current edge. Used internally to check that *di* is a valid key for the object attributes declared on dictionaries.

Parameters *di* (*tuple*) – Or [str], key to be tested for validity.

Returns

(*bool*) – **True** if *di* is 'undirected' or a **tuple** of node names contained in the edge, **False** otherwise.

consensus_edges()

Infers the consensus edge(s) according to the number of supporting sources. This includes direction and sign.

Returns (*list*) – Contains the consensus edge(s) along with the consensus sign. If there is no major directionality, both are returned. The structure is as follows: ['<source>', '<target>', '<(un)directed>', '<sign>']

get_dir(*direction*, *sources=False*)

Returns the state (or *sources* if specified) of the given *direction*.

Parameters

- **direction** (*tuple*) – Or [str] (if 'undirected'). Pair of nodes from which direction information is to be retrieved.
- **sources** (*bool*) – Optional, 'False' by default. Specifies if the *sources* information of the given direction is to be retrieved instead.

Returns (*bool* or *set*) – (if *sources=True*). Presence/absence of the requested direction (or the list of sources if specified). Returns **None** if *direction* is not valid.

get_dirs(*src*, *tgt*, *sources=False*)

Returns all directions with boolean values or list of sources.

Parameters

- **src** (*str*) – Source node.
- **tgt** (*str*) – Target node.
- **sources** (*bool*) – Optional, **False** by default. Specifies whether to return the *sources* attribute instead of *dirs*.

Returns Contains the *dirs* (or *sources* if specified) of the given edge.

get_sign(*direction*, *sign=None*, *sources=False*)

Retrieves the sign information of the edge in the given direction. If specified in *sign*, only that sign's information will be retrieved. If specified in *sources*, the sources of that information will be retrieved instead.

Parameters

- **direction** (*tuple*) – Contains the pair of nodes specifying the directionality of the edge from which the information is to be retrieved.
- **sign** (*str*) – Optional, **None** by default. Denotes whether to retrieve the 'positive' or 'negative' specific information.
- **sources** (*bool*) – Optional, **False** by default. Specifies whether to return the sources instead of sign.

Returns (*list*) – If `sign=None` containing [bool] values denoting the presence of positive and negative sign on that direction, if `sources=True` the [set] of sources for each of them will be returned instead. If *sign* is specified, returns [bool] or [set] (if `sources=True`) of that specific direction and sign.

has_sign (*direction=None*)

Checks whether the edge (or for a specific *direction*) has any signed information (about positive/negative interactions).

Parameters *direction* (*tuple*) – Optional, `None` by default. If specified, only the information of that direction is checked for sign.

Returns

(*bool*) – **True** if there exist any information on the sign of the interaction, `False` otherwise.

is_directed ()

Checks if edge has any directionality information.

Returns (*bool*) – Returns `True` if any of the `:py:attr:`dirs`` attribute values is `True` (except `'undirected'`), `False` otherwise.

is_inhibition (*direction=None*)

Checks if any (or for a specific *direction*) interaction is inhibition (negative interaction).

Parameters *direction* (*tuple*) – Optional, `None` by default. If specified, checks the negative attribute of that specific directionality. If not specified, checks both.

Returns (*bool*) – `True` if any interaction (or the specified *direction*) is inhibitory (negative).

is_stimulation (*direction=None*)

Checks if any (or for a specific *direction*) interaction is activation (positive interaction).

Parameters *direction* (*tuple*) – Optional, `None` by default. If specified, checks the positive attribute of that specific directionality. If not specified, checks both.

Returns (*bool*) – `True` if any interaction (or the specified *direction*) is activatory (positive).

majority_dir ()

Infers which is the major directionality of the edge by number of supporting sources.

Returns (*tuple*) – Contains the pair of nodes denoting the consensus directionality. If the number of sources on both directions is equal, `None` is returned. If there is no directionality information, `'undirected'` will be returned.

majority_sign ()

Infers which is the major sign (activation/inhibition) of the edge by number of supporting sources on both directions.

Returns (*dict*) – Keys are the node tuples on both directions (`straight/reverse`) and values can be either `None` if that direction has no sign information or a list of two [bool] elements corresponding to majority of positive and majority of negative support. In case both elements of the list are `True`, this means the number of supporting sources for both signs in that direction is equal.

merge (*other*)

Merges current edge with another (if and only if they are the same class and contain the same nodes). Updates the attributes `dirs`, `sources`, `positive`, `negative`, `positive_sources` and `negative_sources`.

Parameters *other* (`pypath.main.Direction`) – The new edge object to be merged with the current one.

negative_reverse()

Checks if the `reverse` directionality is a negative interaction.

Returns (*bool*) – True if there is supporting information on the `reverse` direction of the edge as inhibition. False otherwise.

negative_sources_reverse()

Retrieves the list of sources for the `reverse` direction and negative sign.

Returns (*set*) – Contains the names of the sources supporting the `reverse` directionality of the edge with a negative sign.

negative_sources_straight()

Retrieves the list of sources for the `straight` direction and negative sign.

Returns (*set*) – Contains the names of the sources supporting the `straight` directionality of the edge with a negative sign.

negative_straight()

Checks if the `straight` directionality is a negative interaction.

Returns (*bool*) – True if there is supporting information on the `straight` direction of the edge as inhibition. False otherwise.

positive_reverse()

Checks if the `reverse` directionality is a positive interaction.

Returns (*bool*) – True if there is supporting information on the `reverse` direction of the edge as activation. False otherwise.

positive_sources_reverse()

Retrieves the list of sources for the `reverse` direction and positive sign.

Returns (*set*) – Contains the names of the sources supporting the `reverse` directionality of the edge with a positive sign.

positive_sources_straight()

Retrieves the list of sources for the `straight` direction and positive sign.

Returns (*set*) – Contains the names of the sources supporting the `straight` directionality of the edge with a positive sign.

positive_straight()

Checks if the `straight` directionality is a positive interaction.

Returns (*bool*) – True if there is supporting information on the `straight` direction of the edge as activation. False otherwise.

set_dir(direction, source)

Adds directionality information with the corresponding data source named. Modifies self attributes `dirs` and `sources`.

