scikit-network Documentation

Release 0.20.0

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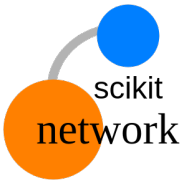
Oct 20, 2020

INSTALLATION REFERENCE



Python package for the analysis of large graphs:

- Memory-efficient representation as sparse matrices in the CSR format of scipy
- Fast algorithms
- Simple API inspired by scikit-learn

CHAPTER

ONE

RESOURCES

- Free software: BSD license
- GitHub: https://github.com/sknetwork-team/scikit-network
- Documentation: https://scikit-network.readthedocs.io

CHAPTER

TWO

QUICKSTART

Install scikit-network:

```
$ pip install scikit-network
```

Import scikit-network in a Python project:

```
import sknetwork as skn
```

See examples in the tutorials; the notebooks are available here.

CHAPTER

THREE

CITING

If you want to cite *scikit-network*, please refer to the publication in the Journal of Machine Learning Research:

```
@article{JMLR:v21:20-412,
  author  = {Thomas Bonald and Nathan de Lara and Quentin Lutz and Bertrand␣
↪Charpentier},
  title   = {Scikit-network: Graph Analysis in Python},
  journal = {Journal of Machine Learning Research},
  year    = {2020},
  volume  = {21},
  number  = {185},
  pages   = {1-6},
  url     = {http://jmlr.org/papers/v21/20-412.html}
}
```

3.1 Installation

3.1.1 Stable release

To install scikit-network, run this command in your terminal:

```
$ pip install scikit-network
```

This is the preferred method to install scikit-network, as it will always install the most recent stable release.

If you don't have pip installed, this Python installation guide can guide you through the process.

3.1.2 From sources

The sources for scikit-network can be downloaded from the Github repo.

You can either clone the public repository:

```
$ git clone git://github.com/sknetwork-team/scikit-network
```

Or download the tarball.

Once you have a copy of the source, if you have an installation of pip:

```
$ pip install <path to the repo/path to the tarball>
```

Or, after having unpacked the tarball if relevant, you can install it with:

```
$ cd <scikit-network folder>
$ python setup.py develop
```

3.2 Reference

3.2.1 Getting started

`scikit-network` is an open-source python package for the analysis of large graphs.

Installation

Install `scikit-network`:

```
$ pip install scikit-network
```

Import `scikit-network` in a Python project:

```
import sknetwork as skn
```

Data format

Each graph is represented by its *adjacency* matrix, either as a dense `numpy array` or a sparse `scipy CSR matrix`. A bipartite graph can be represented by its biadjacency matrix, in the same format.

Documentation

We use the following notations in the documentation:

Graphs

For undirected graphs:

- A is the adjacency matrix of the graph (dimension $n \times n$)
- $d = A1$ is the vector of node weights (node degrees if the matrix A is binary)
- $D = \text{diag}(d)$ the diagonal matrix of node weights

Digraphs

For directed graphs:

- A is the adjacency matrix of the graph (dimension $n \times n$)
- $d^+ = A1$ and $d^- = A^T1$ are the vectors of out-weights and in-weights of nodes (out-degrees and in-degrees if the matrix A is binary)
- $D^+ = \text{diag}(d^+)$ and $D^- = \text{diag}(d^-)$ are the diagonal matrices of out-weights and in-weights

Bigraphs

For bipartite graphs:

- B is the biadjacency matrix of the graph (dimension $n_1 \times n_2$)
- $d_1 = B1$ and $d_2 = B^T 1$ are the vectors of weights (rows and columns)
- $D_1 = \text{diag}(d_1)$ and $D_2 = \text{diag}(d_2)$ are the diagonal matrices of weights.

Notes

- Adjacency and biadjacency matrices have non-negative entries (the weights of the edges).
- Bipartite graphs are undirected but have a special structure that is exploited by some algorithms. These algorithms are identified with the prefix `Bi`.

3.2.2 Data

Tools for importing and exporting data.

Toy graphs

`sknetwork.data.`**`house`**(*metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

House graph.

- Undirected graph
- 5 nodes, 6 edges

Parameters **`metadata`** – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> adjacency.shape
(5, 5)
```

`sknetwork.data.`**`bow_tie`**(*metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Bow tie graph.

- Undirected graph
- 5 nodes, 6 edges

Parameters **`metadata`** – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import bow_tie
>>> adjacency = bow_tie()
>>> adjacency.shape
(5, 5)
```

sknetwork.data.**karate_club**(*metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Karate club graph.

- Undirected graph
- 34 nodes, 78 edges
- 2 labels

Parameters **metadata** – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (labels, positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import karate_club
>>> adjacency = karate_club()
>>> adjacency.shape
(34, 34)
```

References

Zachary's karate club graph https://en.wikipedia.org/wiki/Zachary%27s_karate_club

sknetwork.data.**miserables**(*metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Co-occurrence graph of the characters in the novel Les miserables by Victor Hugo.

- Undirected graph
- 77 nodes, 508 edges
- Names of characters

Parameters **metadata** – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (names, positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import miserables
>>> adjacency = miserables()
>>> adjacency.shape
(77, 77)
```

sknetwork.data.**painters**(*metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Graph of links between some famous painters on Wikipedia.

- Directed graph
- 14 nodes, 50 edges
- Names of painters

Parameters **metadata** – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (names, positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import painters
>>> adjacency = painters()
>>> adjacency.shape
(14, 14)
```

sknetwork.data.**star_wars**(*metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Bipartite graph connecting some Star Wars villains to the movies in which they appear.

- Bipartite graph
- 7 nodes (4 villains, 3 movies), 8 edges
- Names of villains and movies

Parameters **metadata** – If `True`, return a *Bunch* object with metadata.

Returns **biadjacency or graph** – Biadjacency matrix or graph with metadata (names).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import star_wars
>>> biadjacency = star_wars()
>>> biadjacency.shape
(4, 3)
```

sknetwork.data.**movie_actor**(*metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Bipartite graph connecting movies to some actors starring in them.

- Bipartite graph

- 31 nodes (15 movies, 16 actors), 42 edges
- 9 labels (rows)
- Names of movies (rows) and actors (columns)
- Names of movies production company (rows)

Parameters **metadata** – If `True`, return a *Bunch* object with metadata.

Returns **biadjacency or graph** – Biadjacency matrix or graph with metadata (names).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import movie_actor
>>> biadjacency = movie_actor()
>>> biadjacency.shape
(15, 16)
```

Models

`sknetwork.data.`**`linear_graph`**(*n: int = 3*, *metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Linear graph (undirected).

Parameters

- **n** (*int*) – Number of nodes.
- **metadata** (*bool*) – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import linear_graph
>>> adjacency = linear_graph(5)
>>> adjacency.shape
(5, 5)
```

`sknetwork.data.`**`linear_digraph`**(*n: int = 3*, *metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Linear graph (directed).

Parameters

- **n** (*int*) – Number of nodes.
- **metadata** (*bool*) – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import linear_digraph
>>> adjacency = linear_digraph(5)
>>> adjacency.shape
(5, 5)
```

sknetwork.data.**cyclic_graph**(*n: int = 3, metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Cyclic graph (undirected).

Parameters

- **n** (*int*) – Number of nodes.
- **metadata** (*bool*) – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import cyclic_graph
>>> adjacency = cyclic_graph(5)
>>> adjacency.shape
(5, 5)
```

sknetwork.data.**cyclic_digraph**(*n: int = 3, metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Cyclic graph (directed).

Parameters

- **n** (*int*) – Number of nodes.
- **metadata** (*bool*) – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import cyclic_digraph
>>> adjacency = cyclic_digraph(5)
>>> adjacency.shape
(5, 5)
```

sknetwork.data.**grid**(*n1: int = 10, n2: int = 10, metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Grid (undirected).

Parameters

- **n1** (*int*) – Grid dimension.
- **n2** (*int*) – Grid dimension.
- **metadata** (*bool*) – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import grid
>>> adjacency = grid(10, 5)
>>> adjacency.shape
(50, 50)
```

sknetwork.data.**erdos_renyi**(*n: int = 20*, *p: float = 0.3*, *random_state: Optional[int] = None*) → scipy.sparse.csr.csr_matrix

Erdos-Renyi graph.

Parameters

- **n** – Number of nodes.
- **p** – Probability of connection between nodes.
- **random_state** – Seed of the random generator (optional).

Returns **adjacency** – Adjacency matrix.

Return type sparse.csr_matrix

Example

```
>>> from sknetwork.data import erdos_renyi
>>> adjacency = erdos_renyi(7)
>>> adjacency.shape
(7, 7)
```

References

Erdős, P., Rényi, A. (1959). On Random Graphs. Publicationes Mathematicae.

sknetwork.data.**block_model**(*sizes: Iterable*, *p_in: Union[float, list, numpy.ndarray] = 0.2*, *p_out: float = 0.05*, *random_state: Optional[int] = None*, *metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Stochastic block model.

Parameters

- **sizes** – Block sizes.
- **p_in** – Probability of connection within blocks.
- **p_out** – Probability of connection across blocks.
- **random_state** – Seed of the random generator (optional).
- **metadata** – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (labels).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import block_model
>>> sizes = np.array([4, 5])
>>> adjacency = block_model(sizes)
>>> adjacency.shape
(9, 9)
```

References

Airoldi, E., Blei, D., Feinberg, S., Xing, E. (2007). Mixed membership stochastic blockmodels. Journal of Machine Learning Research.

sknetwork.data.**albert_barabasi**(*n: int = 100*, *degree: int = 3*, *undirected: bool = True*, *seed: Optional[int] = None*) → scipy.sparse.csr.csr_matrix

Albert-Barabasi model.

Parameters

- **n** (*int*) – Number of nodes.
- **degree** (*int*) – Degree of incoming nodes (less than **n**).
- **undirected** (*bool*) – If `True`, return an undirected graph.
- **seed** – Seed of the random generator (optional).

Returns **adjacency** – Adjacency matrix.

Return type sparse.csr_matrix

Example

```
>>> from sknetwork.data import albert_barabasi
>>> adjacency = albert_barabasi(30, 3)
>>> adjacency.shape
(30, 30)
```

References

Albert, R., Barabási, L. (2002). Statistical mechanics of complex networks Reviews of Modern Physics.

sknetwork.data.**watts_strogatz**(*n: int = 100*, *degree: int = 6*, *prob: float = 0.05*, *seed: Optional[int] = None*, *metadata: bool = False*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]

Watts-Strogatz model.

Parameters

- **n** – Number of nodes.
- **degree** – Initial degree of nodes.
- **prob** – Probability of edge modification.
- **seed** – Seed of the random generator (optional).
- **metadata** – If `True`, return a *Bunch* object with metadata.

Returns **adjacency or graph** – Adjacency matrix or graph with metadata (positions).

Return type Union[sparse.csr_matrix, Bunch]

Example

```
>>> from sknetwork.data import watts_strogatz
>>> adjacency = watts_strogatz(30, 4, 0.02)
>>> adjacency.shape
(30, 30)
```

References

Watts, D., Strogatz, S. (1998). Collective dynamics of small-world networks, Nature.

Load

You can find some datasets on NetRep.

sknetwork.data.**load_edge_list**(*file: str*, *directed: bool = False*, *bipartite: bool = False*, *weighted: Optional[bool] = None*, *named: Optional[bool] = None*, *comment: str = '%#'*, *delimiter: str = None*, *reindex: bool = True*, *fast_format: bool = True*) → sknetwork.utils.Bunch

Parse Tabulation-Separated, Comma-Separated or Space-Separated (or other) Values datasets in the form of edge lists.

Parameters

- **file** (*str*) – The path to the dataset in TSV format
- **directed** (*bool*) – If `True`, considers the graph as directed.
- **bipartite** (*bool*) – If `True`, returns a biadjacency matrix of shape (n1, n2).
- **weighted** (*Optional[bool]*) – Retrieves the weights in the third field of the file. None makes a guess based on the first lines.
- **named** (*Optional[bool]*) – Retrieves the names given to the nodes and renumbers them. Returns an additional array. None makes a guess based on the first lines.
- **comment** (*str*) – Set of characters denoting lines to ignore.
- **delimiter** (*str*) – delimiter used in the file. None makes a guess
- **reindex** (*bool*) – If True and the graph nodes have numeric values, the size of the returned adjacency will be determined by the maximum of those values. Does not work for bipartite graphs.
- **fast_format** (*bool*) – If True, assumes that the file is well-formatted:
  - no comments except for the header
  - only 2 or 3 columns
  - only int or float values

Returns **graph**

Return type `Bunch`

sknetwork.data.**load_adjacency_list**(*file: str*, *bipartite: bool = False*, *comment: str = '%#'*, *delimiter: str = None*) → sknetwork.utils.Bunch

Parse Tabulation-Separated, Comma-Separated or Space-Separated (or other) Values datasets in the form of adjacency lists.

Parameters

- **file** (*str*) – The path to the dataset in TSV format
- **bipartite** (*bool*) – If `True`, returns a biadjacency matrix of shape (n1, n2).
- **comment** (*str*) – Set of characters denoting lines to ignore.
- **delimiter** (*str*) – delimiter used in the file. None makes a guess

Returns **graph**

Return type `Bunch`

sknetwork.data.**load_graphml**(*file: str*, *weight_key: str = 'weight'*, *max_string_size: int = 512*) → sknetwork.utils.Bunch

Parse GraphML datasets.

Hyperedges and nested graphs are not supported.

Parameters

- **file** (*str*) – The path to the dataset
- **weight_key** (*str*) – The key to be used as a value for edge weights
- **max_string_size** (*int*) – The maximum size for string features of the data

Returns **data** – The dataset in a bunch with the adjacency as a CSR matrix.

Return type `Bunch`

sknetwork.data.**load_netset**(*dataset: Optional[str] = None*, *data_home: Optional[Union[str, pathlib.Path]] = None*) → sknetwork.utils.Bunch

Load a dataset from the NetSet database.

Parameters

- **dataset** (*str*) – The name of the dataset (all low-case). Examples include 'openflights', 'cinema' and 'wikivitals'.
- **data_home** (str or `pathlib.Path`) – The folder to be used for dataset storage.

Returns **graph**

Return type `Bunch`

sknetwork.data.**load_konect**(*dataset: str*, *data_home: Optional[Union[str, pathlib.Path]] = None*, *auto_numpy_bundle: bool = True*) → sknetwork.utils.Bunch

Load a dataset from the Konect database.

Parameters

- **dataset** (*str*) – The internal name of the dataset as specified on the Konect website (e.g. for the Zachary Karate club dataset, the corresponding name is `'ucidata-zachary'`).
- **data_home** (str or `pathlib.Path`) – The folder to be used for dataset storage
- **auto_numpy_bundle** (*bool*) – Denotes if the dataset should be stored in its default format (False) or using Numpy files for faster subsequent access to the dataset (True).

Returns

graph –

An object with the following attributes:

- *adjacency* or *biadjacency*: the adjacency/biadjacency matrix for the dataset
- *meta*: a dictionary containing the metadata as specified by Konect
- each attribute specified by Konect (ent.* file)

Return type `Bunch`

Notes

An attribute *meta* of the *Bunch* class is used to store information about the dataset if present. In any case, *meta* has the attribute *name* which, if not given, is equal to the name of the dataset as passed to this function.

References

Kunegis, J. (2013, May). Konect: the Koblenz network collection. In Proceedings of the 22nd International Conference on World Wide Web (pp. 1343-1350).

`sknetwork.data.`**`convert_edge_list`**(*edge_list: Union[numpy.ndarray, List[Tuple], List[List]]*, *directed: bool = False*, *bipartite: bool = False*, *reindex: bool = True*, *named: Optional[bool] = None*) → sknetwork.utils.Bunch

Turn an edge list into a `Bunch`.

Parameters

- **`edge_list`** (*`Union[np.ndarray, List[Tuple], List[List]]`*) – The edge list to convert, given as a NumPy array of size (n, 2) or (n, 3) or a list of either lists or tuples of length 2 or 3.
- **`directed`** (*`bool`*) – If `True`, considers the graph as directed.
- **`bipartite`** (*`bool`*) – If `True`, returns a biadjacency matrix of shape (n1, n2).
- **`reindex`** (*`bool`*) – If True and the graph nodes have numeric values, the size of the returned adjacency will be determined by the maximum of those values. Does not work for bipartite graphs.
- **`named`** (*`Optional[bool]`*) – Retrieves the names given to the nodes and renumbers them. Returns an additional array. None makes a guess based on the first lines.

Returns **graph**

Return type `Bunch`

Save

sknetwork.data.**save**(*folder: Union[str, pathlib.Path]*, *data: Union[scipy.sparse.csr.csr_matrix, sknetwork.utils.Bunch]*)

Save a Bunch or a CSR matrix in the current directory to a collection of Numpy and Pickle files for faster subsequent loads.

Parameters

- **folder** (str or `pathlib.Path`) – The name to be used for the bundle folder
- **data** (*`Union[sparse.csr_matrix, Bunch]`*) – The data to save

Example

```
>>> from sknetwork.data import save
>>> graph = Bunch()
>>> graph.adjacency = sparse.csr_matrix(np.random.random((10, 10)) < 0.2)
>>> graph.names = np.array(list('abcdefghij'))
>>> save('random_data', graph)
>>> 'random_data' in listdir('.')
True
```

sknetwork.data.**load**(*folder: Union[str, pathlib.Path]*)

Load a Bunch from a previously created bundle from the current directory (inverse function of `save`).

Parameters **folder** (*`str`*) – The name used for the bundle folder

Returns **data** – The original data

Return type Bunch

Example

```
>>> from sknetwork.data import save
>>> graph = Bunch()
>>> graph.adjacency = sparse.csr_matrix(np.random.random((10, 10)) < 0.2)
>>> graph.names = np.array(list('abcdefghij'))
>>> save('random_data', graph)
>>> loaded_graph = load('random_data')
>>> loaded_graph.names[0]
'a'
```

3.2.3 Topology

Algorithms for the analysis of graph topology.

Structure

sknetwork.topology.**connected_components**(*adjacency: scipy.sparse.csr.csr_matrix, connection: str = 'weak'*) → numpy.ndarray

Extract the connected components of the graph.

- Graphs
- Digraphs

Based on SciPy (scipy.sparse.csgraph.connected_components).

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **connection** – Must be `'weak'` (default) or `'strong'`. The type of connection to use for directed graphs.

Returns **labels** – Connected component of each node.

Return type np.ndarray

sknetwork.topology.**largest_connected_component**(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray], return_labels: bool = False*)

Extract the largest connected component of a graph. Bipartite graphs are treated as undirected.

- Graphs
- Digraphs
- Bigraphs

Parameters

- **adjacency** – Adjacency or biadjacency matrix of the graph.
- **return_labels** (*bool*) – Whether to return the indices of the new nodes in the original graph.

Returns

- **new_adjacency** (*sparse.csr_matrix*) – Adjacency or biadjacency matrix of the largest connected component.
- **indices** (*array or tuple of array*) – Indices of the nodes in the original graph. For biadjacency matrices, `indices[0]` corresponds to the rows and `indices[1]` to the columns.

class sknetwork.topology.**CoreDecomposition**

K-core decomposition algorithm.

- Graphs

Variables

- **labels_** (*np.ndarray*) – Core value of each node.
- **core_value_** (*int*) – Maximum core value of the graph

Example