Parameters

- **direction** (*tuple*) – Or [str], the directionality key for which the value on `dirs` has to be set True.
- **source** (*set*) – Contains the name(s) of the source(s) from which such information was obtained.

set_sign(direction, sign, source)

Sets sign and source information on a given direction of the edge. Modifies the attributes `positive` and `positive_sources` or `negative` and `negative_sources` depending on the sign. Direction is also updated accordingly, which also modifies the attributes `dirs` and `sources`.

Parameters

- **direction** (*tuple*) – Pair of edge nodes specifying the direction from which the information is to be set/updated.
- **sign** (*str*) – Specifies the type of interaction. If 'positive', is considered activation, otherwise, is assumed to be negative (inhibition).
- **source** (*set*) – Contains the name(s) of the source(s) from which the information was obtained.

sources_reverse()

Retrieves the list of sources for the `reverse` direction.

Returns (*set*) – Contains the names of the sources supporting the `reverse` directionality of the edge.

sources_straight()

Retrieves the list of sources for the `straight` direction.

Returns (*set*) – Contains the names of the sources supporting the `straight` directionality of the edge.

sources_undirected()

Retrieves the list of sources without directed information.

Returns (*set*) – Contains the names of the sources supporting the edge presence but without specific directionality information.

src(undirected=False)

Returns the name(s) of the source node(s) for each existing direction on the interaction.

Parameters **undirected** (*bool*) – Optional, `False` by default.

Returns (*list*) – Contains the name(s) for the source node(s). This means if the interaction is bidirectional, the list will contain both identifiers on the edge. If the interaction is undirected, an empty list will be returned.

src_by_source(source)

Returns the name(s) of the source node(s) for each existing direction on the interaction for a specific *source*.

Parameters **source** (*str*) – Name of the source according to which the information is to be retrieved.

Returns (*list*) – Contains the name(s) for the source node(s) according to the specified *source*. This means if the interaction is bidirectional, the list will contain both identifiers on the edge. If the specified *source* is not found or invalid, an empty list will be returned.

tgt(undirected=False)

Returns the name(s) of the target node(s) for each existing direction on the interaction.

Parameters **undirected** (*bool*) – Optional, `False` by default.

Returns (*list*) – Contains the name(s) for the target node(s). This means if the interaction is bidirectional, the list will contain both identifiers on the edge. If the interaction is undirected, an empty list will be returned.

tgt_by_source(source)

Returns the name(s) of the target node(s) for each existing direction on the interaction for a specific *source*.

Parameters **source** (*str*) – Name of the source according to which the information is to be retrieved.

Returns (*list*) – Contains the name(s) for the target node(s) according to the specified *source*. This means if the interaction is bidirectional, the list will contain both identifiers on the edge. If the specified *source* is not found or invalid, an empty list will be returned.

translate (*ids*)

Translates the node names/identifiers according to the dictionary *ids*.

Parameters *ids* (*dict*) – Dictionary containing (at least) the current names of the nodes as keys and their translation as values.

Returns (*pypath.main.Direction*) – The copy of current edge object with translated node names.

unset_dir (*direction*, *source=None*)

Removes directionality and/or source information of the specified *direction*. Modifies attribute *dirs* and *sources*.

Parameters

- **direction** (*tuple*) – Or [*str*] (if 'undirected') the pair of nodes specifying the directionality from which the information is to be removed.
- **source** (*set*) – Optional, *None* by default. If specified, determines which specific source(s) is(are) to be removed from *sources* attribute in the specified *direction*.

unset_sign (*direction*, *sign*, *source=None*)

Removes sign and/or source information of the specified *direction* and *sign*. Modifies attribute *positive* and *positive_sources* or *negative* and *negative_sources* (or *positive_attributes/negative_sources* only if *source=True*).

Parameters

- **direction** (*tuple*) – The pair of nodes specifying the directionality from which the information is to be removed.
- **sign** (*str*) – Sign from which the information is to be removed. Must be either 'positive' or 'negative'.
- **source** (*set*) – Optional, *None* by default. If specified, determines which source(s) is(are) to be removed from the sources in the specified *direction* and *sign*.

which_dirs ()

Returns the pair(s) of nodes for which there is information about their directionality.

Returns (*list*) – List of tuples containing the nodes for which their attribute *dirs* is *True*.

class *pypath.main.AttrHelper* (*value*, *name=None*, *defaults={}*)

Attribute helper class.

• Initialization arguments:

- *value* [*dict/str*]?:
- *name* [*str*]?: Optional, *None* by default.
- *defaults* [*dict*]:

• Attributes:

- *value* [*dict*]?:
- *name* [*str*]?:
- *defaults* [*dict*]:
- *id_type* [*type*]:

- **Call arguments:**
 - *instance* []:
 - *this_directed* [tuple?]: Optional, `None` by default.
 - *thisSign* []: Optional, `None` by default.
 - *this_directedSources* []: Optional, `None` by default.
 - *thisSources* []: Optional, `None` by default.
- **Returns:**
 -

2.7 ptm module

WEBSERVICE

New webservice from 14 June 2018: the queries slightly changed, have been largely extended. See the examples below.

One instance of the pypath webservice runs at the domain <http://omnipathdb.org/>, serving not only the OmniPath data but other datasets: TF-target interactions from TF Regulons, a large collection additional enzyme-substrate interactions, and literature curated miRNA-mRNA interactions combined from 4 databases. The webservice implements a very simple REST style API, you can make requests by HTTP protocol (browser, wget, curl or whatever).

The webservice currently recognizes 3 types of queries: `interactions`, `ptms` and `info`. The query types `resources`, `network` and `about` have not been implemented yet in the new webservice.

3.1 Mouse and rat

Except the miRNA interactions all interactions are available for human, mouse and rat. The rodent data has been translated from human using the NCBI Homologene database. Many human proteins have no known homolog in rodents hence rodent datasets are smaller than their human counterparts. Note, if you work with mouse omics data you might do better to translate your dataset to human (for example using the `pypath.homology` module) and use human interaction data.

3.2 Examples

A request without any parameter, gives some basic numbers about the actual loaded dataset:

<http://omnipathdb.org>

The `info` returns a HTML page with comprehensive information about the resources:

<http://omnipathdb.org/info>

The `interactions` query accepts some parameters and returns interactions in tabular format. This example returns all interactions of EGFR (P00533), with sources and references listed.

<http://omnipathdb.org/interactions/?partners=P00533&fields=sources,references>

By default only the OmniPath dataset used, to query the TF Regulons or add the extra enzyme-substrate interactions you need to set additional parameters. For example to query the transcriptional regulators of EGFR:

<http://omnipathdb.org/interactions/?targets=EGFR&types=TF>

The TF Regulons database assigns confidence levels to the interactions. You might want to select only the highest confidence, A category:

http://omnipathdb.org/interactions/?targets=EGFR&types=TF&tfregulons_levels=A

Show the transcriptional targets of Smad2 homology translated to rat including the confidence levels from TF Regulations:

```
http://omnipathdb.org/interactions/?genesymbols=1&fields=type,ncbi_tax_id,tfregulons_level&organisms=10116&sources=Smad2&types=TF
```

Query interactions from PhosphoNetworks which is part of the *kinaseextra* dataset:

```
http://omnipathdb.org/interactions/?genesymbols=1&fields=sources&databases=PhosphoNetworks&datasets=kinaseextra
```

Get the interactions from Signor, SPIKE and Signalink3:

```
http://omnipathdb.org/interactions/?genesymbols=1&fields=sources,references&databases=Signor,SPIKE,Signalink3
```

All interactions of MAP1LC3B:

```
http://omnipathdb.org/interactions/?genesymbols=1&partners=MAP1LC3B
```

By default `partners` queries the interaction where either the source or the target is among the partners. If you set the `source_target` parameter to `AND` both the source and the target must be in the queried set:

```
http://omnipathdb.org/interactions/?genesymbols=1&fields=sources,references&sources=ATG3,ATG7,ATG4B,SQSTM1&targets=MAP1LC3B,MAP1LC3A,MAP1LC3C,Q9H0R8,GABARAP,GABARAPL2&source_target=AND
```

As you see above you can use UniProt IDs and Gene Symbols in the queries and also mix them. Get the miRNA regulating NOTCH1:

```
http://omnipathdb.org/interactions/?genesymbols=1&fields=sources,references&datasets=mirnatarget&targets=NOTCH1
```

Note: with the exception of mandatory fields and genesymbols, the columns appear exactly in the order you provided in your query.

Another query type available is `ptms` which provides enzyme-substrate interactions. It is very similar to the interactions:

```
http://omnipathdb.org/ptms?genesymbols=1&fields=sources,references,isoforms&enzymes=FYN
```

Is there any ubiquitination reaction?

```
http://omnipathdb.org/ptms?genesymbols=1&fields=sources,references&types=ubiquitination
```

And acetylation in mouse?

```
http://omnipathdb.org/ptms?genesymbols=1&fields=sources,references&types=acetylation&organisms=10090
```

Rat interactions, both directly from rat and homology translated from human, from the PhosphoSite database:

```
http://omnipathdb.org/ptms?genesymbols=1&fields=sources,references&organisms=10116&databases=PhosphoSite,PhosphoSite_noref
```

RELEASE HISTORY

Main improvements in the past releases:

4.1 0.1.0

- First release of pypath, for initial testing.

4.2 0.2.0

- Lots of small improvements in almost every module
- Networks can be read from local files, remote files, lists or provided by any function
- Almost all redistributed data have been removed, every source downloaded from the original provider.

4.3 0.3.0

- First version with partial Python 3 support.

4.4 0.4.0

- **pyreact** module with **BioPaxReader** and **PyReact** classes added
- Process description databases, BioPax and PathwayCommons SIF conversion rules are supported
- Format definitions for 6 process description databases included.

4.5 0.5.0

- Many classes have been added to the **plot** module
- All figures and tables in the manuscript can be generated automatically
- This is supported by a new module, **analysis**, which implements a generic workflow in its **Workflow** class.

4.6 0.7.74

- **homology** module: finds the homologs of proteins using the NCBI Homologene database and the homologs of PTM sites using UniProt sequences and PhosphoSitePlus homology table
- **ptm** module: fully integrated way of processing enzyme-substrate interactions from many databases and their translation by homology to other species
- **export** module: creates `pandas.DataFrame` or exports the network into tabular file
- New webservice
- TF Regulons database included and provides much more comprehensive transcriptional regulation resources, including literature curated, in silico predicted, ChIP-Seq and expression pattern based approaches
- Many network resources added, including miRNA-mRNA and TF-miRNA interactions

4.7 Upcoming

- New, more flexible network reader class
- Full support for multi-species molecular interaction networks (e.g. pathogene-host)
- Better support for not protein only molecular interaction networks (metabolites, drug compounds, RNA)
- ChEMBL webservice interface, interface for PubChem and eventually for DrugBank
- Silent mode: a way to suppress messages and progress bars

FEATURES

The primary aim of **pypath** is to build up networks from multiple sources on one **igraph** object. **pypath** handles ambiguous ID conversion, reads custom edge and node attributes from text files and **MySQL**.

Submodules perform various features, e.g. graph visualization, working with **rug** compound data, searching drug targets and compounds in **ChEMBL**.

5.1 ID conversion

The ID conversion module `mapping` can be used independently. It has the feature to translate secondary UniProt IDs to primaries, and Trembl IDs to SwissProt, using primary Gene Symbols to find the connections. This module automatically loads and stores the necessary conversion tables. Many tables are predefined, such as all the IDs in **UniProt mapping service**, while users are able to load any table from **file** or **MySQL**, using the classes provided in the module `input_formats`.

5.2 Pathways

pypath includes data and predefined format descriptions for more than 25 high quality, literature curated databases. The input formats are defined in the `data_formats` module. For some resources data downloaded on the fly, where it is not possible, data is redistributed with the module. Descriptions and comprehensive information about the resources is available in the `descriptions` module.

5.3 Structural features

One of the modules called `intera` provides many classes for representing structures and mechanisms behind protein interactions. These are `Residue` (optionally mutated), `Motif`, `Ptm`, `Domain`, `DomainMotif`, `DomainDomain` and `Interface`. All these classes have `__eq__()` methods to test equality between instances, and also `__contains__()` methods to look up easily if a residue is within a short motif or protein domain, or is the target residue of a PTM.