```
>>> from sknetwork.topology import CoreDecomposition
>>> from sknetwork.data import karate_club
>>> kcore = CoreDecomposition()
>>> adjacency = karate_club()
>>> kcore.fit(adjacency)
>>> kcore.core_value_
4
```

fit(*adjacency: scipy.sparse.csr.csr_matrix*) → sknetwork.topology.kcore.CoreDecomposition
K-core decomposition.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *CoreDecomposition*

fit_transform(*adjacency: scipy.sparse.csr.csr_matrix*)
Fit algorithm to the data and return the core value of each node. Same parameters as the `fit` method.

Returns Core value of the nodes.

Return type labels

sknetwork.topology.**is_bipartite**(*adjacency: scipy.sparse.csr.csr_matrix*, *return_biadjacency: bool = False*) → Union[bool, Tuple[bool, Optional[scipy.sparse.csr.csr_matrix], Optional[numpy.ndarray], Optional[numpy.ndarray]]]
Check whether an undirected graph is bipartite.

- Graphs

Parameters

- **adjacency** – Adjacency matrix of the graph (symmetric).
- **return_biadjacency** – If `True`, return a biadjacency matrix of the graph if bipartite.

Returns

- **is_bipartite** (*bool*) – A boolean denoting if the graph is bipartite.
- **biadjacency** (*sparse.csr_matrix*) – A biadjacency matrix of the graph if bipartite (optional).
- **rows** (*np.ndarray*) – Index of rows in the original graph (optional).
- **cols** (*np.ndarray*) – Index of columns in the original graph (optional).

sknetwork.topology.**is_acyclic**(*adjacency: scipy.sparse.csr.csr_matrix*) → bool
Check whether a graph has no cycle.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **is_acyclic** – A boolean with value True if the graph has no cycle and False otherwise

Return type bool

class sknetwork.topology.**DAG**(*ordering: str = None*)
Build a Directed Acyclic Graph from an adjacency.

- Graphs
- DiGraphs

Parameters **ordering** (*str*) – A method to sort the nodes.

- If None, the default order is the index.
- If `'degree'`, the nodes are sorted by ascending degree.

Variables

- **indptr_** (*np.ndarray*) – Pointer index as for CSR format.
- **indices_** (*np.ndarray*) – Indices as for CSR format.

fit (*adjacency: scipy.sparse.csr.csr_matrix*, *sorted_nodes=None*)
Fit algorithm to the data.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **sorted_nodes** (*np.ndarray*) – An order on the nodes such that the DAG only contains edges (i, j) such that `sorted_nodes[i] < sorted_nodes[j]`.

Counting

class sknetwork.topology.**Triangles** (*parallelize: bool = False*)
Count the number of triangles in a graph, and evaluate the clustering coefficient.

- Graphs

Parameters **parallelize** – If `True`, use a parallel range while listing the triangles.

Variables

- **n_triangles_** (*int*) – Number of triangles.
- **clustering_coef_** (*float*) – Global clustering coefficient of the graph.

Example

```
>>> from sknetwork.data import karate_club
>>> triangles = Triangles()
>>> adjacency = karate_club()
>>> triangles.fit_transform(adjacency)
45
```

fit (*adjacency: scipy.sparse.csr.csr_matrix*) → sknetwork.topology.triangles.Triangles
Count triangles.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *Triangles*

fit_transform (*adjacency: scipy.sparse.csr.csr_matrix*) → int
Fit algorithm to the data and return the number of triangles. Same parameters as the `fit` method.

Returns **n_triangles_** – Number of triangles.

Return type int

class sknetwork.topology.**Cliques**(*k: int*)
Clique counting algorithm.

- Graphs

Parameters **k** (*int*) – k value of cliques to list

Variables **n_cliques_** (*int*) – Number of cliques

Example

```
>>> from sknetwork.data import karate_club
>>> cliques = Cliques(k=3)
>>> adjacency = karate_club()
>>> cliques.fit_transform(adjacency)
45
```

References

Danisch, M., Balalau, O., & Sozio, M. (2018, April). Listing k-cliques in sparse real-world graphs. In Proceedings of the 2018 World Wide Web Conference (pp. 589-598).

fit(*adjacency: scipy.sparse.csr.csr_matrix*) → sknetwork.topology.kcliques.Cliques
K-cliques count.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *Cliques*

fit_transform(*adjacency: scipy.sparse.csr.csr_matrix*) → int
Fit algorithm to the data and return the number of cliques. Same parameters as the `fit` method.

Returns **n_cliques** – Number of k-cliques.

Return type int

Coloring

class sknetwork.topology.**WeisfeilerLehman**(*max_iter: int = - 1*)
Weisfeiler-Lehman algorithm for coloring/labeling graphs in order to check similarity.

Parameters **max_iter** (*int*) – Maximum number of iterations. Negative value means until convergence.

Variables **labels_** (*np.ndarray*) – Label of each node.

Example

```
>>> from sknetwork.topology import WeisfeilerLehman
>>> from sknetwork.data import house
>>> weisfeiler_lehman = WeisfeilerLehman()
>>> adjacency = house()
>>> labels = weisfeiler_lehman.fit_transform(adjacency)
>>> labels
array([0, 2, 1, 1, 2], dtype=int32)
```

References

- Douglas, B. L. (2011). The Weisfeiler-Lehman Method and Graph Isomorphism Testing.
- Shervashidze, N., Schweitzer, P., van Leeuwen, E. J., Melhorn, K., Borgwardt, K. M. (2011) Weisfeiler-Lehman graph kernels. Journal of Machine Learning Research 12, 2011.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.topology.weisfeiler_lehman.WeisfeilerLehman
Fit algorithm to the data.

Parameters **adjacency** (*Union[sparse.csr_matrix, np.ndarray]*) – Adjacency matrix of the graph.

Returns **self**

Return type *WeisfeilerLehman*

fit_transform(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

Similarity

sknetwork.topology.**are_isomorphic**(*adjacency1: scipy.sparse.csr.csr_matrix, adjacency2: scipy.sparse.csr.csr_matrix, max_iter: int = - 1*) → bool
Weisfeiler-Lehman isomorphism test. If the test is False, the graphs cannot be isomorphic, otherwise, they might be.

Parameters

- **adjacency1** – First adjacency matrix.
- **adjacency2** – Second adjacency matrix.
- **max_iter** (*int*) – Maximum number of coloring iterations. Negative value means until convergence.

Returns **test_result**

Return type bool

Example

```
>>> from sknetwork.topology import are_isomorphic
>>> from sknetwork.data import house
>>> adjacency_1 = house()
>>> adjacency_2 = house()
>>> are_isomorphic(adjacency_1, adjacency_2)
True
```

References

- Douglas, B. L. (2011). The Weisfeiler-Lehman Method and Graph Isomorphism Testing.
- Shervashidze, N., Schweitzer, P., van Leeuwen, E. J., Melhorn, K., Borgwardt, K. M. (2011) Weisfeiler-Lehman graph kernels. Journal of Machine Learning Research 12, 2011.

3.2.4 Path

Standard algorithms related to graph traversal.

Most algorithms are adapted from SciPy.

Shortest path

sknetwork.path.**distance**(*adjacency: scipy.sparse.csr.csr_matrix*, *sources: Optional[Union[int, Iterable]] = None*, *method: str = 'D'*, *return_predecessors: bool = False*, *unweighted: bool = False*, *n_jobs: Optional[int] = None*)

Compute distances between nodes.

- Graphs
- Digraphs

Based on SciPy (scipy.sparse.csgraph.shortest_path)

Parameters

- **adjacency** – The adjacency matrix of the graph
- **sources** – If specified, only compute the paths for the points at the given indices. Will not work with `method =='FW'`.
- **method** – The method to be used.
  - `'D'` (Dijkstra),
  - `'BF'` (Bellman-Ford),
  - `'J'` (Johnson).
- **return_predecessors** – If `True`, the size predecessor matrix is returned
- **unweighted** – If `True`, the weights of the edges are ignored
- **n_jobs** – If an integer value is given, denotes the number of workers to use (-1 means the maximum number will be used). If `None`, no parallel computations are made.

Returns

- **dist_matrix** (*np.ndarray*) – The matrix of distances between graph nodes. `dist_matrix[i,j]` gives the shortest distance from point `i` to point `j` along the graph. If no path exists between nodes `i` and `j`, then `dist_matrix[i, j] = np.inf`.
- **predecessors** (*np.ndarray, optional*) – Returned only if `return_predecessors == True`. The matrix of predecessors, which can be used to reconstruct the shortest paths. Row i of the predecessor matrix contains information on the shortest paths from point `i`: each entry `predecessors[i, j]` gives the index of the previous node in the path from point `i` to point `j`. If no path exists between nodes `i` and `j`, then `predecessors[i, j] = -9999`.

Examples

```
>>> from sknetwork.data import cyclic_digraph
>>> adjacency = cyclic_digraph(3)
>>> distance(adjacency, sources=0)
array([0., 1., 2.])
>>> distance(adjacency, sources=0, return_predecessors=True)
(array([0., 1., 2.]), array([-9999,     0,     1]))
```

sknetwork.path.**shortest_path**(*adjacency: scipy.sparse.csr.csr_matrix*, *sources: Union[int, Iterable]*, *targets: Union[int, Iterable]*, *method: str = 'D'*, *unweighted: bool = False*, *n_jobs: Optional[int] = None*)

Compute the shortest paths in the graph.

- Graphs
- Digraphs

Parameters

- **adjacency** – The adjacency matrix of the graph
- **sources** (*int or iterable*) – Sources nodes.
- **targets** (*int or iterable*) – Target nodes.
- **method** – The method to be used.
  - `'D'` (Dijkstra),
  - `'BF'` (Bellman-Ford),
  - `'J'` (Johnson).
- **unweighted** – If `True`, the weights of the edges are ignored
- **n_jobs** – If an integer value is given, denotes the number of workers to use (-1 means the maximum number will be used). If `None`, no parallel computations are made.

Returns **paths** – If single source and single target, return a list containing the nodes on the path from source to target. If multiple sources or multiple targets, return a list of paths as lists. An empty list means that the path does not exist.

Return type list

Examples

```
>>> from sknetwork.data import linear_digraph
>>> adjacency = linear_digraph(3)
>>> shortest_path(adjacency, 0, 2)
[0, 1, 2]
>>> shortest_path(adjacency, 2, 0)
[]
>>> shortest_path(adjacency, 0, [1, 2])
[[0, 1], [0, 1, 2]]
>>> shortest_path(adjacency, [0, 1], 2)
[[0, 1, 2], [1, 2]]
```

Summary of the different methods and their worst-case complexity for n nodes and m edges (for the all-pairs problem):

Method	Worst-case time complexity	Remarks
Dijkstra	$O(n^2 \log n + nm)$	For use on graphs with positive weights only
Bellman-Ford	$O(nm)$	For use on graphs without negative-weight cycles only
Johnson	$O(n^2 \log n + nm)$	

Search

sknetwork.path.**breadth_first_search**(*adjacency: scipy.sparse.csr.csr_matrix*, *source: int*, *return_predecessors: bool = True*)

Breadth-first ordering starting with specified node.

- Graphs
- Digraphs

Based on SciPy (scipy.sparse.csgraph.breadth_first_order)

Parameters

- **adjacency** – The adjacency matrix of the graph
- **source** (*int*) – The node from which to start the ordering
- **return_predecessors** (*bool*) – If `True`, the size predecessor matrix is returned

Returns

- **node_array** (*np.ndarray*) – The breadth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.
- **predecessors** (*np.ndarray*) – Returned only if `return_predecessors == True`. The list of predecessors of each node in a breadth-first tree. If node `i` is in the tree, then its parent is given by `predecessors[i]`. If node `i` is not in the tree (and for the parent node) then `predecessors[i] = -9999`.

sknetwork.path.**depth_first_search**(*adjacency: scipy.sparse.csr.csr_matrix*, *source: int*, *return_predecessors: bool = True*)

Depth-first ordering starting with specified node.

- Graphs
- Digraphs

Based on SciPy (scipy.sparse.csgraph.depth_first_order)

Parameters

- **adjacency** – The adjacency matrix of the graph
- **source** – The node from which to start the ordering
- **return_predecessors** – If `True`, the size predecessor matrix is returned

Returns

- **node_array** (*np.ndarray*) – The depth-first list of nodes, starting with specified node. The length of node_array is the number of nodes reachable from the specified node.
- **predecessors** (*np.ndarray*) – Returned only if `return_predecessors == True`. The list of predecessors of each node in a depth-first tree. If node `i` is in the tree, then its parent is given by `predecessors[i]`. If node `i` is not in the tree (and for the parent node) then `predecessors[i] = -9999`.

Metrics

`sknetwork.path.`**diameter**(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *n_sources: Optional[Union[int, float]] = None*, *n_jobs: Optional[int] = None*) → int

Lower bound on the diameter of a graph which is the length of the longest shortest path between two nodes.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **n_sources** – Number of node sources to use for approximation.
  - If None, compute exact diameter.
  - If int, sample n_sample source nodes at random.
  - If float, sample (n_samples * n) source nodes at random.
- **n_jobs** – If an integer value is given, denotes the number of workers to use (-1 means the maximum number will be used). If `None`, no parallel computations are made.

Returns **diameter**

Return type int

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> d_exact = diameter(adjacency)
>>> d_exact
2
>>> d_approx = diameter(adjacency, 2)
>>> d_approx <= d_exact
True
>>> d_approx = diameter(adjacency, 0.5)
>>> d_approx <= d_exact
True
```

Notes

This is a basic implementation that computes distances between nodes and returns the maximum.

3.2.5 Clustering

Clustering algorithms.

The attribute `labels_` assigns a label (cluster index) to each node of the graph.

Louvain

Here are the available modularities for the Louvain algorithm:

Modularity	Formula	Remarks
Newman (`'newman'`)	$Q = \frac{1}{w}\sum_{i,j}\left(A_{ij} - \gamma\frac{d_i d_j}{w}\right)\delta_{c_i,c_j}$	Ignores edge directions
Dugué (`'dugue'`)	$Q = \frac{1}{w}\sum_{i,j}\left(A_{ij} - \gamma\frac{d_i^+ d_j^-}{w}\right)\delta_{c_i,c_j}$	
Constant Potts (`'potts'`)	$Q = \sum_{i,j}\left(\frac{A_{ij}}{w} - \gamma\frac{1}{n^2}\right)\delta_{c_i,c_j}$	Ignores edge directions

class sknetwork.clustering.**Louvain**(*resolution: float = 1*, *modularity: str = 'dugue'*, *tol_optimization: float = 0.001*, *tol_aggregation: float = 0.001*, *n_aggregations: int = -1*, *shuffle_nodes: bool = False*, *sort_clusters: bool = True*, *return_membership: bool = True*, *return_aggregate: bool = True*, *random_state: Optional[Union[numpy.random.mtrand.RandomState, int]] = None*, *verbose: bool = False*)

Louvain algorithm for clustering graphs by maximization of modularity.

- Graphs
- Digraphs

Parameters

- **resolution** – Resolution parameter.
- **modularity** (*str*) – Which objective function to maximize. Can be `'dugue'`, `'newman'` or `'potts'`.
- **tol_optimization** – Minimum increase in the objective function to enter a new optimization pass.
- **tol_aggregation** – Minimum increase in the objective function to enter a new aggregation pass.
- **n_aggregations** – Maximum number of aggregations. A negative value is interpreted as no limit.
- **shuffle_nodes** – Enables node shuffling before optimization.
- **sort_clusters** – If `True`, sort labels in decreasing order of cluster size.

- **return_membership** – If `True`, return the membership matrix of nodes to each cluster (soft clustering).
- **return_aggregate** – If `True`, return the adjacency matrix of the graph between clusters.
- **random_state** – Random number generator or random seed. If None, numpy.random is used.
- **verbose** – Verbose mode.

Variables

- **labels_** (*np.ndarray*) – Label of each node.
- **membership_** (*sparse.csr_matrix*) – Membership matrix.
- **adjacency_** (*sparse.csr_matrix*) – Adjacency matrix between clusters.

Example

```
>>> from sknetwork.clustering import Louvain
>>> from sknetwork.data import karate_club
>>> louvain = Louvain()
>>> adjacency = karate_club()
>>> labels = louvain.fit_transform(adjacency)
>>> len(set(labels))
4
```

References

- Blondel, V. D., Guillaume, J. L., Lambiotte, R., & Lefebvre, E. (2008). Fast unfolding of communities in large networks. Journal of statistical mechanics: theory and experiment, 2008
- Dugué, N., & Perez, A. (2015). Directed Louvain: maximizing modularity in directed networks (Doctoral dissertation, Université d'Orléans).
- Traag, V. A., Van Dooren, P., & Nesterov, Y. (2011). Narrow scope for resolution-limit-free community detection. Physical Review E, 84(1), 016114.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.clustering.louvain.Louvain
Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *Louvain*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

class sknetwork.clustering.**BiLouvain**(*resolution: float = 1*, *modularity: str = 'dugue'*, *tol_optimization: float = 0.001*, *tol_aggregation: float = 0.001*, *n_aggregations: int = - 1*, *shuffle_nodes: bool = False*, *sort_clusters: bool = True*, *return_membership: bool = True*, *return_aggregate: bool = True*, *random_state: Optional[Union[numpy.random.mtrand.RandomState, int]] = None*, *verbose: bool = False*)

BiLouvain algorithm for the clustering of bipartite graphs.

- Bigraphs

Parameters

- **resolution** – Resolution parameter.
- **modularity** (*str*) – Which objective function to maximize. Can be `'dugue'`, `'newman'` or `'potts'`.
- **tol_optimization** – Minimum increase in the objective function to enter a new optimization pass.
- **tol_aggregation** – Minimum increase in the objective function to enter a new aggregation pass.
- **n_aggregations** – Maximum number of aggregations. A negative value is interpreted as no limit.
- **shuffle_nodes** – Enables node shuffling before optimization.
- **sort_clusters** – If `True`, sort labels in decreasing order of cluster size.
- **return_membership** – If `True`, return the membership matrix of nodes to each cluster (soft clustering).
- **return_aggregate** – If `True`, return the biadjacency matrix of the graph between clusters.
- **random_state** – Random number generator or random seed. If None, numpy.random is used.
- **verbose** – Verbose mode.

Variables

- **labels_** (*np.ndarray*) – Labels of the rows.
- **labels_row_** (*np.ndarray*) – Labels of the rows (copy of **labels_**).
- **labels_col_** (*np.ndarray*) – Labels of the columns.
- **membership_row_** (*sparse.csr_matrix*) – Membership matrix of the rows (copy of **membership_**).
- **membership_col_** (*sparse.csr_matrix*) – Membership matrix of the columns. Only valid if **cluster_both** = *True*.
- **biadjacency_** (*sparse.csr_matrix*) – Biadjacency matrix of the aggregate graph between clusters.

Example

```
>>> from sknetwork.clustering import BiLouvain
>>> from sknetwork.data import movie_actor
>>> bilouvain = BiLouvain()
>>> biadjacency = movie_actor()
>>> labels = bilouvain.fit_transform(biadjacency)
>>> len(labels)
15
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.clustering.louvain.BiLouvain
Apply the Louvain algorithm to the corresponding directed graph, with adjacency matrix:

$$A = \begin{bmatrix} 0 & B \\ 0 & 0 \end{bmatrix}$$

where B is the input (biadjacency matrix).

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns **self**

Return type *BiLouvain*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

Propagation

class sknetwork.clustering.**PropagationClustering**(*n_iter: int = 5*, *node_order: str = 'decreasing'*, *weighted: bool = True*, *sort_clusters: bool = True*, *return_membership: bool = True*, *return_aggregate: bool = True*)

Clustering by label propagation.

- Graphs
- Digraphs

Parameters

- **n_iter** (*int*) – Maximum number of iterations (-1 for infinity).
- **node_order** (*str*) –
  - *'random'*: node labels are updated in random order.
  - *'increasing'*: node labels are updated by increasing order of weight.
  - *'decreasing'*: node labels are updated by decreasing order of weight.
  - Otherwise, node labels are updated by index order.
- **weighted** (*bool*) – If `True`, the vote of each neighbor is proportional to the edge weight. Otherwise, all votes have weight 1.
- **sort_clusters** – If `True`, sort labels in decreasing order of cluster size.

- **return_membership** – If `True`, return the membership matrix of nodes to each cluster (soft clustering).
- **return_aggregate** – If `True`, return the adjacency matrix of the graph between clusters.

Variables

- **labels_** (*np.ndarray*) – Label of each node.
- **membership_** (*sparse.csr_matrix*) – Membership matrix (columns = labels).

Example

```
>>> from sknetwork.clustering import PropagationClustering
>>> from sknetwork.data import karate_club
>>> propagation = PropagationClustering()
>>> graph = karate_club(metadata=True)
>>> adjacency = graph.adjacency
>>> labels = propagation.fit_transform(adjacency)
>>> len(set(labels))
2
```

References

Raghavan, U. N., Albert, R., & Kumara, S. (2007). Near linear time algorithm to detect community structures in large-scale networks. Physical review E, 76(3), 036106.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.clustering.propagation_clustering.PropagationClustering
Clustering by label propagation.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *PropagationClustering*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

class sknetwork.clustering.**BiPropagationClustering**(*n_iter: int = 5*, *node_order: str = 'decreasing'*, *weighted: bool = True*, *sort_clusters: bool = True*, *return_membership: bool = True*, *return_aggregate: bool = True*)
Clustering by label propagation in bipartite graphs.

- Bigraphs

Parameters

- **n_iter** – Maximum number of iteration (-1 for infinity).
- **sort_clusters** – If `True`, sort labels in decreasing order of cluster size.
- **return_membership** – If `True`, return the membership matrix of nodes to each cluster (soft clustering).
- **return_aggregate** – If `True`, return the biadjacency matrix of the graph between clusters.

Variables

- **labels_** (*np.ndarray*) – Label of each row.
- **labels_row_** (*np.ndarray*) – Label of each row (copy of **labels_**).
- **labels_col_** (*np.ndarray*) – Label of each column.
- **membership_** (*sparse.csr_matrix*) – Membership matrix of rows.
- **membership_row_** (*sparse.csr_matrix*) – Membership matrix of rows (copy of **membership_**).
- **membership_col_** (*sparse.csr_matrix*) – Membership matrix of columns.

Example

```
>>> from sknetwork.clustering import BiPropagationClustering
>>> from sknetwork.data import movie_actor
>>> bipropagation = BiPropagationClustering()
>>> graph = movie_actor(metadata=True)
>>> biadjacency = graph.biadjacency
>>> len(bipropagation.fit_transform(biadjacency))
15
>>> len(bipropagation.labels_col_)
16
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.clustering.propagation_clustering.BiPropagationClustering
Clustering.

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns **self**

Return type *BiPropagationClustering*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

K-Means

class sknetwork.clustering.**KMeans**(*n_clusters: int = 8, embedding_method: sknetwork.embedding.base.BaseEmbedding = GSVD(n_components=10, regularization=None, relative_regularization=True, factor_row=0.5, factor_col=0.5, factor_singular=0.0, normalized=True, solver='auto')*, *sort_clusters: bool = True*, *return_membership: bool = True*, *return_aggregate: bool = True*)

K-means applied in the embedding space.

- Graphs
- Digraphs

Parameters

- **n_clusters** – Number of desired clusters.
- **embedding_method** – Embedding method (default = GSVD in dimension 10, projected on the unit sphere).
- **sort_clusters** – If `True`, sort labels in decreasing order of cluster size.
- **return_membership** – If `True`, return the membership matrix of nodes to each cluster (soft clustering).
- **return_aggregate** – If `True`, return the adjacency matrix of the graph between clusters.

Variables

- **labels_** (*np.ndarray*) – Label of each node.
- **membership_** (*sparse.csr_matrix*) – Membership matrix.
- **adjacency_** (*sparse.csr_matrix*) – Adjacency matrix between clusters.

Example

```
>>> from sknetwork.clustering import KMeans
>>> from sknetwork.data import karate_club
>>> kmeans = KMeans(n_clusters=3)
>>> adjacency = karate_club()
>>> labels = kmeans.fit_transform(adjacency)
>>> len(set(labels))
3
```

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.clustering.kmeans.KMeans

Apply embedding method followed by K-means.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *KMeans*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

class sknetwork.clustering.**BiKMeans**(*n_clusters: int = 2*, *embedding_method: sknetwork.embedding.base.BaseBiEmbedding = GSVD(n_components=10, regularization=None, relative_regularization=True, factor_row=0.5, factor_col=0.5, factor_singular=0.0, normalized=True, solver='auto')*, *co_cluster: bool = False*, *sort_clusters: bool = True*, *return_membership: bool = True*, *return_aggregate: bool = True*)
KMeans clustering of bipartite graphs applied in the embedding space.

- Bigraphs

Parameters

- **n_clusters** – Number of clusters.
- **embedding_method** – Embedding method (default = GSVD in dimension 10, projected on the unit sphere).
- **co_cluster** – If `True`, co-cluster rows and columns (default = `False`).
- **sort_clusters** – If `True`, sort labels in decreasing order of cluster size.
- **return_membership** – If `True`, return the membership matrix of nodes to each cluster (soft clustering).
- **return_aggregate** – If `True`, return the biadjacency matrix of the graph between clusters.

Variables

- **labels_** (*np.ndarray*) – Labels of the rows.
- **labels_row_** (*np.ndarray*) – Labels of the rows (copy of **labels_**).
- **labels_col_** (*np.ndarray*) – Labels of the columns. Only valid if **co_cluster** = *True*.
- **membership_** (*sparse.csr_matrix*) – Membership matrix of the rows.
- **membership_row_** (*sparse.csr_matrix*) – Membership matrix of the rows (copy of **membership_**).
- **membership_col_** (*sparse.csr_matrix*) – Membership matrix of the columns. Only valid if **co_cluster** = *True*.
- **biadjacency_** (*sparse.csr_matrix*) – Biadjacency matrix of the graph between clusters.

Example

```
>>> from sknetwork.clustering import BiKMeans
>>> from sknetwork.data import movie_actor
>>> bikmeans = BiKMeans()
>>> biadjacency = movie_actor()
>>> labels = bikmeans.fit_transform(biadjacency)
>>> len(labels)
15
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.clustering.kmeans.BiKMeans
Apply embedding method followed by clustering to the graph.

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns **self**

Return type *BiKMeans*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

Metrics

sknetwork.clustering.**modularity**(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *labels: numpy.ndarray*, *weights: Union[str, numpy.ndarray] = 'degree'*, *weights_in: Union[str, numpy.ndarray] = 'degree'*, *resolution: float = 1*, *return_all: bool = False*) → Union[float, Tuple[float, float, float]]
Modularity of a clustering (node partition).

- Graphs
- Digraphs

The modularity of a clustering is

$Q = \frac{1}{w}\sum_{i,j}\left(A_{ij} - \gamma\frac{d_i d_j}{w}\right)\delta_{c_i,c_j}$ for graphs,

$Q = \frac{1}{w}\sum_{i,j}\left(A_{ij} - \gamma\frac{d_i^+ d_j^-}{w}\right)\delta_{c_i,c_j}$ for digraphs,

where

- c_i is the cluster of node i,
- d_i is the weight of node i,
- d_i^+, d_i^- are the out-weight, in-weight of node i (for digraphs),
- $w = 1^T A 1$ is the total weight,
- δ is the Kronecker symbol,
- $\gamma \geq 0$ is the resolution parameter.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **labels** – Labels of nodes, vector of size n .
- **weights** – Weights of nodes. `'degree'` (default), `'uniform'` or custom weights.
- **weights_in** – In-weights of nodes. `None` (default), `'degree'`, `'uniform'` or custom weights. If `None`, taken equal to weights.
- **resolution** – Resolution parameter (default = 1).
- **return_all** – If `True`, return modularity, fit, diversity.

Returns

- **modularity** (*float*)
- **fit** (*float, optional*)
- **diversity** (*float, optional*)

Example

```
>>> from sknetwork.clustering import modularity
>>> from sknetwork.data import house
>>> adjacency = house()
>>> labels = np.array([0, 0, 1, 1, 0])
>>> np.round(modularity(adjacency, labels), 2)
0.11
```

sknetwork.clustering.**bimodularity**(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *labels: numpy.ndarray*, *labels_col: numpy.ndarray*, *weights: Union[str, numpy.ndarray] = 'degree'*, *weights_col: Union[str, numpy.ndarray] = 'degree'*, *resolution: float = 1*, *return_all: bool = False*) → Union[float, Tuple[float, float, float]]

Bimodularity of a clustering (node partition).

- Bigraphs

The bimodularity of a clustering is

$$Q = \sum_i \sum_j \left(\frac{B_{ij}}{w} - \gamma \frac{d_{1,i} d_{2,j}}{w^2} \right) \delta_{c_{1,i}, c_{2,j}}$$

where

- $c_{1,i}, c_{2,j}$ are the clusters of nodes i (row) and j (column),
- $d_{1,i}, d_{2,j}$ are the weights of nodes i (row) and j (column),
- $w = 1^T B 1$ is the total weight,
- δ is the Kronecker symbol,
- $\gamma \geq 0$ is the resolution parameter.

Parameters

- **biadjacency** – Biadjacency matrix of the graph (shape $n_1 \times n_2$).
- **labels** – Labels of rows, vector of size n_1.

- **labels_col** – Labels of columns, vector of size n_2.
- **weights** – Weights of nodes. `'degree'` (default), `'uniform'` or custom weights.
- **weights_col** – Weights of columns. `'degree'` (default), `'uniform'` or custom weights.
- **resolution** – Resolution parameter (default = 1).
- **return_all** – If `True`, return modularity, fit, diversity.

Returns

- **modularity** (*float*)
- **fit** (*float, optional*)
- **diversity** (*float, optional*)

Example

```
>>> from sknetwork.clustering import bimodularity
>>> from sknetwork.data import star_wars
>>> biadjacency = star_wars()
>>> labels = np.array([1, 1, 0, 0])
>>> labels_col = np.array([1, 0, 0])
>>> np.round(bimodularity(biadjacency, labels, labels_col), 2)
0.22
```

sknetwork.clustering.**comodularity**(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *labels: numpy.ndarray*, *resolution: float = 1*, *return_all: bool = False*) → Union[float, Tuple[float, float, float]]

Modularity of a clustering in the normalized co-neighborhood graph.

- Graphs
- Digraphs
- Bigraphs

Quality metric of a clustering given by:

$$Q = \frac{1}{w} \sum_{i,j} \left((AD_2^{-1}A^T)_{ij} - \gamma \frac{d_i d_j}{w} \right) \delta_{c_i,c_j}$$

where

- c_i is the cluster of node i,
- δ is the Kronecker symbol,
- $\gamma \geq 0$ is the resolution parameter.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **labels** – Labels of the nodes.
- **resolution** – Resolution parameter (default = 1).
- **return_all** – If `True`, return modularity, fit, diversity.

Returns

- **modularity** (*float*)
- **fit** (*float, optional*)
- **diversity** (*float, optional*)

Example

```
>>> from sknetwork.clustering import comodularity
>>> from sknetwork.data import house
>>> adjacency = house()
>>> labels = np.array([0, 0, 1, 1, 0])
>>> np.round(comodularity(adjacency, labels), 2)
0.06
```

Notes

Does not require the computation of the adjacency matrix of the normalized co-neighborhood graph.

sknetwork.clustering.**normalized_std**(*labels: numpy.ndarray*) → float

Normalized standard deviation of cluster sizes.

A score of 1 means perfectly balanced clustering.

Parameters **labels** – Labels of nodes.

Returns

Return type float

Example

```
>>> from sknetwork.clustering import normalized_std
>>> labels = np.array([0, 0, 1, 1])
>>> normalized_std(labels)
1.0
```

Post-processing

sknetwork.clustering.postprocess.**reindex_labels**(*labels: numpy.ndarray, consecutive: bool = True*) → numpy.ndarray

Reindex clusters in decreasing order of size.

Parameters

- **labels** – label of each node.
- **consecutive** – If `True`, the set of labels must be from 0 to $k-1$, where k is the number of labels. Lead to faster computation.

Returns **new_labels** – New label of each node.

Return type np.ndarray

Example

```
>>> from sknetwork.clustering import reindex_labels
>>> labels = np.array([0, 1, 1])
>>> reindex_labels(labels)
array([1, 0, 0])
```

3.2.6 Hierarchy

Hierarchical clustering algorithms.

The attribute `dendrogram_` gives the dendrogram.

A dendrogram is an array of size $(n-1) \times 4$ representing the successive merges of nodes. Each row gives the two merged nodes, their distance and the size of the resulting cluster. Any new node resulting from a merge takes the first available index (e.g., the first merge corresponds to node n).

Paris

class sknetwork.hierarchy.**Paris**(*weights: unicode = 'degree'*, *reorder: bool = True*)

Agglomerative clustering algorithm that performs greedy merge of nodes based on their similarity.

- Graphs
- Digraphs

The similarity between nodes i, j is $\dfrac{A_{ij}}{w_i w_j}$ where

- A_{ij} is the weight of edge i, j,
- w_i, w_j are the weights of nodes i, j

Parameters

- **weights** – Weights of nodes. `'degree'` (default) or `'uniform'`.
- **reorder** – If `True`, reorder the dendrogram in non-decreasing order of height.

Variables **dendrogram_** (*numpy array of shape (total number of nodes - 1, 4)*) – Dendrogram.

Examples

```
>>> from sknetwork.hierarchy import Paris
>>> from sknetwork.data import house
>>> paris = Paris()
>>> adjacency = house()
>>> dendrogram = paris.fit_transform(adjacency)
>>> np.round(dendrogram, 2)
array([[3.        , 2.        , 0.17      , 2.        ],
       [1.        , 0.        , 0.25      , 2.        ],
       [6.        , 4.        , 0.31      , 3.        ],
       [7.        , 5.        , 0.67      , 5.        ]])
```

Notes

Each row of the dendrogram = i, j, distance, size of cluster $i + j$.

See also:

`scipy.cluster.hierarchy.linkage`

References

T. Bonald, B. Charpentier, A. Galland, A. Hollocou (2018). Hierarchical Graph Clustering using Node Pair Sampling. Workshop on Mining and Learning with Graphs.

fit (*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.hierarchy.paris.Paris
Agglomerative clustering using the nearest neighbor chain.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *Paris*

fit_transform (**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the dendrogram. Same parameters as the `fit` method.

Returns **dendrogram** – Dendrogram.

Return type np.ndarray

class sknetwork.hierarchy.**BiParis** (*weights: unicode = 'degree'*, *reorder: bool = True*)
Hierarchical clustering of bipartite graphs by the Paris method.

- Bigraphs

Parameters

- **weights** – Weights of nodes. `'degree'` (default) or `'uniform'`.
- **reorder** – If `True`, reorder the dendrogram in non-decreasing order of height.

Variables

- **dendrogram_** – Dendrogram for the rows.
- **dendrogram_row_** – Dendrogram for the rows (copy of **dendrogram_**).
- **dendrogram_col_** – Dendrogram for the columns.
- **dendrogram_full_** – Dendrogram for both rows and columns, indexed in this order.

Examples

```
>>> from sknetwork.hierarchy import BiParis
>>> from sknetwork.data import star_wars
>>> biparis = BiParis()
>>> biadjacency = star_wars()
>>> dendrogram = biparis.fit_transform(biadjacency)
>>> np.round(dendrogram, 2)
array([[1.        , 2.        , 0.37      , 2.        ],
       [4.        , 0.        , 0.55      , 3.        ],
       [5.        , 3.        , 0.75      , 4.        ]])
```

Notes

Each row of the dendrogram = i, j, height, size of cluster.

See also:

`scipy.cluster.hierarchy.linkage`

References

T. Bonald, B. Charpentier, A. Galland, A. Hollocou (2018). Hierarchical Graph Clustering using Node Pair Sampling. Workshop on Mining and Learning with Graphs.

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.hierarchy.paris.BiParis
Apply the Paris algorithm to

$$A = \begin{bmatrix} 0 & B \\ B^T & 0 \end{bmatrix}$$

where B is the biadjacency matrix of the graph.

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns **self**

Return type *BiParis*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the dendrogram. Same parameters as the `fit` method.

Returns **dendrogram** – Dendrogram.

Return type np.ndarray

Louvain

class sknetwork.hierarchy.**LouvainHierarchy**(*depth: int = 3*, *resolution: float = 1*, *tol_optimization: float = 0.001*, *tol_aggregation: float = 0.001*, *n_aggregations: int = -1*, *shuffle_nodes: bool = False*, *random_state: Optional[Union[numpy.random.mtrand.RandomState, int]] = None*, *verbose: bool = False*)
Hierarchical clustering by successive instances of Louvain (top-down).

- Graphs
- Digraphs

Parameters

- **depth** – Depth of the tree. A negative value is interpreted as no limit (return a tree of maximum depth).
- **resolution** – Resolution parameter.
- **tol_optimization** – Minimum increase in the objective function to enter a new optimization pass.

- **tol_aggregation** – Minimum increase in the objective function to enter a new aggregation pass.
- **n_aggregations** – Maximum number of aggregations. A negative value is interpreted as no limit.
- **shuffle_nodes** – Enables node shuffling before optimization.
- **random_state** – Random number generator or random seed. If `None`, numpy.random is used.
- **verbose** – Verbose mode.

Variables **dendrogram_** (*np.ndarray*) – Dendrogram.

Example