5.4 Sequences

The module `seq` contains a simple class for quick lookup any residue or segment in **UniProt** protein sequences while being aware of isoforms.

5.5 Tissue expression

For 3 protein expression databases there are functions and modules for downloading and combining the expression data with the network. These are the Human Protein Atlas, the ProteomicsDB and GIANT. The `giant` and `proteomicsdb` modules can be used also as stand alone Python clients for these resources.

5.6 Functional annotations

GSEA and **Gene Ontology** are two approaches for annotating genes and gene products, and enrichment analysis technics aims to use these annotations to highlight the biological functions a given set of genes is related to. Here the `enrich` module gives abstract classes to calculate enrichment statistics, while the `go` and the `gsea` modules give access to GO and GSEA data, and make it easy to count enrichment statistics for sets of genes.

5.7 Drug compounds

UniChem submodule provides an interface to effectively query the UniChem service, use connectivity search with custom settings, and translate SMILES to ChEMBL IDs with ChEMBL web service.

ChEMBL submodule queries directly your own ChEMBL MySQL instance, has the features to search targets and compounds from custom assay types and relationship types, to get activity values, binding domains, and action types. You need to download the ChEMBL MySQL dump, and load into your own server.

5.8 Technical

MySQL submodule helps to manage MySQL connections and track queries. It is able to run queries parallelly to optimize CPU and memory usage on the server, handling queues, and serve the result by server side or client side storage. The `chembl` and potentially the `mapping` modules rely on this `mysql` module.

The most important function in module `dataio` is a very flexible **download manager** built around `curl`. The function `dataio.curl()` accepts numerous arguments, tries to deal in a smart way with local **cache**, authentication, redirects, uncompression, character encodings, FTP and HTTP transactions, and many other stuff. Cache can grow to several GBs, and takes place in `./cache` by default. Please be aware of this, and use for example symlinks in case of using multiple working directories.

A simple **webservice** comes with this module: the `server` module based on `twisted.web.server` opens a custom port and serves plain text tables over HTTP with REST style querying.

OMNIPATH IN R

You can download the data from the webservice and load into R. Look [here](#) for an example.

PYTHON MODULE INDEX

p

- `pypath.annot`, 7
- `pypath.complex`, 8
- `pypath.intera`, 9
- `pypath.intercell`, 9
- `pypath.main`, 9
- `pypath.ptm`, 56

A

AbstractComplexResource (class in *py-path.complex*), 8
 acsn_effects() (*py-path.main.PyPath* method), 12
 add_genesets() (*py-path.main.PyPath* method), 12
 add_grouped_eattr() (*py-path.main.PyPath* method), 12
 add_grouped_set_eattr() (*py-path.main.PyPath* method), 12
 add_list_eattr() (*py-path.main.PyPath* method), 13
 add_set_eattr() (*py-path.main.PyPath* method), 13
 add_update_edge() (*py-path.main.PyPath* method), 13
 add_update_vertex() (*py-path.main.PyPath* method), 13
 Adhesome (class in *py-path.annot*), 7
 affects() (*py-path.main.PyPath* method), 14
 all_between() (*py-path.main.PyPath* method), 14
 all_neighbours() (*py-path.main.PyPath* method), 14
 all_uniprot() (*py-path.annot.AnnotationBase* method), 7
 AnnotationBase (class in *py-path.annot*), 7
 apply_list() (*py-path.main.PyPath* method), 14
 apply_negative() (*py-path.main.PyPath* method), 14
 attach_network() (*py-path.main.PyPath* method), 14
 AttrHelper (class in *py-path.main*), 55

B

basic_stats() (*py-path.main.PyPath* method), 15
 basic_stats_intergroup() (*py-path.main.PyPath* method), 15

C

cancer_drivers_list() (*py-path.main.PyPath* method), 15
 cancer_gene_census_list() (*py-path.main.PyPath* method), 15
 CellPhoneDB (class in *py-path.annot*), 7

CellPhoneDB (class in *py-path.complex*), 8
 CellPhoneDBComplex (class in *py-path.annot*), 7
 CellSurfaceProteinAtlas (class in *py-path.annot*), 7
 check_nodes() (*py-path.main.Direction* method), 50
 check_param() (*py-path.main.Direction* method), 50
 clean_graph() (*py-path.main.PyPath* method), 15
 collapse_by_name() (*py-path.main.PyPath* method), 15
 combine_attr() (*py-path.main.PyPath* method), 15
 communities() (*py-path.main.PyPath* method), 16
 Compleat (class in *py-path.complex*), 8
 complex_comembership_network() (*py-path.main.PyPath* method), 16
 ComplexAggregator (class in *py-path.complex*), 8
 complexes() (*py-path.main.PyPath* method), 16
 complexes_in_network() (*py-path.main.PyPath* method), 16
 ComplexPortal (class in *py-path.complex*), 8
 compounds_from_chembl() (*py-path.main.PyPath* method), 16
 consensus_edges() (*py-path.main.Direction* method), 51
 consistency() (*py-path.main.PyPath* method), 16
 copy() (*py-path.main.PyPath* method), 16
 copy_edges() (*py-path.main.PyPath* method), 17
 Corum (class in *py-path.annot*), 7
 Corum (class in *py-path.complex*), 8
 CorumFuncat (class in *py-path.annot*), 7
 CorumGO (class in *py-path.annot*), 7
 count_sol() (*py-path.main.PyPath* method), 17
 coverage() (*py-path.main.PyPath* method), 17
 cspa_list() (*py-path.main.PyPath* method), 17
 curation_effort() (*py-path.main.PyPath* method), 17
 curation_stats() (*py-path.main.PyPath* method), 17
 curation_tab() (*py-path.main.PyPath* method), 17
 curators_work() (*py-path.main.PyPath* method), 17

D

databases_similarity() (*py-path.main.PyPath*

`method`), 17
`degree_dist()` (*pypath.main.PyPath method*), 17
`degree_dists()` (*pypath.main.PyPath method*), 18
`delete_by_organism()` (*pypath.main.PyPath method*), 18
`delete_by_source()` (*pypath.main.PyPath method*), 18
`delete_unknown()` (*pypath.main.PyPath method*), 18
`delete_unmapped()` (*pypath.main.PyPath method*), 18
`dgenesymbol()` (*pypath.main.PyPath method*), 18
`dgenesymbols()` (*pypath.main.PyPath method*), 19
`dgs()` (*pypath.main.PyPath method*), 19
`dgss()` (*pypath.main.PyPath method*), 19
`Direction` (*class in pypath.main*), 50
`disease_genes_list()` (*pypath.main.PyPath method*), 19
`dneighbors()` (*pypath.main.PyPath method*), 19
`dp()` (*pypath.main.PyPath method*), 19
`dproteins()` (*pypath.main.PyPath method*), 19
`dps()` (*pypath.main.PyPath method*), 19
`druggability_list()` (*pypath.main.PyPath method*), 19
`duniprot()` (*pypath.main.PyPath method*), 19
`duniprots()` (*pypath.main.PyPath method*), 19
`dup()` (*pypath.main.PyPath method*), 19
`dups()` (*pypath.main.PyPath method*), 19
`dv()` (*pypath.main.PyPath method*), 19
`dvs()` (*pypath.main.PyPath method*), 19

E

`edge_exists()` (*pypath.main.PyPath method*), 20
`edge_loc()` (*pypath.main.PyPath method*), 20
`edge_names()` (*pypath.main.PyPath method*), 20
`edges_3d()` (*pypath.main.PyPath method*), 20
`edges_between()` (*pypath.main.PyPath method*), 20
`edges_expression()` (*pypath.main.PyPath method*), 20
`edges_in_complexes()` (*pypath.main.PyPath method*), 20
`edges_ptms()` (*pypath.main.PyPath method*), 20
`edgeseq_inverse()` (*pypath.main.PyPath method*), 20
`Exocarta` (*class in pypath.annot*), 7
`export_dot()` (*pypath.main.PyPath method*), 20
`export_edgelist()` (*pypath.main.PyPath method*), 21
`export_graphml()` (*pypath.main.PyPath method*), 21
`export_ptms_tab()` (*pypath.main.PyPath method*), 22
`export_sif()` (*pypath.main.PyPath method*), 22

`export_struct_tab()` (*pypath.main.PyPath method*), 22
`export_tab()` (*pypath.main.PyPath method*), 22

F

`filters()` (*pypath.main.PyPath method*), 22
`find_all_paths()` (*pypath.main.PyPath method*), 22
`find_all_paths2()` (*pypath.main.PyPath method*), 23
`find_complex()` (*pypath.main.PyPath method*), 23
`first_neighbours()` (*pypath.main.PyPath method*), 23
`fisher_enrichment()` (*pypath.main.PyPath method*), 23

G

`geneset_enrichment()` (*pypath.main.PyPath method*), 23
`genesymbol()` (*pypath.main.PyPath method*), 23
`genesymbol_labels()` (*pypath.main.PyPath method*), 24
`genesymbols()` (*pypath.main.PyPath method*), 24
`get_attrs()` (*pypath.main.PyPath method*), 24
`get_db()` (*in module pypath.annot*), 8
`get_db()` (*in module pypath.complex*), 8
`get_dir()` (*pypath.main.Direction method*), 51
`get_directed()` (*pypath.main.PyPath method*), 24
`get_dirs()` (*pypath.main.Direction method*), 51
`get_dirs_signs()` (*pypath.main.PyPath method*), 24
`get_edge()` (*pypath.main.PyPath method*), 24
`get_edges()` (*pypath.main.PyPath method*), 24
`get_function()` (*pypath.main.PyPath method*), 25
`get_giant()` (*pypath.main.PyPath method*), 25
`get_go()` (*pypath.main.PyPath method*), 25
`get_max()` (*pypath.main.PyPath method*), 25
`get_network()` (*pypath.main.PyPath method*), 25
`get_node()` (*pypath.main.PyPath method*), 25
`get_node_d()` (*pypath.main.PyPath method*), 25
`get_node_pair()` (*pypath.main.PyPath method*), 26
`get_nodes()` (*pypath.main.PyPath method*), 26
`get_nodes_d()` (*pypath.main.PyPath method*), 26
`get_pathways()` (*pypath.main.PyPath method*), 26
`get_proteomicsdb()` (*pypath.main.PyPath method*), 26
`get_sign()` (*pypath.main.Direction method*), 51
`get_sub()` (*pypath.main.PyPath method*), 26
`get_subset()` (*pypath.annot.AnnotationBase method*), 7
`get_taxon()` (*pypath.main.PyPath method*), 26
`go_annotate_graph()` (*pypath.main.PyPath method*), 26
`go_enrichment()` (*pypath.main.PyPath method*), 26

GOIntercell (class in pypath.annot), 7
gs() (pypath.main.PyPath method), 26
gs_affected_by() (pypath.main.PyPath method), 26
gs_affects() (pypath.main.PyPath method), 26
gs_edge() (pypath.main.PyPath method), 27
gs_in_directed() (pypath.main.PyPath method), 27
gs_in_undirected() (pypath.main.PyPath method), 27
gs_inhibited_by() (pypath.main.PyPath method), 27
gs_inhibits() (pypath.main.PyPath method), 27
gs_neighborhood() (pypath.main.PyPath method), 27
gs_neighbors() (pypath.main.PyPath method), 27
gs_stimulated_by() (pypath.main.PyPath method), 27
gs_stimulates() (pypath.main.PyPath method), 27
gss() (pypath.main.PyPath method), 27
guide2pharma() (pypath.main.PyPath method), 27
GuideToPharmacology (class in pypath.annot), 7
GuideToPharmacology (class in pypath.complex), 8

H

has_sign() (pypath.main.Direction method), 52
having_attr() (pypath.main.PyPath method), 27
having_eattr() (pypath.main.PyPath method), 27
having_ptm() (pypath.main.PyPath method), 28
having_vattr() (pypath.main.PyPath method), 28
Havugimana (class in pypath.complex), 8
Hgnc (class in pypath.annot), 7
homology_translation() (pypath.main.PyPath method), 28
Hpmr (class in pypath.complex), 8
HpmrComplex (class in pypath.annot), 7
http_stats() (pypath.main.PyPath method), 28
HumanPlasmaMembraneReceptome (class in pypath.annot), 7
Humap (class in pypath.complex), 8