```
>>> from sknetwork.hierarchy import LouvainHierarchy
>>> from sknetwork.data import house
>>> louvain = LouvainHierarchy()
>>> adjacency = house()
>>> louvain.fit_transform(adjacency)
array([[3., 2., 0., 2.],
       [4., 1., 0., 2.],
       [6., 0., 0., 3.],
       [5., 7., 1., 5.]])
```

Notes

Each row of the dendrogram = merge nodes, distance, size of cluster.

See also:

`scipy.cluster.hierarchy.dendrogram`

fit (*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.hierarchy.louvain_hierarchy.LouvainHierarchy
Fit algorithm to data.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *LouvainHierarchy*

fit_transform (**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the dendrogram. Same parameters as the `fit` method.

Returns **dendrogram** – Dendrogram.

Return type np.ndarray

class sknetwork.hierarchy.**BiLouvainHierarchy** (***kwargs*)
Hierarchical clustering of bipartite graphs by successive instances of Louvain (top-down).

- Bigraphs

Parameters

- **depth** – Depth of the tree. A negative value is interpreted as no limit (return a tree of maximum depth).

- **resolution** – Resolution parameter.
- **tol_optimization** – Minimum increase in the objective function to enter a new optimization pass.
- **tol_aggregation** – Minimum increase in the objective function to enter a new aggregation pass.
- **n_aggregations** – Maximum number of aggregations. A negative value is interpreted as no limit.
- **shuffle_nodes** – Enables node shuffling before optimization.
- **random_state** – Random number generator or random seed. If None, numpy.random is used.
- **verbose** – Verbose mode.

Variables

- **dendrogram_** – Dendrogram for the rows.
- **dendrogram_row_** – Dendrogram for the rows (copy of **dendrogram_**).
- **dendrogram_col_** – Dendrogram for the columns.
- **dendrogram_full_** – Dendrogram for both rows and columns, indexed in this order.

Examples

```
>>> from sknetwork.hierarchy import BiLouvainHierarchy
>>> from sknetwork.data import star_wars
>>> bilouvain = BiLouvainHierarchy()
>>> biadjacency = star_wars()
>>> bilouvain.fit_transform(biadjacency)
array([[3., 2., 1., 2.],
       [1., 0., 1., 2.],
       [5., 4., 2., 4.]])
```

Notes

Each row of the dendrogram = i, j, height, size of cluster.

See also:

`scipy.cluster.hierarchy.linkage`

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.hierarchy.louvain_hierarchy.BiLouvainHierarchy

Applies Louvain hierarchical clustering to

$$A = \begin{bmatrix} 0 & B \\ B^T & 0 \end{bmatrix}$$

where B is the biadjacency matrix of the graphs.

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns **self**

Return type *BiLouvainHierarchy*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the dendrogram. Same parameters as the `fit` method.

Returns **dendrogram** – Dendrogram.

Return type np.ndarray

Ward

class sknetwork.hierarchy.**Ward**(*embedding_method: sknetwork.embedding.base.BaseEmbedding = GSVD(n_components=10, regularization=None, relative_regularization=True, factor_row=0.5, factor_col=0.5, factor_singular=0.0, normalized=True, solver='auto')*)
Hierarchical clustering by the Ward method.

- Graphs
- Digraphs

Parameters **embedding_method** – Embedding method (default = GSVD in dimension 10, projected on the unit sphere).

Examples

```
>>> from sknetwork.hierarchy import Ward
>>> from sknetwork.data import karate_club
>>> ward = Ward()
>>> adjacency = karate_club()
>>> dendrogram = ward.fit_transform(adjacency)
>>> dendrogram.shape
(33, 4)
```

References

- Ward, J. H., Jr. (1963). Hierarchical grouping to optimize an objective function. Journal of the American Statistical Association.
- Murtagh, F., & Contreras, P. (2012). Algorithms for hierarchical clustering: an overview. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.hierarchy.ward.Ward
Applies embedding method followed by the Ward algorithm.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *Ward*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the dendrogram. Same parameters as the `fit` method.

Returns **dendrogram** – Dendrogram.

Return type np.ndarray

class sknetwork.hierarchy.**BiWard**(*embedding_method: sknetwork.embedding.base.BaseBiEmbedding = GSVD(n_components=10, regularization=None, relative_regularization=True, factor_row=0.5, factor_col=0.5, factor_singular=0.0, normalized=True, solver='auto')*, *cluster_col: bool = False*, *cluster_both: bool = False*)

Hierarchical clustering of bipartite graphs by the Ward method.

- Bigraphs

Parameters

- **embedding_method** – Embedding method (default = GSVD in dimension 10, projected on the unit sphere).
- **cluster_col** – If `True`, return a dendrogram for the columns (default = `False`).
- **cluster_both** – If `True`, return a dendrogram for all nodes (co-clustering rows + columns, default = `False`).

Variables

- **dendrogram_** – Dendrogram for the rows.
- **dendrogram_row_** – Dendrogram for the rows (copy of **dendrogram_**).
- **dendrogram_col_** – Dendrogram for the columns.
- **dendrogram_full_** – Dendrogram for both rows and columns, indexed in this order.

Examples

```
>>> from sknetwork.hierarchy import BiWard
>>> from sknetwork.data import movie_actor
>>> biward = BiWard()
>>> biadjacency = movie_actor()
>>> biward.fit_transform(biadjacency).shape
(14, 4)
```

References

- Ward, J. H., Jr. (1963). Hierarchical grouping to optimize an objective function. Journal of the American Statistical Association, 58, 236–244.
- Murtagh, F., & Contreras, P. (2012). Algorithms for hierarchical clustering: an overview. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2(1), 86-97.

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.hierarchy.ward.BiWard

Applies the embedding method followed by the Ward algorithm.

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns self

Return type *BiWard*

fit_transform(**args*, ***kwargs*) → numpy.ndarray

Fit algorithm to data and return the dendrogram. Same parameters as the `fit` method.

Returns **dendrogram** – Dendrogram.

Return type np.ndarray

Metrics

sknetwork.hierarchy.**dasgupta_cost**(*adjacency: scipy.sparse.csr.csr_matrix, dendrogram: numpy.ndarray, weights: str = 'uniform', normalized: bool = False*) → float

Dasgupta's cost of a hierarchy.

- Graphs
- Digraphs

Expected size (weights = `'uniform'`) or expected weight (weights = `'degree'`) of the cluster induced by random edge sampling (closest ancestor of the two nodes in the hierarchy).

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **dendrogram** – Dendrogram.
- **weights** – Weights of nodes. `'degree'` or `'uniform'` (default).
- **normalized** – If `True`, normalized cost (between 0 and 1).

Returns **cost** – Cost.

Return type float

Example

```
>>> from sknetwork.hierarchy import dasgupta_score, Paris
>>> from sknetwork.data import house
>>> paris = Paris()
>>> adjacency = house()
>>> dendrogram = paris.fit_transform(adjacency)
>>> cost = dasgupta_cost(adjacency, dendrogram)
>>> np.round(cost, 2)
3.33
```

References

Dasgupta, S. (2016). A cost function for similarity-based hierarchical clustering. Proceedings of ACM symposium on Theory of Computing.

sknetwork.hierarchy.**dasgupta_score**(*adjacency: scipy.sparse.csr.csr_matrix, dendrogram: numpy.ndarray, weights: str = 'uniform'*) → float

Dasgupta's score of a hierarchy (quality metric, between 0 and 1).

- Graphs
- Digraphs

Defined as 1 - normalized Dasgupta's cost.

Parameters

- **adjacency** – Adjacency matrix of the graph.

- **dendrogram** – Dendrogram.
- **weights** – Weights of nodes. `'degree'` or `'uniform'` (default).

Returns **score** – Score.

Return type float

Example

```
>>> from sknetwork.hierarchy import dasgupta_score, Paris
>>> from sknetwork.data import house
>>> paris = Paris()
>>> adjacency = house()
>>> dendrogram = paris.fit_transform(adjacency)
>>> score = dasgupta_score(adjacency, dendrogram)
>>> np.round(score, 2)
0.33
```

References

Dasgupta, S. (2016). A cost function for similarity-based hierarchical clustering. Proceedings of ACM symposium on Theory of Computing.

`sknetwork.hierarchy.`**`tree_sampling_divergence`**(*adjacency: scipy.sparse.csr.csr_matrix*, *dendrogram: numpy.ndarray*, *weights: str = 'degree'*, *normalized: bool = True*) → float

Tree sampling divergence of a hierarchy (quality metric).

- Graphs
- Digraphs

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **dendrogram** – Dendrogram.
- **weights** – Weights of nodes. `'degree'` (default) or `'uniform'`.
- **normalized** – If `True`, normalized score (between 0 and 1).

Returns **score** – Score.

Return type float

Example

```
>>> from sknetwork.hierarchy import tree_sampling_divergence, Paris
>>> from sknetwork.data import house
>>> paris = Paris()
>>> adjacency = house()
>>> dendrogram = paris.fit_transform(adjacency)
>>> score = tree_sampling_divergence(adjacency, dendrogram)
>>> np.round(score, 2)
0.52
```

References

Charpentier, B. & Bonald, T. (2019). Tree Sampling Divergence: An Information-Theoretic Metric for Hierarchical Graph Clustering. Proceedings of IJCAI.

Cuts

sknetwork.hierarchy.**cut_straight**(*dendrogram: numpy.ndarray*, *n_clusters: Optional[int] = None*, *threshold: Optional[float] = None*, *sort_clusters: bool = True*, *return_dendrogram: bool = False*) → Union[numpy.ndarray, Tuple[numpy.ndarray, numpy.ndarray]]

Cut a dendrogram and return the corresponding clustering.

Parameters

- **dendrogram** – Dendrogram.
- **n_clusters** – Number of clusters (optional).
- **threshold** – Threshold on height (optional). If both n_clusters and threshold are `None`, n_clusters is set to 2.
- **sort_clusters** – If `True`, sorts clusters in decreasing order of size.
- **return_dendrogram** – If `True`, returns the dendrogram formed by the clusters up to the root.

Returns

- **labels** (*np.ndarray*) – Cluster of each node.
- **dendrogram_aggregate** (*np.ndarray*) – Dendrogram starting from clusters (leaves = clusters).

Example

```
>>> from sknetwork.hierarchy import cut_straight
>>> dendrogram = np.array([[0, 1, 0, 2], [2, 3, 1, 3]])
>>> cut_straight(dendrogram)
array([0, 0, 1])
```

sknetwork.hierarchy.**cut_balanced**(*dendrogram: numpy.ndarray*, *max_cluster_size: int = 20*, *sort_clusters: bool = True*, *return_dendrogram: bool = False*) → Union[numpy.ndarray, Tuple[numpy.ndarray, numpy.ndarray]]

Cuts a dendrogram with a constraint on the cluster size and returns the corresponding clustering.

Parameters

- **dendrogram** – Dendrogram
- **max_cluster_size** – Maximum size of each cluster.
- **sort_clusters** – If `True`, sort labels in decreasing order of cluster size.
- **return_dendrogram** – If `True`, returns the dendrogram formed by the clusters up to the root.

Returns

- **labels** (*np.ndarray*) – Label of each node.
- **dendrogram_aggregate** (*np.ndarray*) – Dendrogram starting from clusters (leaves = clusters).

Example

```
>>> from sknetwork.hierarchy import cut_balanced
>>> dendrogram = np.array([[0, 1, 0, 2], [2, 3, 1, 3]])
>>> cut_balanced(dendrogram, 2)
array([0, 0, 1])
```

3.2.7 Ranking

Node ranking algorithms.

The attribute `scores_` assigns a score of importance to each node of the graph.

PageRank

class sknetwork.ranking.**PageRank**(*damping_factor: float = 0.85, solver: str = 'piteration', n_iter: int = 10, tol: float = 1e-06*)

PageRank of each node, corresponding to its frequency of visit by a random walk.

The random walk restarts with some fixed probability. The restart distribution can be personalized by the user. This variant is known as Personalized PageRank.

- Graphs
- Digraphs

Parameters

- **damping_factor** (*float*) – Probability to continue the random walk.
- **solver** (*str*) –
  - `'piteration'`, use power iteration for a given number of iterations.
  - `'diteration'`, use asynchronous parallel diffusion for a given number of iterations.
  - `'lanczos'`, use eigensolver with a given tolerance.
  - `'bicgstab'`, use Biconjugate Gradient Stabilized method for a given tolerance.
  - `'RH'`, use a Ruffini-Horner polynomial evaluation.
- **n_iter** (*int*) – Number of iterations for some solvers.
- **tol** (*float*) – Tolerance for the convergence of some solvers.

Variables **scores_** (*np.ndarray*) – PageRank score of each node.

Example

```
>>> from sknetwork.ranking import PageRank
>>> from sknetwork.data import house
>>> pagerank = PageRank()
>>> adjacency = house()
>>> seeds = {0: 1}
>>> scores = pagerank.fit_transform(adjacency, seeds)
>>> np.round(scores, 2)
array([0.29, 0.24, 0.12, 0.12, 0.24])
```

References

Page, L., Brin, S., Motwani, R., & Winograd, T. (1999). The PageRank citation ranking: Bringing order to the web. Stanford InfoLab.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray, scipy.sparse.linalg.interface.LinearOperator]*, *seeds: Optional[Union[numpy.ndarray, dict]] = None*) → sknetwork.ranking.pagerank.PageRank
Fit algorithm to data.

Parameters

- **adjacency** – Adjacency matrix.
- **seeds** – Parameter to be used for Personalized PageRank. Restart distribution as a vector or a dict (node: weight). If `None`, the uniform distribution is used (no personalization, default).

Returns self

Return type *PageRank*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

class sknetwork.ranking.**BiPageRank**(*damping_factor: float = 0.85*, *solver: str = 'piteration'*, *n_iter: int = 10*, *tol: float = 0*)
Compute the PageRank of each node through a random walk in the bipartite graph.

- Bigraphs

Parameters

- **damping_factor** (*float*) – Probability to continue the random walk.
- **solver** (*str*) –
  - *piteration*, use power iteration for a given number of iterations.
  - *diteration*, use asynchronous parallel diffusion for a given number of iterations.
  - *lanczos*, use eigensolver for a given tolerance.
  - *bicgstab*, use Biconjugate Gradient Stabilized method for a given tolerance.
- **n_iter** (*int*) – Number of iterations for some solvers.
- **tol** (*float*) – Tolerance for the convergence of some solvers.

Variables

- **scores_** (*np.ndarray*) – PageRank score of each row.
- **scores_row_** (*np.ndarray*) – PageRank score of each row (copy of **scores_**).
- **scores_col_** (*np.ndarray*) – PageRank score of each column.

Example

```
>>> from sknetwork.ranking import BiPageRank
>>> from sknetwork.data import star_wars
>>> bipagerank = BiPageRank()
>>> biadjacency = star_wars()
>>> seeds = {0: 1}
>>> scores = bipagerank.fit_transform(biadjacency, seeds)
>>> np.round(scores, 2)
array([0.45, 0.11, 0.28, 0.17])
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds_row: Optional[Union[numpy.ndarray, dict]] = None*, *seeds_col: Optional[Union[numpy.ndarray, dict]] = None*) → sknetwork.ranking.pagerank.BiPageRank
Fit algorithm to data.

Parameters

- **biadjacency** – Biadjacency matrix.
- **seeds_row** – Parameter to be used for Personalized BiPageRank. Restart distribution as vectors or dicts on rows, columns (node: weight). If both seeds_row and seeds_col are None (default), the uniform distribution on rows is used.
- **seeds_col** – Parameter to be used for Personalized BiPageRank. Restart distribution as vectors or dicts on rows, columns (node: weight). If both seeds_row and seeds_col are None (default), the uniform distribution on rows is used.

Returns self

Return type *BiPageRank*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the fit method.

Returns **scores** – Scores.

Return type np.ndarray

Diffusion

class sknetwork.ranking.**Diffusion**(*n_iter: int = 3*, *damping_factor: Optional[float] = None*)
Ranking by diffusion along the edges (heat equation).

- Graphs
- Digraphs

Parameters

- **n_iter** (*int*) – Number of steps of the diffusion in discrete time (must be positive).
- **damping_factor** (*float (optional)*) – Damping factor (default value = 1).

Variables **scores_** (*np.ndarray*) – Score of each node (= temperature).

Example

```
>>> from sknetwork.data import house
>>> diffusion = Diffusion(n_iter=2)
>>> adjacency = house()
>>> seeds = {0: 1, 2: 0}
>>> scores = diffusion.fit_transform(adjacency, seeds)
>>> np.round(scores, 2)
array([0.58, 0.56, 0.38, 0.58, 0.42])
```

References

Chung, F. (2007). The heat kernel as the pagerank of a graph. Proceedings of the National Academy of Sciences.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds: Optional[Union[numpy.ndarray, dict]] = None*, *init: Optional[float] = None*) → sknetwork.ranking.diffusion.Diffusion
Compute the diffusion (temperatures at equilibrium).

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **seeds** – Temperatures of seed nodes in initial state (dictionary or vector). Negative temperatures ignored.
- **init** – Temperature of non-seed nodes in initial state. If `None`, use the average temperature of seed nodes (default).

Returns **self**

Return type *Diffusion*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

class sknetwork.ranking.**BiDiffusion**(*n_iter: int = 3*, *damping_factor: Optional[float] = None*)
Ranking by diffusion along the edges of a bipartite graph (heat equation).

- Bigraphs

Parameters

- **n_iter** (*int*) – Number of steps of the diffusion in discrete time (must be positive).
- **damping_factor** (*float (optional)*) – Damping factor (default value = 1).

Variables

- **scores_** (*np.ndarray*) – Scores of rows.
- **scores_row_** (*np.ndarray*) – Scores of rows (copy of **scores_**).
- **scores_col_** (*np.ndarray*) – Scores of columns.

Example

```
>>> from sknetwork.ranking import BiDiffusion
>>> from sknetwork.data import star_wars
>>> bidiffusion = BiDiffusion(n_iter=2)
>>> biadjacency = star_wars()
>>> scores = bidiffusion.fit_transform(biadjacency, seeds_row = {0: 1, 2: 0})
>>> np.round(scores, 2)
array([0.5 , 0.5 , 0.46, 0.44])
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds_row: Optional[Union[numpy.ndarray, dict]] = None*, *seeds_col: Optional[Union[numpy.ndarray, dict]] = None*, *init: Optional[float] = None*) → sknetwork.ranking.diffusion.BiDiffusion
Compute the diffusion (temperatures at equilibrium).

Parameters

- **biadjacency** – Biadjacency matrix, shape (n_row, n_col).
- **seeds_row** – Temperatures of seed rows in initial state (dictionary or vector of size n_row). Negative temperatures ignored.
- **seeds_col** – Temperatures of seed columns in initial state (dictionary or vector of size n_col). Negative temperatures ignored.
- **init** – Temperature of non-seed nodes in initial state. If `None`, use the average temperature of seed nodes (default).

Returns self

Return type *BiDiffusion*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

Dirichlet

class sknetwork.ranking.**Dirichlet**(*n_iter: int = 10*, *damping_factor: Optional[float] = None*, *verbose: bool = False*)
Ranking by the Dirichlet problem (heat diffusion with boundary constraints).

- Graphs
- Digraphs

Parameters

- **n_iter** (*int*) – If positive, number of steps of the diffusion in discrete time. Otherwise, solve the Dirichlet problem by the bi-conjugate gradient stabilized method.
- **damping_factor** (*float (optional)*) – Damping factor (default value = 1).
- **verbose** (*bool*) – Verbose mode.

Variables **scores_** (*np.ndarray*) – Score of each node (= temperature).

Example

```
>>> from sknetwork.ranking import Dirichlet
>>> from sknetwork.data import house
>>> dirichlet = Dirichlet()
>>> adjacency = house()
>>> seeds = {0: 1, 2: 0}
>>> scores = dirichlet.fit_transform(adjacency, seeds)
>>> np.round(scores, 2)
array([1.  , 0.54, 0.  , 0.31, 0.62])
```

References

Chung, F. (2007). The heat kernel as the pagerank of a graph. Proceedings of the National Academy of Sciences.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds: Optional[Union[numpy.ndarray, dict]] = None*, *init: Optional[float] = None*) → sknetwork.ranking.diffusion.Dirichlet
Compute the solution to the Dirichlet problem (temperatures at equilibrium).

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **seeds** – Temperatures of seed nodes (dictionary or vector). Negative temperatures ignored.
- **init** – Temperature of non-seed nodes in initial state. If `None`, use the average temperature of seed nodes (default).

Returns **self**

Return type *Dirichlet*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

class sknetwork.ranking.**BiDirichlet**(*n_iter: int = 10*, *damping_factor: Optional[float] = None*, *verbose: bool = False*)
Ranking by the Dirichlet problem in bipartite graphs (heat diffusion with boundary constraints).

- Bigraphs

Parameters

- **n_iter** (*int*) – If positive, number of steps of the diffusion in discrete time. Otherwise, solve the Dirichlet problem by the bi-conjugate gradient stabilized method.
- **damping_factor** (*float (optional)*) – Damping factor (default value = 1).
- **verbose** (*bool*) – Verbose mode.

Variables

- **scores_** (*np.ndarray*) – Scores of rows.
- **scores_row_** (*np.ndarray*) – Scores of rows (copy of **scores_**).

- **scores_col_** (*np.ndarray*) – Scores of columns.

Example

```
>>> from sknetwork.ranking import BiDirichlet
>>> from sknetwork.data import star_wars
>>> bidirichlet = BiDirichlet()
>>> biadjacency = star_wars()
>>> scores = bidirichlet.fit_transform(biadjacency, seeds_row = {0: 1, 2: 0})
>>> np.round(scores, 2)
array([1.  , 0.5 , 0.  , 0.29])
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds_row: Optional[Union[numpy.ndarray, dict]] = None*, *seeds_col: Optional[Union[numpy.ndarray, dict]] = None*, *init: Optional[float] = None*) → sknetwork.ranking.diffusion.BiDirichlet
Compute the solution to the Dirichlet problem (temperatures at equilibrium).

Parameters

- **biadjacency** – Biadjacency matrix, shape (n_row, n_col).
- **seeds_row** – Temperatures of seed rows (dictionary or vector of size n_row). Negative temperatures ignored.
- **seeds_col** – Temperatures of seed columns (dictionary or vector of size n_col). Negative temperatures ignored.
- **init** – Temperature of non-seed nodes in initial state. If `None`, use the average temperature of seed nodes (default).

Returns self

Return type *BiDirichlet*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

Katz

class sknetwork.ranking.**Katz**(*damping_factor: float = 0.5*, *path_length: int = 4*)
Katz centrality:

$\sum_{k=1}^{K} \alpha^k (A^k)^T \mathbf{1}$.

- Graphs
- Digraphs

Parameters

- **damping_factor** (*float*) – Decay parameter for path contributions.
- **path_length** (*int*) – Maximum length of the paths to take into account.

Examples

```
>>> from sknetwork.data.toy_graphs import house
>>> adjacency = house()
>>> katz = Katz()
>>> scores = katz.fit_transform(adjacency)
>>> np.round(scores, 2)
array([6.5 , 8.25, 5.62, 5.62, 8.25])
```

References

Katz, L. (1953). A new status index derived from sociometric analysis. Psychometrika, 18(1), 39-43.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray, scipy.sparse.linalg.interface.LinearOperator]*) → sknetwork.ranking.katz.Katz
Katz centrality.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *Katz*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

class sknetwork.ranking.**BiKatz**(*damping_factor: float = 0.5*, *path_length: int = 4*)
Katz centrality for bipartite graphs.

- Bigraphs

Parameters

- **damping_factor** (*float*) – Decay parameter for path contributions.
- **path_length** (*int*) – Maximum length of the paths to take into account.

Examples

```
>>> from sknetwork.data.toy_graphs import star_wars
>>> biadjacency = star_wars()
>>> bikatz = BiKatz()
>>> scores = bikatz.fit_transform(biadjacency)
>>> np.round(scores, 2)
array([6.38, 3.06, 8.81, 5.75])
```

References

Katz, L. (1953). A new status index derived from sociometric analysis. Psychometrika, 18(1), 39-43.

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.ranking.katz.BiKatz
Katz centrality.

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns **self**

Return type *BiKatz*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

HITS

class sknetwork.ranking.**HITS**(*solver: Union[str, sknetwork.linalg.svd_solver.SVDSolver] = 'auto'*, ***kwargs*)
Hub and authority scores of each node. For bipartite graphs, the hub score is computed on rows and the authority score on columns.

- Graphs
- Digraphs
- Bigraphs

Parameters

- **solver** (`'auto'`, `'halko'`, `'lanczos'` or `SVDSolver`) – Which singular value solver to use.
  - `'auto'` call the auto_solver function.
  - `'halko'`: randomized method, fast but less accurate than `'lanczos'` for ill-conditioned matrices.
  - `'lanczos'`: power-iteration based method.
  - `SVDSolver`: custom solver.
- ****kwargs** – See *sknetwork.linalg.svd_solver.LanczosSVD* or *sknetwork.linalg.svd_solver.HalkoSVD*.

Variables

- **scores_** (*np.ndarray*) – Hub score of each row.
- **scores_row_** (*np.ndarray*) – Hub score of each row (copy of **scores_row_**).
- **scores_col_** (*np.ndarray*) – Authority score of each column.

Example

```
>>> from sknetwork.ranking import HITS
>>> from sknetwork.data import star_wars
>>> hits = HITS()
>>> biadjacency = star_wars()
>>> scores = hits.fit_transform(biadjacency)
>>> np.round(scores, 2)
array([0.5 , 0.23, 0.69, 0.46])
```

References

Kleinberg, J. M. (1999). Authoritative sources in a hyperlinked environment. Journal of the ACM (JACM), 46(5), 604-632.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.ranking.hits.HITS
Compute HITS algorithm with a spectral method.

Parameters **adjacency** – Adjacency or biadjacency matrix of the graph.

Returns **self**

Return type *HITS*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

Betweenness centrality

class sknetwork.ranking.**Betweenness**(*normalized: bool = False*)
Betweenness centrality, based on Brandes' algorithm.

- Graphs

Variables **scores_** (*np.ndarray*) – Betweenness centrality value of each node

Example

```
>>> from sknetwork.ranking import Betweenness
>>> from sknetwork.data.toy_graphs import bow_tie
>>> betweenness = Betweenness()
>>> adjacency = bow_tie()
>>> scores = betweenness.fit_transform(adjacency)
>>> scores
array([4., 0., 0., 0., 0.])
```

References

Brandes, Ulrik (2001). A faster algorithm for betweenness centrality. Journal of Mathematical Sociology.

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

Closeness centrality

class sknetwork.ranking.**Closeness**(*method: str = 'exact'*, *tol: float = 0.1*, *n_jobs: Optional[int] = None*)
Closeness centrality of each node in a connected graph, corresponding to the average length of the shortest paths from that node to all the other ones.

For a directed graph, the closeness centrality is computed in terms of outgoing paths.

- Graphs
- Digraphs

Parameters

- **method** – Denotes if the results should be exact or approximate.
- **tol** (*float*) – If `method=='approximate'`, the allowed tolerance on each score entry.
- **n_jobs** – If an integer value is given, denotes the number of workers to use (-1 means the maximum number will be used). If `None`, no parallel computations are made.

Variables **scores_** (*np.ndarray*) – Closeness centrality of each node.

Example

```
>>> from sknetwork.ranking import Closeness
>>> from sknetwork.data import cyclic_digraph
>>> closeness = Closeness()
>>> adjacency = cyclic_digraph(3)
>>> scores = closeness.fit_transform(adjacency)
>>> np.round(scores, 2)
array([0.67, 0.67, 0.67])
```

References

Eppstein, D., & Wang, J. (2001, January). Fast approximation of centrality. In Proceedings of the twelfth annual ACM-SIAM symposium on Discrete algorithms (pp. 228-229). Society for Industrial and Applied Mathematics.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.ranking.closeness.Closeness
Closeness centrality for connected graphs.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *Closeness*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

Harmonic centrality

class sknetwork.ranking.**Harmonic**(*n_jobs: Optional[int] = None*)
Harmonic centrality of each node in a connected graph, corresponding to the average inverse length of the shortest paths from that node to all the other ones.

For a directed graph, the harmonic centrality is computed in terms of outgoing paths.

- Graphs
- Digraphs

Parameters **n_jobs** – If an integer value is given, denotes the number of workers to use (-1 means the maximum number will be used). If `None`, no parallel computations are made.

Variables **scores_** (*np.ndarray*) – Harmonic centrality of each node.

Example

```
>>> from sknetwork.ranking import Harmonic
>>> from sknetwork.data import house
>>> harmonic = Harmonic()
>>> adjacency = house()
>>> scores = harmonic.fit_transform(adjacency)
>>> np.round(scores, 2)
array([3. , 3.5, 3. , 3. , 3.5])
```

References

Marchiori, M., & Latora, V. (2000). Harmony in the small-world. Physica A: Statistical Mechanics and its Applications, 285(3-4), 539-546.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.ranking.harmonic.Harmonic
Harmonic centrality for connected graphs.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *Harmonic*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to data and return the scores. Same parameters as the `fit` method.

Returns **scores** – Scores.

Return type np.ndarray

Post-processing

sknetwork.ranking.**top_k**(*scores: numpy.ndarray*, *k: int = 1*)

Index of the k elements with highest value.

Parameters

- **scores** (*np.ndarray*) – Array of values.
- **k** (*int*) – Number of elements to return.

Examples

```
>>> scores = np.array([0, 1, 0, 0.5])
>>> top_k(scores, k=2)
array([1, 3])
```

Notes

This is a basic implementation that sorts the entire array to find its top k elements.

3.2.8 Classification

Node classification algorithms.

The attribute `labels_` assigns a label to each node of the graph.

PageRank

class sknetwork.classification.**PageRankClassifier**(*damping_factor: float = 0.85*, *solver: str = 'piteration'*, *n_iter: int = 10*, *tol: float = 0.0*, *n_jobs: Optional[int] = None*, *verbose: bool = False*)

Node classification by multiple personalized PageRanks.

- Graphs
- Digraphs

Parameters

- **damping_factor** – Probability to continue the random walk.
- **solver** (`str`) – Which solver to use: 'piteration', 'diteration', 'bicgstab', 'lanczos'.
- **n_iter** (*int*) – Number of iterations for some of the solvers such as `'piteration'` or `'diteration'`.
- **tol** (*float*) – Tolerance for the convergence of some solvers such as `'bicgstab'` or `'lanczos'`.

Variables

- **labels_** (*np.ndarray*) – Label of each node (hard classification).

- **membership_** (*sparse.csr_matrix*) – Membership matrix (soft classification, columns = labels).

Example

```
>>> from sknetwork.classification import PageRankClassifier
>>> from sknetwork.data import karate_club
>>> pagerank = PageRankClassifier()
>>> graph = karate_club(metadata=True)
>>> adjacency = graph.adjacency
>>> labels_true = graph.labels
>>> seeds = {0: labels_true[0], 33: labels_true[33]}
>>> labels_pred = pagerank.fit_transform(adjacency, seeds)
>>> np.round(np.mean(labels_pred == labels_true), 2)
0.97
```

References

Lin, F., & Cohen, W. W. (2010). Semi-supervised classification of network data using very few labels. In IEEE International Conference on Advances in Social Networks Analysis and Mining.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds: Union[numpy.ndarray, dict]*) → sknetwork.classification.base_rank.RankClassifier
Fit algorithm to the data.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **seeds** – Seed nodes (labels as dictionary or array; negative values ignored).

Returns self

Return type RankClassifier

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

class sknetwork.classification.**BiPageRankClassifier**(*damping_factor: float = 0.85*, *solver: str = 'piteration'*, *n_iter: int = 10*, *tol: float = 0.0*, *n_jobs: Optional[int] = None*, *verbose: bool = False*)
Node classification for bipartite graphs by multiple personalized PageRanks .

- Bigraphs

Parameters

- **damping_factor** – Probability to continue the random walk.
- **solver** (*str*) – Which solver to use: 'piteration', 'diteration', 'bicgstab', 'lanczos'.
- **n_iter** (*int*) – Number of iterations for some of the solvers such as `'piteration'` or `'diteration'`.
- **tol** (*float*) – Tolerance for the convergence of some solvers such as `'bicgstab'` or `'lanczos'`.

Variables

- **labels_** (*np.ndarray*) – Label of each row.
- **labels_row_** (*np.ndarray*) – Label of each row (copy of **labels_**).
- **labels_col_** (*np.ndarray*) – Label of each column.
- **membership_** (*sparse.csr_matrix*) – Membership matrix of rows (soft classification, labels on columns).
- **membership_row_** (*sparse.csr_matrix*) – Membership matrix of rows (copy of **membership_**).
- **membership_col_** (*sparse.csr_matrix*) – Membership matrix of columns.

Example

```
>>> from sknetwork.classification import BiPageRankClassifier
>>> from sknetwork.data import star_wars
>>> bipagerank = BiPageRankClassifier()
>>> biadjacency = star_wars()
>>> seeds = {0: 1, 2: 0}
>>> bipagerank.fit_transform(biadjacency, seeds)
array([1, 1, 0, 0])
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds_row: Union[numpy.ndarray, dict]*, *seeds_col: Optional[Union[numpy.ndarray, dict]] = None*) → sknetwork.classification.base_rank.RankClassifier
Compute labels.

Parameters

- **biadjacency** – Biadjacency matrix of the graph.
- **seeds_row** – Seed rows (labels as dictionary or array; negative values ignored).
- **seeds_col** – Seed columns (optional). Same format.

Returns self

Return type *BiPageRankClassifier*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

Diffusion

class sknetwork.classification.**DiffusionClassifier**(*n_iter: int = 10*, *damping_factor: Optional[float] = None*, *n_jobs: Optional[int] = None*)

Node classification using multiple diffusions.

- Graphs
- Digraphs

Parameters

- **n_iter** (*int*) – Number of steps of the diffusion in discrete time (must be positive).
- **damping_factor** (*float (optional)*) – Damping factor (default value = 1).
- **n_jobs** – If positive, number of parallel jobs allowed (-1 means maximum number). If None, no parallel computations are made.

Variables

- **labels_** (*np.ndarray*) – Label of each node (hard classification).
- **membership_** (*sparse.csr_matrix*) – Membership matrix (soft classification, labels on columns).

Example

```
>>> from sknetwork.data import karate_club
>>> diffusion = DiffusionClassifier()
>>> graph = karate_club(metadata=True)
>>> adjacency = graph.adjacency
>>> labels_true = graph.labels
>>> seeds = {0: labels_true[0], 33: labels_true[33]}
>>> labels_pred = diffusion.fit_transform(adjacency, seeds)
>>> np.round(np.mean(labels_pred == labels_true), 2)
0.94
```

References

- de Lara, N., & Bonald, T. (2020). A Consistent Diffusion-Based Algorithm for Semi-Supervised Classification on Graphs. arXiv preprint arXiv:2008.11944.
- Zhu, X., Lafferty, J., & Rosenfeld, R. (2005). Semi-supervised learning with graphs (Doctoral dissertation, Carnegie Mellon University, language technologies institute, school of computer science).

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds: Union[numpy.ndarray, dict]*) → sknetwork.classification.base_rank.RankClassifier
Fit algorithm to the data.

Parameters

- **adjacency** – Adjacency matrix of the graph.

- **seeds** – Seed nodes (labels as dictionary or array; negative values ignored).

Returns self

Return type RankClassifier

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the fit method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

class sknetwork.classification.**BiDiffusionClassifier**(*n_iter: int = 10*, *damping_factor: Optional[float] = None*, *n_jobs: Optional[int] = None*)
Node classification using multiple diffusions.

- Bigraphs

Parameters

- **n_iter** (*int*) – Number of steps of the diffusion in discrete time (must be positive).
- **damping_factor** (*float (optional)*) – Damping factor (default value = 1).
- **n_jobs** – If positive, number of parallel jobs allowed (-1 means maximum number). If None, no parallel computations are made.

Variables

- **labels_** (*np.ndarray*) – Label of each row.
- **labels_row_** (*np.ndarray*) – Label of each row (copy of **labels_**).
- **labels_col_** (*np.ndarray*) – Label of each column.
- **membership_** (*sparse.csr_matrix*) – Membership matrix of rows (soft classification, labels on columns).
- **membership_row_** (*sparse.csr_matrix*) – Membership matrix of rows (copy of **membership_**).
- **membership_col_** (*sparse.csr_matrix*) – Membership matrix of columns.

Example

```
>>> from sknetwork.classification import BiDiffusionClassifier
>>> from sknetwork.data import star_wars
>>> bidiffusion = BiDiffusionClassifier(n_iter=2)
>>> biadjacency = star_wars()
>>> seeds = {0: 1, 2: 0}
>>> bidiffusion.fit_transform(biadjacency, seeds)
array([1, 1, 0, 0])
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds_row: Union[numpy.ndarray, dict]*, *seeds_col: Optional[Union[numpy.ndarray, dict]] = None*) → sknetwork.classification.base_rank.RankClassifier
Compute labels.

Parameters

- **biadjacency** – Biadjacency matrix of the graph.
- **seeds_row** – Seed rows (labels as dictionary or array; negative values ignored).
- **seeds_col** – Seed columns (optional). Same format.

Returns self

Return type *BiPageRankClassifier*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

Dirichlet

class sknetwork.classification.**DirichletClassifier**(*n_iter: int = 10*, *damping_factor: Optional[float] = None*, *n_jobs: Optional[int] = None*, *verbose: bool = False*)
Node classification using multiple Dirichlet problems.

- Graphs
- Digraphs

Parameters

- **n_iter** (*int*) – If positive, the solution to the Dirichlet problem is approximated by power iteration for n_iter steps. Otherwise, the solution is computed through BiConjugate Stabilized Gradient descent.
- **damping_factor** (*float (optional)*) – Damping factor (default value = 1).