I

in_complex() (pypath.main.PyPath method), 28
in_directed() (pypath.main.PyPath method), 28
in_undirected() (pypath.main.PyPath method), 28
info() (pypath.main.PyPath method), 28
init_complex_attr() (pypath.main.PyPath method), 28
init_db() (in module pypath.annot), 8
init_db() (in module pypath.complex), 9
init_edge_attr() (pypath.main.PyPath method), 28
init_gsea() (pypath.main.PyPath method), 29
init_network() (pypath.main.PyPath method), 29

init_vertex_attr() (pypath.main.PyPath method), 29
Integrins (class in pypath.annot), 7
IntercellRole (class in pypath.intercell), 9
intergroup_shortest_paths() (pypath.main.PyPath method), 29
intogen_cancer_drivers_list() (pypath.main.PyPath method), 29
is_directed() (pypath.main.Direction method), 52
is_inhibition() (pypath.main.Direction method), 52
is_stimulation() (pypath.main.Direction method), 52
iter_interactions() (pypath.main.PyPath method), 29

J

jaccard_edges() (pypath.main.PyPath method), 29
jaccard_meta() (pypath.main.PyPath method), 30

K

kegg_directions() (pypath.main.PyPath method), 30
kegg_pathways() (pypath.main.PyPath method), 30
kinase_stats() (pypath.main.PyPath method), 30
kinases_list() (pypath.main.PyPath method), 30
Kirouac2010 (class in pypath.annot), 7

L

label() (pypath.main.PyPath method), 30
label_by_go() (pypath.main.PyPath method), 30
label_edges() (pypath.main.PyPath method), 30
label_vertices() (pypath.main.PyPath method), 30
laudanna_directions() (pypath.main.PyPath method), 30
laudanna_effects() (pypath.main.PyPath method), 30
license() (pypath.main.PyPath static method), 30
LigandReceptor (class in pypath.annot), 7
list_resources() (pypath.main.PyPath static method), 30
load_3dcomplexes() (pypath.main.PyPath method), 30
load_3did_ddi() (pypath.main.PyPath method), 30
load_3did_ddi2() (pypath.main.PyPath method), 30
load_3did_dmi() (pypath.main.PyPath method), 30
load_3did_interfaces() (pypath.main.PyPath method), 30
load_all_pathways() (pypath.main.PyPath method), 30
load_compleat() (pypath.main.PyPath method), 30

`load_complexportal()` (*pypath.main.PyPath method*), 31
`load_comppi()` (*pypath.main.PyPath method*), 31
`load_corum()` (*pypath.main.PyPath method*), 31
`load_dbptm()` (*pypath.main.PyPath method*), 31
`load_ddi()` (*pypath.main.PyPath method*), 31
`load_ddis()` (*pypath.main.PyPath method*), 31
`load_depod_dmi()` (*pypath.main.PyPath method*), 31
`load_disgenet()` (*pypath.main.PyPath method*), 31
`load_dmi()` (*pypath.main.PyPath method*), 31
`load_dmis()` (*pypath.main.PyPath method*), 31
`load_domino_dmi()` (*pypath.main.PyPath method*), 31
`load_elm()` (*pypath.main.PyPath method*), 31
`load_exocarta_attrs()` (*pypath.main.PyPath method*), 31
`load_expression()` (*pypath.main.PyPath method*), 31
`load_go()` (*pypath.main.PyPath method*), 31
`load_havugimana()` (*pypath.main.PyPath method*), 32
`load_hpa()` (*pypath.main.PyPath method*), 32
`load_hprd_ptms()` (*pypath.main.PyPath method*), 32
`load_ielm()` (*pypath.main.PyPath method*), 32
`load_interfaces()` (*pypath.main.PyPath method*), 32
`load_li2012_ptms()` (*pypath.main.PyPath method*), 32
`load_ligand_receptor_network()` (*pypath.main.PyPath method*), 32
`load_list()` (*pypath.main.PyPath method*), 32
`load_lmpid()` (*pypath.main.PyPath method*), 32
`load_matrisome_attrs()` (*pypath.main.PyPath method*), 32
`load_membranome_attrs()` (*pypath.main.PyPath method*), 32
`load_mimp_dmi()` (*pypath.main.PyPath method*), 32
`load_mutations()` (*pypath.main.PyPath method*), 32
`load_negatives()` (*pypath.main.PyPath method*), 32
`load_old_omnipath()` (*pypath.main.PyPath method*), 32
`load_omnipath()` (*pypath.main.PyPath method*), 32
`load_pathways()` (*pypath.main.PyPath method*), 32
`load_pdb()` (*pypath.main.PyPath method*), 33
`load_pepcyber()` (*pypath.main.PyPath method*), 33
`load_pfam()` (*pypath.main.PyPath method*), 33
`load_pfam2()` (*pypath.main.PyPath method*), 33
`load_pfam3()` (*pypath.main.PyPath method*), 33
`load_phospho_dmi()` (*pypath.main.PyPath method*), 33
`load_phosphoelm()` (*pypath.main.PyPath method*), 33
`load_pisa()` (*pypath.main.PyPath method*), 33
`load_pnetworks_dmi()` (*pypath.main.PyPath method*), 33
`load_psite_phos()` (*pypath.main.PyPath method*), 33
`load_psite_reg()` (*pypath.main.PyPath method*), 33
`load_ptms()` (*pypath.main.PyPath method*), 33
`load_ptms2()` (*pypath.main.PyPath method*), 33
`load_resource()` (*pypath.main.PyPath method*), 34
`load_resources()` (*pypath.main.PyPath method*), 34
`load_signor_ptms()` (*pypath.main.PyPath method*), 35
`load_surfaceome_attrs()` (*pypath.main.PyPath method*), 35
`load_tfrequlons()` (*pypath.main.PyPath method*), 35
`load_uniprots()` (*pypath.annot.AnnotationBase method*), 7
`load_vesiclepedia_attrs()` (*pypath.main.PyPath method*), 35
`Locate` (*class in pypath.annot*), 8
`lookup_cache()` (*pypath.main.PyPath method*), 35
`loop_edges()` (*pypath.main.PyPath method*), 36