- **n_jobs** – If an integer value is given, denotes the number of workers to use (-1 means the maximum number will be used). If `None`, no parallel computations are made.
- **verbose** – Verbose mode.

Variables

- **labels_** (*np.ndarray*) – Label of each node (hard classification).
- **membership_** (*sparse.csr_matrix*) – Membership matrix (soft classification, labels on columns).

Example

```
>>> from sknetwork.data import karate_club
>>> dirichlet = DirichletClassifier()
>>> graph = karate_club(metadata=True)
>>> adjacency = graph.adjacency
>>> labels_true = graph.labels
>>> seeds = {0: labels_true[0], 33: labels_true[33]}
>>> labels_pred = dirichlet.fit_transform(adjacency, seeds)
>>> np.round(np.mean(labels_pred == labels_true), 2)
0.97
```

References

Zhu, X., Lafferty, J., & Rosenfeld, R. (2005). Semi-supervised learning with graphs (Doctoral dissertation, Carnegie Mellon University, language technologies institute, school of computer science).

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds: Union[numpy.ndarray, dict]*) → sknetwork.classification.base_rank.RankClassifier
Fit algorithm to the data.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **seeds** – Seed nodes (labels as dictionary or array; negative values ignored).

Returns self

Return type `RankClassifier`

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

class sknetwork.classification.**BiDirichletClassifier**(*n_iter: int = 10, damping_factor: Optional[float] = None, n_jobs: Optional[int] = None, verbose: bool = False*)

Node classification using multiple diffusions.

- Bigraphs

Parameters

- **n_iter** (*int*) – If positive, the solution to the Dirichlet problem is approximated by power iteration for n_iter steps. Otherwise, the solution is computed through BiConjugate Stabilized Gradient descent.
- **damping_factor** (*float (optional)*) – Damping factor (default value = 1).
- **n_jobs** – If positive, number of parallel jobs allowed (-1 means maximum number). If None, no parallel computations are made.
- **verbose** – Verbose mode.

Variables

- **labels_** (*np.ndarray*) – Label of each row.
- **labels_row_** (*np.ndarray*) – Label of each row (copy of **labels_**).
- **labels_col_** (*np.ndarray*) – Label of each column.
- **membership_** (*sparse.csr_matrix*) – Membership matrix of rows (soft classification, labels on columns).
- **membership_row_** (*sparse.csr_matrix*) – Membership matrix of rows (copy of **membership_**).
- **membership_col_** (*sparse.csr_matrix*) – Membership matrix of columns.

Example

```
>>> from sknetwork.data import star_wars
>>> bidirichlet = BiDirichletClassifier()
>>> biadjacency = star_wars()
>>> seeds = {0: 1, 2: 0}
>>> bidirichlet.fit_transform(biadjacency, seeds)
array([1, 1, 0, 0])
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray], seeds_row: Union[numpy.ndarray, dict], seeds_col: Optional[Union[numpy.ndarray, dict]] = None*) → sknetwork.classification.base_rank.RankClassifier

Compute labels.

Parameters

- **biadjacency** – Biadjacency matrix of the graph.
- **seeds_row** – Seed rows (labels as dictionary or array; negative values ignored).
- **seeds_col** – Seed columns (optional). Same format.

Returns self

Return type *BiPageRankClassifier*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

Propagation

class sknetwork.classification.**Propagation**(*n_iter: int = - 1*, *node_order: str = None*, *weighted: bool = True*)
Node classification by label propagation.

- Graphs
- Digraphs

Parameters

- **n_iter** (*int*) – Maximum number of iterations (-1 for infinity).
- **node_order** (*str*) –
  - *'random'*: node labels are updated in random order.
  - *'increasing'*: node labels are updated by increasing order of (in-)weight.
  - *'decreasing'*: node labels are updated by decreasing order of (in-)weight.
  - Otherwise, node labels are updated by index order.
- **weighted** (*bool*) – If `True`, the vote of each neighbor is proportional to the edge weight. Otherwise, all votes have weight 1.

Variables

- **labels_** (*np.ndarray*) – Label of each node.
- **membership_** (*sparse.csr_matrix*) – Membership matrix (columns = labels).

Example

```
>>> from sknetwork.classification import Propagation
>>> from sknetwork.data import karate_club
>>> propagation = Propagation()
>>> graph = karate_club(metadata=True)
>>> adjacency = graph.adjacency
>>> labels_true = graph.labels
>>> seeds = {0: labels_true[0], 33: labels_true[33]}
>>> labels_pred = propagation.fit_transform(adjacency, seeds)
>>> np.round(np.mean(labels_pred == labels_true), 2)
0.94
```

References

Raghavan, U. N., Albert, R., & Kumara, S. (2007). Near linear time algorithm to detect community structures in large-scale networks. Physical review E, 76(3), 036106.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds: Union[numpy.ndarray, dict] = None*) → sknetwork.classification.propagation.Propagation
Node classification by label propagation.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **seeds** – Seed nodes. Can be a dict {node: label} or an array where "-1" means no label.

Returns **self**

Return type *Propagation*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

class sknetwork.classification.**BiPropagation**(*n_iter: int = - 1*)
Node classification by label propagation in bipartite graphs.

- Bigraphs

Parameters **n_iter** – Maximum number of iteration (-1 for infinity).

Variables

- **labels_** (*np.ndarray*) – Label of each row.
- **labels_row_** (*np.ndarray*) – Label of each row (copy of **labels_**).
- **labels_col_** (*np.ndarray*) – Label of each column.
- **membership_** (*sparse.csr_matrix*) – Membership matrix of rows.
- **membership_row_** (*sparse.csr_matrix*) – Membership matrix of rows (copy of **membership_**).
- **membership_col_** (*sparse.csr_matrix*) – Membership matrix of columns.

Example

```
>>> from sknetwork.classification import BiPropagation
>>> from sknetwork.data import movie_actor
>>> bipropagation = BiPropagation()
>>> graph = movie_actor(metadata=True)
>>> biadjacency = graph.biadjacency
>>> seeds_row = {0: 0, 1: 2, 2: 1}
>>> len(bipropagation.fit_transform(biadjacency, seeds_row))
15
>>> len(bipropagation.labels_col_)
16
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds_row: Union[numpy.ndarray, dict]*, *seeds_col: Optional[Union[numpy.ndarray, dict]] = None*) → sknetwork.classification.propagation.BiPropagation
Node classification by k-nearest neighbors in the embedding space.

Parameters

- **biadjacency** – Biadjacency matrix of the graph.
- **seeds_row** – Seed rows. Can be a dict {node: label} or an array where "-1" means no label.
- **seeds_col** – Seed columns (optional). Same format.

Returns self

Return type *BiPropagation*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

Nearest neighbors

class sknetwork.classification.**KNN**(*embedding_method: sknetwork.embedding.base.BaseEmbedding = GSVD(n_components=10, regularization=None, relative_regularization=True, factor_row=0.5, factor_col=0.5, factor_singular=0.0, normalized=True, solver='auto')*, *n_neighbors: int = 5*, *factor_distance: float = 2*, *leaf_size: int = 16*, *p: float = 2*, *tol_nn: float = 0.01*, *n_jobs: Optional[int] = None*)
Node classification by K-nearest neighbors in the embedding space.

- Graphs
- Digraphs

- Bigraphs

For bigraphs, classify rows only (see `BiKNN` for joint classification of rows and columns).

Parameters

- **embedding_method** – Which algorithm to use to project the nodes in vector space. Default is `GSVD`.
- **n_neighbors** – Number of nearest neighbors to consider.
- **factor_distance** – Power weighting factor α applied to the distance to each neighbor. Neighbor at distance :math:`d` has weight $1/d^\alpha$. Default is 2.
- **leaf_size** – Leaf size passed to KDTree.
- **p** – Which Minkowski p-norm to use. Default is 2 (Euclidean distance).
- **tol_nn** – Tolerance in nearest neighbors search; the k-th returned value is guaranteed to be no further than `1 + tol_nn` times the distance to the actual k-th nearest neighbor.
- **n_jobs** – Number of jobs to schedule for parallel processing. If -1 is given all processors are used.

Variables

- **labels_** (*np.ndarray*) – Label of each node.
- **membership_** (*sparse.csr_matrix*) – Membership matrix (columns = labels).

Example

```
>>> from sknetwork.classification import KNN
>>> from sknetwork.embedding import GSVD
>>> from sknetwork.data import karate_club
>>> knn = KNN(GSVD(3), n_neighbors=1)
>>> graph = karate_club(metadata=True)
>>> adjacency = graph.adjacency
>>> labels_true = graph.labels
>>> seeds = {0: labels_true[0], 33: labels_true[33]}
>>> labels_pred = knn.fit_transform(adjacency, seeds)
>>> np.round(np.mean(labels_pred == labels_true), 2)
0.97
```

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray], seeds: Union[numpy.ndarray, dict]*) → sknetwork.classification.knn.KNN
Node classification by k-nearest neighbors in the embedding space.

Parameters

- **adjacency** – Adjacency or biadjacency matrix of the graph.
- **seeds** – Seed nodes. Can be a dict {node: label} or an array where "-1" means no label.

Returns self

Return type *KNN*

fit_transform(**args, **kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

class sknetwork.classification.**BiKNN**(*embedding_method: sknetwork.embedding.base.BaseEmbedding = GSVD(n_components=10, regularization=None, relative_regularization=True, factor_row=0.5, factor_col=0.5, factor_singular=0.0, normalized=True, solver='auto')*, *n_neighbors: int = 5*, *factor_distance: float = 2*, *leaf_size: int = 16*, *p: float = 2*, *tol_nn: float = 0.01*, *n_jobs: int = 1*)
Node classification by K-nearest neighbors in the embedding space.

- Bigraphs

Parameters

- **embedding_method** – Which algorithm to use to project the nodes in vector space. Default is `GSVD`.
- **n_neighbors** – Number of nearest neighbors to consider.
- **factor_distance** – Power weighting factor :math:`\alpha` applied to the distance to each neighbor. Neighbor at distance :math:`d` has weight :math:`1 / d^\alpha`. Default is 2.
- **leaf_size** – Leaf size passed to KDTree.
- **p** – Which Minkowski p-norm to use. Default is 2 (Euclidean distance).
- **tol_nn** – Tolerance in nearest neighbors search; the k-th returned value is guaranteed to be no further than `1 + tol_nn` times the distance to the actual k-th nearest neighbor.
- **n_jobs** – Number of jobs to schedule for parallel processing. If -1 is given all processors are used.

Variables

- **labels_** (*np.ndarray*) – Label of each row.
- **labels_row_** (*np.ndarray*) – Label of each row (copy of **labels_**).
- **labels_col_** (*np.ndarray*) – Label of each column.
- **membership_** (*sparse.csr_matrix*) – Membership matrix of rows.
- **membership_row_** (*sparse.csr_matrix*) – Membership matrix of rows (copy of **membership_**).
- **membership_col_** (*sparse.csr_matrix*) – Membership matrix of columns.

Example

```
>>> from sknetwork.classification import BiKNN
>>> from sknetwork.data import movie_actor
>>> biknn = BiKNN(n_neighbors=2)
>>> graph = movie_actor(metadata=True)
>>> biadjacency = graph.biadjacency
>>> seeds_row = {0: 0, 1: 2, 2: 1}
>>> len(biknn.fit_transform(biadjacency, seeds_row))
15
>>> len(biknn.labels_col_)
16
```

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *seeds_row: Union[numpy.ndarray, dict]*, *seeds_col: Optional[Union[numpy.ndarray, dict]] = None*) → sknetwork.classification.knn.BiKNN
Node classification by k-nearest neighbors in the embedding space.

Parameters

- **biadjacency** – Biadjacency matrix of the graph.
- **seeds_row** – Seed rows. Can be a dict {node: label} or an array where "-1" means no label.
- **seeds_col** – Seed columns (optional). Same format.

Returns self

Return type *BiKNN*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit algorithm to the data and return the labels. Same parameters as the `fit` method.

Returns **labels** – Labels.

Return type np.ndarray

score(*label: int*)
Classification scores for a given label.

Parameters **label** (*int*) – The label index of the class.

Returns **scores** – Classification scores of shape (number of nodes,).

Return type np.ndarray

Metrics

sknetwork.classification.**accuracy_score**(*y_true: numpy.ndarray*, *y_pred: numpy.ndarray*) → float

Accuracy: number of correctly labeled samples over total number of elements. In the case of binary classification, this is

$$P = \frac{TP + TN}{TP + TN + FP + FN}.$$

Parameters

- **y_true** (*np.ndarray*) – True labels.
- **y_pred** (*np.ndarray*) – Predicted labels

Returns **precision** – A score between 0 and 1.

Return type float

Examples

```
>>> import numpy as np
>>> y_true = np.array([0, 0, 1, 1])
>>> y_pred = np.array([0, 0, 0, 1])
>>> accuracy_score(y_true, y_pred)
0.75
```

3.2.9 Embedding

Graph embedding algorithms.

The attribute `embedding_` assigns a vector to each node of the graph.

Spectral

class sknetwork.embedding.**Spectral**(*n_components: int = 2*, *regularization: Union[None, float] = 0.01*, *relative_regularization: bool = True*, *scaling: float = 0.5*, *normalized: bool = True*, *solver: str = 'auto'*)

Spectral embedding of graphs, based the spectral decomposition of the transition matrix $P = D^{-1}A$. Eigenvectors are considered in decreasing order of eigenvalues, skipping the first eigenvector.

- Graphs

See *BiSpectral* for digraphs and bigraphs.

Parameters

- **n_components** (int (default = 2)) – Dimension of the embedding space.
- **regularization** (None or float (default = 0.01)) – Add edges of given weight between all pairs of nodes.
- **relative_regularization** (bool (default = True)) – If True, consider the regularization as relative to the total weight of the graph.
- **scaling** (float (non-negative, default = 0.5)) – Scaling factor α so that each component is divided by $(1 - \lambda)^\alpha$, with λ the corresponding eigenvalue of the transition matrix P. Require regularization if positive and the graph is not connected. The default value $\alpha = \frac{1}{2}$ equalizes the energy levels of the corresponding mechanical system.
- **normalized** (bool (default = True)) – If True, normalize the embedding so that each vector has norm 1 in the embedding space, i.e., each vector lies on the unit sphere.
- **solver** ('auto', 'halko', 'lanczos' (default = 'auto')) – Which eigenvalue solver to use.
  - 'auto' call the auto_solver function.
  - 'halko': randomized method, fast but less accurate than 'lanczos' for ill-conditioned matrices.
  - 'lanczos': power-iteration based method.

Variables

- **embedding_** (*array, shape = (n, n_components)*) – Embedding of the nodes.
- **eigenvalues_** (*array, shape = (n_components)*) – Eigenvalues in decreasing order (first eigenvalue ignored).
- **eigenvectors_** (*array, shape = (n, n_components)*) – Corresponding eigenvectors.
- **regularization_** (None or float) – Regularization factor added to all pairs of nodes.

Example

```
>>> from sknetwork.embedding import Spectral
>>> from sknetwork.data import karate_club
>>> spectral = Spectral()
>>> adjacency = karate_club()
>>> embedding = spectral.fit_transform(adjacency)
>>> embedding.shape
(34, 2)
```

References

Belkin, M. & Niyogi, P. (2003). Laplacian Eigenmaps for Dimensionality Reduction and Data Representation, Neural computation.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.embedding.spectral.Spectral
Compute the graph embedding.

Parameters **adjacency** – Adjacency matrix of the graph (symmetric matrix).

Returns **self**

Return type *Spectral*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit to data and return the embedding. Same parameters as the `fit` method.

Returns **embedding** – Embedding.

Return type np.ndarray

predict(*adjacency_vectors: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → numpy.ndarray
Predict the embedding of new nodes, defined by their adjacency vectors.

Parameters **adjacency_vectors** – Adjacency vectors of nodes. Array of shape (n_col,) (single vector) or (n_vectors, n_col)

Returns **embedding_vectors** – Embedding of the nodes.

Return type np.ndarray

class sknetwork.embedding.**BiSpectral**(*n_components: int = 2*, *regularization: Union[None, float] = 0.01*, *relative_regularization: bool = True*, *scaling: float = 0.5*, *normalized: bool = True*, *solver: str = 'auto'*)
Spectral embedding of bipartite and directed graphs, based the spectral embedding of the corresponding undirected graph, with adjacency matrix:

$$A = \begin{bmatrix} 0 & B \\ B^T & 0 \end{bmatrix}$$

where B is the biadjacency matrix of the bipartite graph or the adjacency matrix of the directed graph.

- Digraphs
- Bigraphs

Parameters

- **n_components** (*int (default = 2)*) – Dimension of the embedding space.
- **regularization** (None or float (default = 0.01)) – Add edges of given weight between all pairs of nodes.
- **relative_regularization** (bool (default = True)) – If True, consider the regularization as relative to the total weight of the graph.
- **scaling** (float (non-negative, default = 0.5)) – Scaling factor α so that each component is divided by $(1 - \lambda)^\alpha$, with λ the corresponding eigenvalue of the transition matrix P. Require regularization if positive and the graph is not connected. The default value $\alpha = \frac{1}{2}$ equalizes the energy levels of the corresponding mechanical system.
- **normalized** (bool (default = True)) – If True, normalized the embedding so that each vector has norm 1 in the embedding space, i.e., each vector lies on the unit sphere.
- **solver** ('auto', 'halko', 'lanczos' (default = 'auto')) – Which eigenvalue solver to use.
  - 'auto' call the auto_solver function.
  - 'halko': randomized method, fast but less accurate than 'lanczos' for ill-conditioned matrices.
  - 'lanczos': power-iteration based method.

Variables

- **embedding_** (*array, shape = (n_row, n_components)*) – Embedding of the rows.
- **embedding_row_** (*array, shape = (n_row, n_components)*) – Embedding of the rows (copy of **embedding_**).
- **embedding_col_** (*array, shape = (n_col, n_components)*) – Embedding of the columns.
- **eigenvalues_** (*array, shape = (n_components)*) – Eigenvalues in increasing order (first eigenvalue ignored).
- **eigenvectors_** (*array, shape = (n, n_components)*) – Corresponding eigenvectors.
- **regularization_** (None or float) – Regularization factor added to all pairs of nodes.

Example

```
>>> from sknetwork.embedding import BiSpectral
>>> from sknetwork.data import movie_actor
>>> bispectral = BiSpectral()
>>> biadjacency = movie_actor()
>>> embedding = bispectral.fit_transform(biadjacency)
>>> embedding.shape
(15, 2)
```

References

Belkin, M. & Niyogi, P. (2003). Laplacian Eigenmaps for Dimensionality Reduction and Data Representation, Neural computation.

fit(*biadjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.embedding.spectral.BiSpectral
Spectral embedding of the bipartite graph considered as undirected, with adjacency matrix:

$$A = \begin{bmatrix} 0 & B \\ B^T & 0 \end{bmatrix}$$

where B is the biadjacency matrix (or the adjacency matrix of a directed graph).

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns **self**

Return type *BiSpectral*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit to data and return the embedding. Same parameters as the `fit` method.

Returns **embedding** – Embedding.

Return type np.ndarray

predict(*adjacency_vectors: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → numpy.ndarray
Predict the embedding of new rows, defined by their adjacency vectors.

Parameters **adjacency_vectors** – Adjacency vectors of nodes. Array of shape (n_col,) (single vector) or (n_vectors, n_col)

Returns **embedding_vectors** – Embedding of the nodes.

Return type np.ndarray

class sknetwork.embedding.**LaplacianEmbedding**(*n_components: int = 2*, *regularization: Union[None, float] = 0.01*, *relative_regularization: bool = True*, *scaling: float = 0.5*, *normalized: bool = True*, *solver: str = 'auto'*)
Spectral embedding of graphs, based the spectral decomposition of the Laplacian matrix $L = D - A$. Eigenvectors are considered in increasing order of eigenvalues, skipping the first eigenvector.

- Graphs

Parameters

- **n_components** (*int (default = 2)*) – Dimension of the embedding space.

- **regularization** (None or float (default = 0.01)) – Add edges of given weight between all pairs of nodes.
- **relative_regularization** (bool (default = True)) – If True, consider the regularization as relative to the total weight of the graph.
- **scaling** (float (non-negative, default = 0.5)) – Scaling factor α so that each component is divided by λ^α, with λ the corresponding eigenvalue of the Laplacian matrix L. Require regularization if positive and the graph is not connected. The default value $\alpha = \frac{1}{2}$ equalizes the energy levels of the corresponding mechanical system.
- **normalized** (bool (default = True)) – If True, normalize the embedding so that each vector has norm 1 in the embedding space, i.e., each vector lies on the unit sphere.
- **solver** ('auto', 'halko', 'lanczos' (default = 'auto')) – Which eigenvalue solver to use.
  - 'auto' call the auto_solver function.
  - 'halko': randomized method, fast but less accurate than 'lanczos' for ill-conditioned matrices.
  - 'lanczos': power-iteration based method.

Variables

- **embedding_** (*array, shape = (n, n_components)*) – Embedding of the nodes.
- **eigenvalues_** (*array, shape = (n_components)*) – Eigenvalues in increasing order (first eigenvalue ignored).
- **eigenvectors_** (*array, shape = (n, n_components)*) – Corresponding eigenvectors.
- **regularization_** (None or float) – Regularization factor added to all pairs of nodes.

Example

```
>>> from sknetwork.embedding import Spectral
>>> from sknetwork.data import karate_club
>>> laplacian = LaplacianEmbedding()
>>> adjacency = karate_club()
>>> embedding = laplacian.fit_transform(adjacency)
>>> embedding.shape
(34, 2)
```

References

Belkin, M. & Niyogi, P. (2003). Laplacian Eigenmaps for Dimensionality Reduction and Data Representation, Neural computation.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.embedding.spectral.LaplacianEmbedding
Compute the graph embedding.

Parameters **adjacency** – Adjacency matrix of the graph (symmetric matrix).

Returns **self**

Return type *LaplacianEmbedding*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit to data and return the embedding. Same parameters as the `fit` method.

Returns **embedding** – Embedding.

Return type np.ndarray

SVD

class sknetwork.embedding.**SVD**(*n_components=2*, *regularization: Union[None, float] = None*, *relative_regularization: bool = True*, *factor_singular: float = 0.0*, *normalized: bool = False*, *solver: Union[str, sknetwork.linalg.svd_solver.SVDSolver] = 'auto'*)
Graph embedding by Singular Value Decomposition of the adjacency or biadjacency matrix.

- Graphs
- Digraphs
- Bigraphs

Parameters

- **n_components** (*int*) – Dimension of the embedding.
- **regularization** (`None` or float (default = `None`)) – Implicitly add edges of given weight between all pairs of nodes.
- **relative_regularization** (bool (default = `True`)) – If `True`, consider the regularization as relative to the total weight of the graph.
- **factor_singular** (*float (default = 0.)*) – Power factor α applied to the singular values on right singular vectors. The embedding of rows and columns are respectively $U\Sigma^{1-\alpha}$ and $V\Sigma^{\alpha}$ where:
  - U is the matrix of left singular vectors, shape (n_row, n_components)
  - V is the matrix of right singular vectors, shape (n_col, n_components)
  - Σ is the diagonal matrix of singular values, shape (n_components, n_components)
- **normalized** (bool (default = `False`)) – If `True`, normalized the embedding so that each vector has norm 1 in the embedding space, i.e., each vector lies on the unit sphere.
- **solver** (`'auto'`, `'halko'`, `'lanczos'` or `SVDSolver`) – Which singular value solver to use.
  - `'auto'`: call the auto_solver function.
  - `'halko'`: randomized method, fast but less accurate than `'lanczos'` for ill-conditioned matrices.
  - `'lanczos'`: power-iteration based method.
  - `SVDSolver`: custom solver.

Variables

- **embedding_** (*np.ndarray, shape = (n_row, n_components)*) – Embedding of the rows.

- **embedding_row_** (*np.ndarray, shape = (n_row, n_components)*) – Embedding of the rows (copy of **embedding_**).
- **embedding_col_** (*np.ndarray, shape = (n_col, n_components)*) – Embedding of the columns.
- **singular_values_** (*np.ndarray, shape = (n_components)*) – Singular values.
- **singular_vectors_left_** (*np.ndarray, shape = (n_row, n_components)*) – Left singular vectors.
- **singular_vectors_right_** (*np.ndarray, shape = (n_col, n_components)*) – Right singular vectors.
- **regularization_** (None or float) – Regularization factor added to all pairs of nodes.

Example

```
>>> from sknetwork.embedding import SVD
>>> from sknetwork.data import karate_club
>>> svd = SVD()
>>> adjacency = karate_club()
>>> embedding = svd.fit_transform(adjacency)
>>> embedding.shape
(34, 2)
```

References

Abdi, H. (2007). Singular value decomposition (SVD) and generalized singular value decomposition. Encyclopedia of measurement and statistics, 907-912.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.embedding.svd.GSVD
Compute the GSVD of the adjacency or biadjacency matrix.

Parameters **adjacency** – Adjacency or biadjacency matrix of the graph.

Returns **self**

Return type *GSVD*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit to data and return the embedding. Same parameters as the `fit` method.

Returns **embedding** – Embedding.

Return type np.ndarray

predict(*adjacency_vectors: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → numpy.ndarray
Predict the embedding of new rows, defined by their adjacency vectors.

Parameters **adjacency_vectors** – Adjacency vectors of nodes. Array of shape (n_col,) (single vector) or (n_vectors, n_col)

Returns **embedding_vectors** – Embedding of the nodes.

Return type np.ndarray

GSVD

class sknetwork.embedding.**GSVD**(*n_components=2*, *regularization: Union[None, float] = None*, *relative_regularization: bool = True*, *factor_row: float = 0.5*, *factor_col: float = 0.5*, *factor_singular: float = 0.0*, *normalized: bool = True*, *solver: Union[str, sknetwork.linalg.svd_solver.SVDSolver] = 'auto'*)

Graph embedding by Generalized Singular Value Decomposition of the adjacency or biadjacency matrix A. This is equivalent to the Singular Value Decomposition of the matrix $D_1^{-\alpha_1} A D_2^{-\alpha_2}$ where D_1, D_2 are the diagonal matrices of row weights and columns weights, respectively, and α_1, α_2 are parameters.

- Graphs
- Digraphs
- Bigraphs

Parameters

- **n_components** (*int*) – Dimension of the embedding.
- **regularization** (None or float (default = None)) – Implicitly add edges of given weight between all pairs of nodes.
- **relative_regularization** (bool (default = True)) – If True, consider the regularization as relative to the total weight of the graph.
- **factor_row** (*float (default = 0.5)*) – Power factor α_1 applied to the diagonal matrix of row weights.
- **factor_col** (*float (default = 0.5)*) – Power factor α_2 applied to the diagonal matrix of column weights.
- **factor_singular** (*float (default = 0.)*) – Parameter α applied to the singular values on right singular vectors. The embedding of rows and columns are respectively $D_1^{-\alpha_1} U \Sigma^{1-\alpha}$ and $D_2^{-\alpha_2} V \Sigma^{\alpha}$ where:
  - U is the matrix of left singular vectors, shape (n_row, n_components)
  - V is the matrix of right singular vectors, shape (n_col, n_components)
  - Σ is the diagonal matrix of singular values, shape (n_components, n_components)
- **normalized** (bool (default = True)) – If True, normalized the embedding so that each vector has norm 1 in the embedding space, i.e., each vector lies on the unit sphere.
- **solver** ('auto', 'halko', 'lanczos' or SVDSolver) – Which singular value solver to use.
  - 'auto': call the auto_solver function.
  - 'halko': randomized method, fast but less accurate than 'lanczos' for ill-conditioned matrices.
  - 'lanczos': power-iteration based method.
  - SVDSolver: custom solver.

Variables

- **embedding_** (*np.ndarray, shape = (n1, n_components)*) – Embedding of the rows.
- **embedding_row_** (*np.ndarray, shape = (n1, n_components)*) – Embedding of the rows (copy of **embedding_**).

- **embedding_col_** (*np.ndarray, shape = (n2, n_components)*) – Embedding of the columns.
- **singular_values_** (*np.ndarray, shape = (n_components)*) – Singular values.
- **singular_vectors_left_** (*np.ndarray, shape = (n_row, n_components)*) – Left singular vectors.
- **singular_vectors_right_** (*np.ndarray, shape = (n_col, n_components)*) – Right singular vectors.
- **regularization_** (None or float) – Regularization factor added to all pairs of nodes.
- **weights_col_** (*np.ndarray, shape = (n2)*) – Weights applied to columns.

Example

```
>>> from sknetwork.embedding import GSVD
>>> from sknetwork.data import karate_club
>>> gsvd = GSVD()
>>> adjacency = karate_club()
>>> embedding = gsvd.fit_transform(adjacency)
>>> embedding.shape
(34, 2)
```

References

Abdi, H. (2007). Singular value decomposition (SVD) and generalized singular value decomposition. Encyclopedia of measurement and statistics, 907-912.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → sknetwork.embedding.svd.GSVD
Compute the GSVD of the adjacency or biadjacency matrix.

Parameters **adjacency** – Adjacency or biadjacency matrix of the graph.

Returns **self**

Return type *GSVD*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit to data and return the embedding. Same parameters as the `fit` method.

Returns **embedding** – Embedding.

Return type np.ndarray

predict(*adjacency_vectors: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → numpy.ndarray
Predict the embedding of new rows, defined by their adjacency vectors.

Parameters **adjacency_vectors** – Adjacency vectors of nodes. Array of shape (n_col,) (single vector) or (n_vectors, n_col)

Returns **embedding_vectors** – Embedding of the nodes.

Return type np.ndarray

Louvain

class sknetwork.embedding.**LouvainEmbedding**(*resolution: float = 1, merge_isolated: bool = True, modularity: str = 'dugue', tol_optimization: float = 0.001, tol_aggregation: float = 0.001, n_aggregations: int = -1, shuffle_nodes: bool = False, random_state: Optional[Union[numpy.random.mtrand.RandomState, int]] = None*)

Embedding of graphs from a clustering obtained with Louvain.

Parameters

- **resolution** – Resolution parameter.
- **merge_isolated** (*bool*) – Denotes if clusters consisting of just one node should be merged.
- **modularity** (*str*) – Which objective function to maximize. Can be `'dugue'`, `'newman'` or `'potts'`.
- **tol_optimization** – Minimum increase in the objective function to enter a new optimization pass.
- **tol_aggregation** – Minimum increase in the objective function to enter a new aggregation pass.
- **n_aggregations** – Maximum number of aggregations. A negative value is interpreted as no limit.
- **shuffle_nodes** – Enables node shuffling before optimization.
- **random_state** – Random number generator or random seed. If None, numpy.random is used.

Variables **embedding_** (*array, shape = (n, n_components)*) – Embedding of the nodes.

Example

```
>>> from sknetwork.embedding import LouvainEmbedding
>>> from sknetwork.data import karate_club
>>> louvain = LouvainEmbedding()
>>> adjacency = karate_club()
>>> embedding = louvain.fit_transform(adjacency)
>>> embedding.shape
(34, 7)
```

fit(*adjacency*)

Embedding of graphs from a clustering obtained with Louvain.

Parameters **adjacency** – Adjacency matrix of the graph.

Returns **self**

Return type *LouvainEmbedding*

fit_transform(**args*, ***kwargs*) → numpy.ndarray

Fit to data and return the embedding. Same parameters as the `fit` method.

Returns **embedding** – Embedding.

Return type np.ndarray

predict(*adjacency_vectors: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → numpy.ndarray
Predict the embedding of new nodes, defined by their adjacency vectors.

Parameters **adjacency_vectors** – Adjacency vectors of nodes. Array of shape (n_col,) (single vector) or (n_vectors, n_col)

Returns **embedding_vectors** – Embedding of the nodes.

Return type np.ndarray

class sknetwork.embedding.**BiLouvainEmbedding**(*resolution: float = 1*, *merge_isolated: bool = True*, *modularity: str = 'dugue'*, *tol_optimization: float = 0.001*, *tol_aggregation: float = 0.001*, *n_aggregations: int = - 1*, *shuffle_nodes: bool = False*, *random_state: Optional[Union[numpy.random.mtrand.RandomState, int]] = None*)
Embedding of bipartite graphs from a clustering obtained with Louvain.

Parameters

- **resolution** (*float*) – Resolution parameter.
- **merge_isolated** (*bool*) – Denotes if clusters consisting of just one node should be merged.
- **modularity** (*str*) – Which objective function to maximize. Can be `'dugue'`, `'newman'` or `'potts'`.
- **tol_optimization** – Minimum increase in the objective function to enter a new optimization pass.
- **tol_aggregation** – Minimum increase in the objective function to enter a new aggregation pass.
- **n_aggregations** – Maximum number of aggregations. A negative value is interpreted as no limit.
- **shuffle_nodes** – Enables node shuffling before optimization.
- **random_state** – Random number generator or random seed. If None, numpy.random is used.

Variables

- **embedding_** (*array, shape = (n, n_components)*) – Embedding of the nodes.
- **embedding_row_** (*array, shape = (n_row, n_components)*) – Embedding of the rows (copy of **embedding_**).
- **embedding_col_** (*array, shape = (n_col, n_components)*) – Embedding of the columns.

Example

```
>>> from sknetwork.embedding import BiLouvainEmbedding
>>> from sknetwork.data import movie_actor
>>> bilouvain = BiLouvainEmbedding()
>>> biadjacency = movie_actor()
>>> embedding = bilouvain.fit_transform(biadjacency)
>>> embedding.shape
(15, 5)
```

fit(*biadjacency*)
Embedding of bipartite graphs from a clustering obtained with Louvain.

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns self

Return type *BiLouvainEmbedding*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit to data and return the embedding. Same parameters as the `fit` method.

Returns **embedding** – Embedding.

Return type np.ndarray

predict(*adjacency_vectors: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → numpy.ndarray
Predict the embedding of new rows, defined by their adjacency vectors.

Parameters **adjacency_vectors** – Adjacency vectors of rows. Array of shape (n_col,) (single vector) or (n_vectors, n_col)

Returns **embedding_vectors** – Embedding of the nodes.

Return type np.ndarray

Force Atlas 2

class sknetwork.embedding.**ForceAtlas2**(*n_components: int = 2*, *n_iter: int = 50*, *approx_radius: float = - 1*, *lin_log: bool = False*, *gravity_factor: float = 0.01*, *repulsive_factor: float = 0.1*, *tolerance: float = 0.1*, *speed: float = 0.1*, *speed_max: float = 10*)

Force Atlas 2 layout for displaying graphs.

- Graphs
- Digraphs

Parameters

- **n_components** (*int*) – Dimension of the graph layout.
- **n_iter** (*int*) – Number of iterations to update positions. If `None`, use the value of self.n_iter.
- **approx_radius** (*float*) – If a positive value is provided, only the nodes within this distance a given node are used to compute the repulsive force.
- **lin_log** (*bool*) – If `True`, use lin-log mode.
- **gravity_factor** (*float*) – Gravity force scaling constant.

- **repulsive_factor** (*float*) – Repulsive force scaling constant.
- **tolerance** (*float*) – Tolerance defined in the swinging constant.
- **speed** (*float*) – Speed constant.
- **speed_max** (*float*) – Constant used to impose constrain on speed.

Variables **embedding_** (*np.ndarray*) – Layout in given dimension.

Example

```
>>> from sknetwork.embedding.force_atlas import ForceAtlas2
>>> from sknetwork.data import karate_club
>>> force_atlas = ForceAtlas2()
>>> adjacency = karate_club()
>>> embedding = force_atlas.fit_transform(adjacency)
>>> embedding.shape
(34, 2)
```

References

Jacomy M., Venturini T., Heymann S., Bastian M. (2014). ForceAtlas2, a Continuous Graph Layout Algorithm for Handy Network Visualization Designed for the Gephi Software. Plos One.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *pos_init: Optional[numpy.ndarray] = None*, *n_iter: Optional[int] = None*) → sknetwork.embedding.force_atlas.ForceAtlas2
Compute layout.

Parameters

- **adjacency** – Adjacency matrix of the graph, treated as undirected.
- **pos_init** – Position to start with. Random if not provided.
- **n_iter** (*int*) – Number of iterations to update positions. If `None`, use the value of self.n_iter.

Returns **self**

Return type *ForceAtlas2*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit to data and return the embedding. Same parameters as the `fit` method.

Returns **embedding** – Embedding.

Return type np.ndarray

Spring

class sknetwork.embedding.**Spring**(*n_components: int = 2*, *strength: float = None*, *n_iter: int = 50*, *tol: float = 0.0001*, *approx_radius: float = - 1*, *position_init: str = 'random'*)

Spring layout for displaying small graphs.

- Graphs
- Digraphs

Parameters

- **n_components** (*int*) – Dimension of the graph layout.
- **strength** (*float*) – Intensity of the force that moves the nodes.
- **n_iter** (*int*) – Number of iterations to update positions.
- **tol** (*float*) – Minimum relative change in positions to continue updating.
- **approx_radius** (*float*) – If a positive value is provided, only the nodes within this distance a given node are used to compute the repulsive force.
- **position_init** (*str*) – How to initialize the layout. If 'spectral', use Spectral embedding in dimension 2, otherwise, use random initialization.

Variables **embedding_** (*np.ndarray*) – Layout.

Example

```
>>> from sknetwork.embedding import Spring
>>> from sknetwork.data import karate_club
>>> spring = Spring()
>>> adjacency = karate_club()
>>> embedding = spring.fit_transform(adjacency)
>>> embedding.shape
(34, 2)
```

Notes

Simple implementation designed to display small graphs.

References

Fruchterman, T. M. J., Reingold, E. M. (1991). Graph Drawing by Force-Directed Placement. Software – Practice & Experience.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *position_init: Optional[numpy.ndarray] = None*, *n_iter: Optional[int] = None*) → sknetwork.embedding.spring.Spring

Compute layout.