M

`majority_dir()` (*pypath.main.Direction method*), 52
`majority_sign()` (*pypath.main.Direction method*), 52
`map_edge()` (*pypath.main.PyPath method*), 36
`map_item()` (*pypath.main.PyPath method*), 36
`map_list()` (*pypath.main.PyPath method*), 36
`Matrisome` (*class in pypath.annot*), 8
`Matrixdb` (*class in pypath.annot*), 8
`mean_reference_per_interaction()` (*pypath.main.PyPath method*), 36
`Membranome` (*class in pypath.annot*), 8
`merge()` (*pypath.main.Direction method*), 52
`merge_lists()` (*pypath.main.PyPath method*), 37
`merge_nodes()` (*pypath.main.PyPath method*), 37
`mimp_directions()` (*pypath.main.PyPath method*), 37
`mutated_edges()` (*pypath.main.PyPath method*), 37

N

`name_edgelist()` (*pypath.main.PyPath method*), 37
`names2vids()` (*pypath.main.PyPath method*), 37
`negative_report()` (*pypath.main.PyPath method*), 37
`negative_reverse()` (*pypath.main.Direction method*), 52

`negative_sources_reverse()` (*pypath.main.Direction method*), 53
`negative_sources_straight()` (*pypath.main.Direction method*), 53
`negative_straight()` (*pypath.main.Direction method*), 53
`neighborhood()` (*pypath.main.PyPath method*), 37
`neighbors()` (*pypath.main.PyPath method*), 38
`neighbourhood_network()` (*pypath.main.PyPath method*), 38
`network_by_go()` (*pypath.main.PyPath method*), 38
`network_filter()` (*pypath.main.PyPath method*), 38
`network_stats()` (*pypath.main.PyPath method*), 38
`new_edges()` (*pypath.main.PyPath method*), 38
`new_nodes()` (*pypath.main.PyPath method*), 39
`node_exists()` (*pypath.main.PyPath method*), 39
`numof_directed_edges()` (*pypath.main.PyPath method*), 39
`numof_reference_interaction_pairs()` (*pypath.main.PyPath method*), 39
`numof_references()` (*pypath.main.PyPath method*), 39
`numof_undirected_edges()` (*pypath.main.PyPath method*), 39

O

`Opm` (*class in pypath.annot*), 8
`orthology_translation()` (*pypath.main.PyPath method*), 39

P

`p()` (*pypath.main.PyPath method*), 39
`pathway_attributes()` (*pypath.main.PyPath method*), 39
`pathway_members()` (*pypath.main.PyPath method*), 39
`pathway_names()` (*pypath.main.PyPath method*), 39
`pathway_similarity()` (*pypath.main.PyPath method*), 39
`pathways_table()` (*pypath.main.PyPath method*), 39
`Pdb` (*class in pypath.complex*), 8
`pfam_regions()` (*pypath.main.PyPath method*), 39
`phosfonetworks_directions()` (*pypath.main.PyPath method*), 40
`phosphopoint_directions()` (*pypath.main.PyPath method*), 40
`phosphorylation_directions()` (*pypath.main.PyPath method*), 40
`phosphorylation_signs()` (*pypath.main.PyPath method*), 40
`phosphosite_directions()` (*pypath.main.PyPath method*), 40

`positive_reverse()` (*pypath.main.Direction method*), 53
`positive_sources_reverse()` (*pypath.main.Direction method*), 53
`positive_sources_straight()` (*pypath.main.Direction method*), 53
`positive_straight()` (*pypath.main.Direction method*), 53
`prdb_tissue_expr()` (*pypath.main.PyPath method*), 40
`process_direction()` (*pypath.main.PyPath method*), 40
`process_directions()` (*pypath.main.PyPath method*), 40
`process_dmi()` (*pypath.main.PyPath method*), 40
`process_sign()` (*pypath.main.PyPath method*), 40
`protein()` (*pypath.main.PyPath method*), 40
`protein_edge()` (*pypath.main.PyPath method*), 41
`proteins()` (*pypath.main.PyPath method*), 41
`proteome_list()` (*pypath.main.PyPath method*), 41
`ps()` (*pypath.main.PyPath method*), 41
`PyPath` (*class in pypath.main*), 9
`pypath.annot` (*module*), 7
`pypath.complex` (*module*), 8
`pypath.intera` (*module*), 9
`pypath.intercell` (*module*), 9
`pypath.main` (*module*), 9
`pypath.ptm` (*module*), 56

R

`Ramilowski2015` (*class in pypath.annot*), 8
`random_walk_with_return()` (*pypath.main.PyPath method*), 41
`random_walk_with_return2()` (*pypath.main.PyPath method*), 41
`read_data_file()` (*pypath.main.PyPath method*), 41
`read_from_cache()` (*pypath.main.PyPath method*), 42
`read_list_file()` (*pypath.main.PyPath method*), 42
`receptors_list()` (*pypath.main.PyPath method*), 42
`reference_edge_ratio()` (*pypath.main.PyPath method*), 42
`reference_hist()` (*pypath.main.PyPath method*), 42
`reload()` (*pypath.annot.AnnotationBase method*), 7
`reload()` (*pypath.main.PyPath method*), 42
`remove_htp()` (*pypath.main.PyPath method*), 42
`remove_undirected()` (*pypath.main.PyPath method*), 42
`role` (*pypath.intercell.IntercellRole attribute*), 9
`run_batch()` (*pypath.main.PyPath method*), 43

S

`save_network()` (*pypath.main.PyPath method*), 43
`save_session()` (*pypath.main.PyPath method*), 43
`search_attr_and()` (*pypath.main.PyPath method*), 43
`search_attr_or()` (*pypath.main.PyPath method*), 43
`second_neighbours()` (*pypath.main.PyPath method*), 43
`select_by_go()` (*pypath.main.PyPath method*), 43
`select_by_go_all()` (*pypath.main.PyPath method*), 44
`select_by_go_expr()` (*pypath.main.PyPath method*), 44
`separate()` (*pypath.main.PyPath method*), 44
`separate_by_category()` (*pypath.main.PyPath method*), 44
`sequences()` (*pypath.main.PyPath method*), 44
`set_boolean_vattr()` (*pypath.main.PyPath method*), 44
`set_categories()` (*pypath.main.PyPath method*), 44
`set_chembl_mysql()` (*pypath.main.PyPath method*), 44
`set_dir()` (*pypath.main.Direction method*), 53
`set_disease_genes()` (*pypath.main.PyPath method*), 45
`set_druggability()` (*pypath.main.PyPath method*), 45
`set_drugtargets()` (*pypath.main.PyPath method*), 45
`set_kinases()` (*pypath.main.PyPath method*), 45
`set_plasma_membrane_proteins_cspa()` (*pypath.main.PyPath method*), 45
`set_plasma_membrane_proteins_cspa_surfaceome()` (*pypath.main.PyPath method*), 45
`set_plasma_membrane_proteins_surfaceome()` (*pypath.main.PyPath method*), 45
`set_receptors()` (*pypath.main.PyPath method*), 45
`set_sign()` (*pypath.main.Direction method*), 53
`set_signaling_proteins()` (*pypath.main.PyPath method*), 45
`set_tfs()` (*pypath.main.PyPath method*), 45
`set_transcription_factors()` (*pypath.main.PyPath method*), 45
`shortest_path_dist()` (*pypath.main.PyPath method*), 45
`signaling_proteins_list()` (*pypath.main.PyPath method*), 46
`Signor` (*class in pypath.complex*), 8
`signor_pathways()` (*pypath.main.PyPath method*), 46
`similarity_groups()` (*pypath.main.PyPath method*), 46
`small_plot()` (*pypath.main.PyPath method*), 46
`sorensen_pathways()` (*pypath.main.PyPath method*), 46
`source` (*pypath.intercell.IntercellRole attribute*), 9
`source_diagram()` (*pypath.main.PyPath method*), 46
`source_network()` (*pypath.main.PyPath method*), 46
`source_similarity()` (*pypath.main.PyPath method*), 46
`source_stats()` (*pypath.main.PyPath method*), 46
`sources_hist()` (*pypath.main.PyPath method*), 46
`sources_overlap()` (*pypath.main.PyPath method*), 47
`sources_reverse()` (*pypath.main.Direction method*), 54
`sources_straight()` (*pypath.main.Direction method*), 54
`sources_undirected()` (*pypath.main.Direction method*), 54
`sources_venn_data()` (*pypath.main.PyPath method*), 47
`src()` (*pypath.main.Direction method*), 54
`src_by_source()` (*pypath.main.Direction method*), 54
`straight_between()` (*pypath.main.PyPath method*), 47
`string_effects()` (*pypath.main.PyPath method*), 47
`sum_in_complex()` (*pypath.main.PyPath method*), 47
`Surfaceome` (*class in pypath.annot*), 8
`surfaceome_list()` (*pypath.main.PyPath method*), 47
`table_latex()` (*pypath.main.PyPath method*), 47
`tfs_list()` (*pypath.main.PyPath method*), 47
`tgt()` (*pypath.main.Direction method*), 54
`tgt_by_source()` (*pypath.main.Direction method*), 54
`third_source_directions()` (*pypath.main.PyPath method*), 47
`tissue_network()` (*pypath.main.PyPath method*), 47
`Topdb` (*class in pypath.annot*), 8
`transcription_factors()` (*pypath.main.PyPath method*), 48
`translate()` (*pypath.main.Direction method*), 55

U

`uniprot()` (*pypath.main.PyPath method*), 48
`uniprots()` (*pypath.main.PyPath method*), 48

uniq_node_list() (*pypath.main.PyPath method*),
 48
 uniq_ptm() (*pypath.main.PyPath method*), 48
 uniq_ptms() (*pypath.main.PyPath method*), 48
 unset_dir() (*pypath.main.Direction method*), 55
 unset_sign() (*pypath.main.Direction method*), 55
 up() (*pypath.main.PyPath method*), 48
 up_affected_by() (*pypath.main.PyPath method*),
 48
 up_affects() (*pypath.main.PyPath method*), 48
 up_edge() (*pypath.main.PyPath method*), 48
 up_in_directed() (*pypath.main.PyPath method*),
 48
 up_in_undirected() (*pypath.main.PyPath*
 method), 48
 up_inhibited_by() (*pypath.main.PyPath method*),
 48
 up_inhibits() (*pypath.main.PyPath method*), 48
 up_neighborhood() (*pypath.main.PyPath method*),
 48
 up_neighbors() (*pypath.main.PyPath method*), 48
 up_stimulated_by() (*pypath.main.PyPath*
 method), 48
 up_stimulates() (*pypath.main.PyPath method*), 48
 update_adjlist() (*pypath.main.PyPath method*),
 48
 update_attrs() (*pypath.main.PyPath method*), 48
 update_cats() (*pypath.main.PyPath method*), 49
 update_db_dict() (*pypath.main.PyPath method*),
 49
 update_pathway_types() (*pypath.main.PyPath*
 method), 49
 update_pathways() (*pypath.main.PyPath method*),
 49
 update_sources() (*pypath.main.PyPath method*),
 49
 update_vertex_sources() (*pypath.main.PyPath*
 method), 49
 update_vindex() (*pypath.main.PyPath method*), 49
 update_vname() (*pypath.main.PyPath method*), 49
 ups() (*pypath.main.PyPath method*), 49

V

v() (*pypath.main.PyPath method*), 49
 vertex_pathways() (*pypath.main.PyPath method*),
 49
 Vesiclepedia (*class in pypath.annot*), 8
 vsgs() (*pypath.main.PyPath method*), 49
 vsup() (*pypath.main.PyPath method*), 49

W

wang_effects() (*pypath.main.PyPath method*), 49
 which_dirs() (*pypath.main.Direction method*), 55
 write_table() (*pypath.main.PyPath method*), 49

Z

Zhong2015 (*class in pypath.annot*), 8