Parameters

- **adjacency** – Adjacency matrix of the graph, treated as undirected.
- **position_init** (*np.ndarray*) – Custom initial positions of the nodes. Shape must be (n, 2). If None, use the value of self.pos_init.

- **n_iter** (*int*) – Number of iterations to update positions. If None, use the value of self.n_iter.

Returns self

Return type *Spring*

fit_transform(**args*, ***kwargs*) → numpy.ndarray
Fit to data and return the embedding. Same parameters as the fit method.

Returns **embedding** – Embedding.

Return type np.ndarray

predict(*adjacency_vectors: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*) → numpy.ndarray
Predict the embedding of new rows, defined by their adjacency vectors.

Parameters **adjacency_vectors** – Adjacency vectors of nodes. Array of shape (n_col,) (single vector) or (n_vectors, n_col)

Returns **embedding_vectors** – Embedding of the nodes.

Return type np.ndarray

Metrics

sknetwork.embedding.**cosine_modularity**(*adjacency*, *embedding: numpy.ndarray*, *embedding_col=None*, *resolution=1.0*, *weights='degree'*, *return_all: bool = False*)
Quality metric of an embedding x defined by:

$$Q = \sum_{ij} \left(\frac{A_{ij}}{w} - \gamma \frac{w_i^+ w_j^-}{w^2} \right) \left(\frac{1 + \cos(x_i, x_j)}{2} \right)$$

where

- w_i^+, w_i^- are the out-weight, in-weight of node i (for digraphs),
- $w = 1^T A 1$ is the total weight of the graph.

For bipartite graphs with column embedding y, the metric is

$$Q = \sum_{ij} \left(\frac{B_{ij}}{w} - \gamma \frac{w_{1,i} w_{2,j}}{w^2} \right) \left(\frac{1 + \cos(x_i, y_j)}{2} \right)$$

where

- $w_{1,i}, w_{2,j}$ are the weights of nodes i (row) and j (column),
- $w = 1^T B 1$ is the total weight of the graph.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **embedding** – Embedding of the nodes.
- **embedding_col** – Embedding of the columns (for bipartite graphs).
- **resolution** – Resolution parameter.
- **weights** ('degree' or 'uniform') – Weights of the nodes.
- **return_all** – If True, also return fit and diversity

Returns

- **modularity** (*float*)
- **fit** (*float, optional*)
- **diversity** (*float, optional*)

Example

```
>>> from sknetwork.embedding import cosine_modularity
>>> from sknetwork.data import karate_club
>>> graph = karate_club(metadata=True)
>>> adjacency = graph.adjacency
>>> embedding = graph.position
>>> np.round(cosine_modularity(adjacency, embedding), 2)
0.35
```

3.2.10 Link prediction

Link prediction algorithms.

The method `predict` assigns a scores to edges.

First order methods

class sknetwork.linkpred.**CommonNeighbors**

Link prediction by common neighbors:

$s(i, j) = |\Gamma_i \cap \Gamma_j|$.

Variables

- **indptr_** (*np.ndarray*) – Pointer index for neighbors.
- **indices_** (*np.ndarray*) – Concatenation of neighbors.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> cn = CommonNeighbors()
>>> similarities = cn.fit_predict(adjacency, 0)
>>> similarities
array([2, 1, 1, 1, 1])
>>> similarities = cn.predict([0, 1])
>>> similarities
array([[2, 1, 1, 1, 1],
       [1, 3, 0, 2, 1]])
>>> similarities = cn.predict((0, 1))
>>> similarities
1
>>> similarities = cn.predict([(0, 1), (1, 2)])
>>> similarities
array([1, 0])
```

fit (*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*)
Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph

Returns **self**

Return type FirstOrder

fit_predict (*adjacency*, *query*)
Fit algorithm to data and compute scores for requested edges.

predict (*query: Union[int, Iterable, Tuple]*)
Compute similarity scores.

Parameters **query** (*int, list, array or Tuple*) –

- If int i, return the similarities s(i, j) for all j.
- If list or array integers, return s(i, j) for i in query, for all j as array.
- If tuple (i, j), return the similarity s(i, j).
- If list of tuples or array of shape (n_queries, 2), return s(i, j) for (i, j) in query as array.

Returns **predictions** – The prediction scores.

Return type int, float or array

class sknetwork.linkpred.**JaccardIndex**
Link prediction by Jaccard Index:

$$s(i,j) = \frac{|\Gamma_i \cap \Gamma_j|}{|\Gamma_i \cup \Gamma_j|}.$$

Variables

- **indptr_** (*np.ndarray*) – Pointer index for neighbors.
- **indices_** (*np.ndarray*) – Concatenation of neighbors.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> jaccard = JaccardIndex()
>>> similarities = jaccard.fit_predict(adjacency, 0)
>>> similarities.round(2)
array([1.  , 0.25, 0.33, 0.33, 0.25])
>>> similarities = jaccard.predict([0, 1])
>>> similarities.round(2)
array([[1.  , 0.25, 0.33, 0.33, 0.25],
       [0.25, 1.  , 0.  , 0.67, 0.2 ]])
>>> similarities = jaccard.predict((0, 1))
>>> similarities.round(2)
0.25
>>> similarities = jaccard.predict([(0, 1), (1, 2)])
>>> similarities.round(2)
array([0.25, 0.  ])
```

References

Jaccard, P. (1901) étude comparative de la distribution florale dans une portion des Alpes et du Jura. Bulletin de la Société Vaudoise des Sciences Naturelles, 37, 547-579.

fit (*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*)
Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph

Returns **self**

Return type FirstOrder

fit_predict (*adjacency*, *query*)
Fit algorithm to data and compute scores for requested edges.

predict (*query: Union[int, Iterable, Tuple]*)
Compute similarity scores.

Parameters **query** (*int, list, array or Tuple*) –

- If int i, return the similarities s(i, j) for all j.
- If list or array integers, return s(i, j) for i in query, for all j as array.
- If tuple (i, j), return the similarity s(i, j).
- If list of tuples or array of shape (n_queries, 2), return s(i, j) for (i, j) in query as array.

Returns **predictions** – The prediction scores.

Return type int, float or array

class sknetwork.linkpred.**SaltonIndex**
Link prediction by Salton Index:

$$s(i,j) = \frac{|\Gamma_i \cap \Gamma_j|}{\sqrt{|\Gamma_i|.|\Gamma_j|}}.$$

Variables

- **indptr_** (*np.ndarray*) – Pointer index for neighbors.
- **indices_** (*np.ndarray*) – Concatenation of neighbors.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> salton = SaltonIndex()
>>> similarities = salton.fit_predict(adjacency, 0)
>>> similarities.round(2)
array([1.  , 0.41, 0.5 , 0.5 , 0.41])
>>> similarities = salton.predict([0, 1])
>>> similarities.round(2)
array([[1.  , 0.41, 0.5 , 0.5 , 0.41],
       [0.41, 1.  , 0.  , 0.82, 0.33]])
>>> similarities = salton.predict((0, 1))
>>> similarities.round(2)
0.41
>>> similarities = salton.predict([(0, 1), (1, 2)])
```

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```
>>> similarities.round(2)
array([0.41, 0.  ])
```

References

Martínez, V., Berzal, F., & Cubero, J. C. (2016). A survey of link prediction in complex networks. ACM computing surveys (CSUR), 49(4), 1-33.

fit (*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*)
Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph

Returns **self**

Return type FirstOrder

fit_predict (*adjacency*, *query*)
Fit algorithm to data and compute scores for requested edges.

predict (*query: Union[int, Iterable, Tuple]*)
Compute similarity scores.

Parameters **query** (*int, list, array or Tuple*) –

- If int i, return the similarities s(i, j) for all j.
- If list or array integers, return s(i, j) for i in query, for all j as array.
- If tuple (i, j), return the similarity s(i, j).
- If list of tuples or array of shape (n_queries, 2), return s(i, j) for (i, j) in query as array.

Returns **predictions** – The prediction scores.

Return type int, float or array

class sknetwork.linkpred.**SorensenIndex**
Link prediction by Salton Index:

$$s(i,j) = \frac{2|\Gamma_i \cap \Gamma_j|}{|\Gamma_i| + |\Gamma_j|}.$$

Variables

- **indptr_** (*np.ndarray*) – Pointer index for neighbors.
- **indices_** (*np.ndarray*) – Concatenation of neighbors.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> sorensen = SorensenIndex()
>>> similarities = sorensen.fit_predict(adjacency, 0)
>>> similarities.round(2)
array([1. , 0.4, 0.5, 0.5, 0.4])
>>> similarities = sorensen.predict([0, 1])
>>> similarities.round(2)
array([[1.  , 0.4 , 0.5 , 0.5 , 0.4 ],
```

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```
       [0.4 , 1.  , 0.  , 0.8 , 0.33]])
>>> similarities = sorensen.predict((0, 1))
>>> similarities.round(2)
0.4
>>> similarities = sorensen.predict([(0, 1), (1, 2)])
>>> similarities.round(2)
array([0.4, 0. ])
```

References

- Sørensen, T. J. (1948). A method of establishing groups of equal amplitude in plant sociology based on similarity of species content and its application to analyses of the vegetation on Danish commons. I kommission hos E. Munksgaard.
- Martínez, V., Berzal, F., & Cubero, J. C. (2016). A survey of link prediction in complex networks. ACM computing surveys (CSUR), 49(4), 1-33.

fit (*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*)
Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph

Returns **self**

Return type FirstOrder

fit_predict (*adjacency*, *query*)
Fit algorithm to data and compute scores for requested edges.

predict (*query: Union[int, Iterable, Tuple]*)
Compute similarity scores.

Parameters **query** (*int, list, array or Tuple*) –

- If int i, return the similarities s(i, j) for all j.
- If list or array integers, return s(i, j) for i in query, for all j as array.
- If tuple (i, j), return the similarity s(i, j).
- If list of tuples or array of shape (n_queries, 2), return s(i, j) for (i, j) in query as array.

Returns **predictions** – The prediction scores.

Return type int, float or array

class sknetwork.linkpred.**HubPromotedIndex**
Link prediction by Hub Promoted Index:

$$s(i,j) = \frac{2|\Gamma_i \cap \Gamma_j|}{min(|\Gamma_i|, |\Gamma_j|)}.$$

Variables

- **indptr_** (*np.ndarray*) – Pointer index for neighbors.
- **indices_** (*np.ndarray*) – Concatenation of neighbors.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> hpi = HubPromotedIndex()
>>> similarities = hpi.fit_predict(adjacency, 0)
>>> similarities.round(2)
array([1. , 0.5, 0.5, 0.5, 0.5])
>>> similarities = hpi.predict([0, 1])
>>> similarities.round(2)
array([[1.  , 0.5 , 0.5 , 0.5 , 0.5 ],
       [0.5 , 1.  , 0.  , 1.  , 0.33]])
>>> similarities = hpi.predict((0, 1))
>>> similarities.round(2)
0.5
>>> similarities = hpi.predict([(0, 1), (1, 2)])
>>> similarities.round(2)
array([0.5, 0. ])
```

References

Ravasz, E., Somera, A. L., Mongru, D. A., Oltvai, Z. N., & Barabási, A. L. (2002). Hierarchical organization of modularity in metabolic networks. science, 297(5586), 1551-1555.

fit (*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*)
Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph

Returns **self**

Return type FirstOrder

fit_predict (*adjacency*, *query*)
Fit algorithm to data and compute scores for requested edges.

predict (*query: Union[int, Iterable, Tuple]*)
Compute similarity scores.

Parameters **query** (*int, list, array or Tuple*) –

- If int i, return the similarities s(i, j) for all j.
- If list or array integers, return s(i, j) for i in query, for all j as array.
- If tuple (i, j), return the similarity s(i, j).
- If list of tuples or array of shape (n_queries, 2), return s(i, j) for (i, j) in query as array.

Returns **predictions** – The prediction scores.

Return type int, float or array

class sknetwork.linkpred.**HubDepressedIndex**
Link prediction by Hub Depressed Index:

$$s(i,j) = \frac{2|\Gamma_i \cap \Gamma_j|}{max(|\Gamma_i|, |\Gamma_j|)}.$$

Variables

- **indptr_** (*np.ndarray*) – Pointer index for neighbors.

- **indices_** (*np.ndarray*) – Concatenation of neighbors.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> hdi = HubDepressedIndex()
>>> similarities = hdi.fit_predict(adjacency, 0)
>>> similarities.round(2)
array([1.  , 0.33, 0.5 , 0.5 , 0.33])
>>> similarities = hdi.predict([0, 1])
>>> similarities.round(2)
array([[1.  , 0.33, 0.5 , 0.5 , 0.33],
       [0.33, 1.  , 0.  , 0.67, 0.33]])
>>> similarities = hdi.predict((0, 1))
>>> similarities.round(2)
0.33
>>> similarities = hdi.predict([(0, 1), (1, 2)])
>>> similarities.round(2)
array([0.33, 0.  ])
```

References

Ravasz, E., Somera, A. L., Mongru, D. A., Oltvai, Z. N., & Barabási, A. L. (2002). Hierarchical organization of modularity in metabolic networks. science, 297(5586), 1551-1555.

fit (*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*)
Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph

Returns **self**

Return type FirstOrder

fit_predict (*adjacency*, *query*)
Fit algorithm to data and compute scores for requested edges.

predict (*query: Union[int, Iterable, Tuple]*)
Compute similarity scores.

Parameters **query** (*int, list, array or Tuple*) –

- If int i, return the similarities s(i, j) for all j.
- If list or array integers, return s(i, j) for i in query, for all j as array.
- If tuple (i, j), return the similarity s(i, j).
- If list of tuples or array of shape (n_queries, 2), return s(i, j) for (i, j) in query as array.

Returns **predictions** – The prediction scores.

Return type int, float or array

class sknetwork.linkpred.**AdamicAdar**
Link prediction by Adamic-Adar index:

$$s(i,j) = \sum_{z \in \Gamma_i \cap \Gamma_j} \frac{1}{\log |\Gamma_z|}.$$

Variables

- **indptr_** (*np.ndarray*) – Pointer index for neighbors.
- **indices_** (*np.ndarray*) – Concatenation of neighbors.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> aa = AdamicAdar()
>>> similarities = aa.fit_predict(adjacency, 0)
>>> similarities.round(2)
array([1.82, 0.91, 0.91, 0.91, 0.91])
>>> similarities = aa.predict([0, 1])
>>> similarities.round(2)
array([[1.82, 0.91, 0.91, 0.91, 0.91],
       [0.91, 3.8 , 0.  , 2.35, 1.44]])
>>> similarities = aa.predict((0, 1))
>>> similarities.round(2)
0.91
>>> similarities = aa.predict([(0, 1), (1, 2)])
>>> similarities.round(2)
array([0.91, 0.  ])
```

References

Adamic, L. A., & Adar, E. (2003). Friends and neighbors on the web. Social networks, 25(3), 211-230.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*)
Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph

Returns self

Return type FirstOrder

fit_predict(*adjacency*, *query*)
Fit algorithm to data and compute scores for requested edges.

predict(*query: Union[int, Iterable, Tuple]*)
Compute similarity scores.

Parameters **query** (*int, list, array or Tuple*) –

- If int i, return the similarities s(i, j) for all j.
- If list or array integers, return s(i, j) for i in query, for all j as array.
- If tuple (i, j), return the similarity s(i, j).
- If list of tuples or array of shape (n_queries, 2), return s(i, j) for (i, j) in query as array.

Returns **predictions** – The prediction scores.

Return type int, float or array

class sknetwork.linkpred.**ResourceAllocation**
Link prediction by Resource Allocation index:

$$s(i,j) = \sum_{z \in \Gamma_i \cap \Gamma_j} \frac{1}{|\Gamma_z|}.$$

Variables

- **indptr_** (*np.ndarray*) – Pointer index for neighbors.
- **indices_** (*np.ndarray*) – Concatenation of neighbors.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> ra = ResourceAllocation()
>>> similarities = ra.fit_predict(adjacency, 0)
>>> similarities.round(2)
array([0.67, 0.33, 0.33, 0.33, 0.33])
>>> similarities = ra.predict([0, 1])
>>> similarities.round(2)
array([[0.67, 0.33, 0.33, 0.33, 0.33],
       [0.33, 1.33, 0.  , 0.83, 0.5 ]])
>>> similarities = ra.predict((0, 1))
>>> similarities.round(2)
0.33
>>> similarities = ra.predict([(0, 1), (1, 2)])
>>> similarities.round(2)
array([0.33, 0.  ])
```

References

Zhou, T., Lü, L., & Zhang, Y. C. (2009). Predicting missing links via local information. The European Physical Journal B, 71(4), 623-630.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*)
Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph

Returns **self**

Return type FirstOrder

fit_predict(*adjacency*, *query*)
Fit algorithm to data and compute scores for requested edges.

predict(*query: Union[int, Iterable, Tuple]*)
Compute similarity scores.

Parameters **query** (*int, list, array or Tuple*) –

- If int i, return the similarities s(i, j) for all j.
- If list or array integers, return s(i, j) for i in query, for all j as array.
- If tuple (i, j), return the similarity s(i, j).
- If list of tuples or array of shape (n_queries, 2), return s(i, j) for (i, j) in query as array.

Returns **predictions** – The prediction scores.

Return type int, float or array

class sknetwork.linkpred.**PreferentialAttachment**

Link prediction by Preferential Attachment index:

$s(i, j) = |\Gamma_i||\Gamma_j|$.

Variables

- **indptr_** (*np.ndarray*) – Pointer index for neighbors.
- **indices_** (*np.ndarray*) – Concatenation of neighbors.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> pa = PreferentialAttachment()
>>> similarities = pa.fit_predict(adjacency, 0)
>>> similarities
array([4, 6, 4, 4, 6], dtype=int32)
>>> similarities = pa.predict([0, 1])
>>> similarities
array([[4, 6, 4, 4, 6],
       [6, 9, 6, 6, 9]], dtype=int32)
>>> similarities = pa.predict((0, 1))
>>> similarities
6
>>> similarities = pa.predict([(0, 1), (1, 2)])
>>> similarities
array([6, 6], dtype=int32)
```

References

Albert, R., Barabási, L. (2002). Statistical mechanics of complex networks Reviews of Modern Physics.

fit(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*)

Fit algorithm to the data.

Parameters **adjacency** – Adjacency matrix of the graph

Returns **self**

Return type FirstOrder

fit_predict(*adjacency*, *query*)

Fit algorithm to data and compute scores for requested edges.

predict(*query: Union[int, Iterable, Tuple]*)

Compute similarity scores.

Parameters **query** (*int, list, array or Tuple*) –

- If int i, return the similarities s(i, j) for all j.
- If list or array integers, return s(i, j) for i in query, for all j as array.
- If tuple (i, j), return the similarity s(i, j).
- If list of tuples or array of shape (n_queries, 2), return s(i, j) for (i, j) in query as array.

Returns **predictions** – The prediction scores.

Return type int, float or array

Post-processing

sknetwork.linkpred.**is_edge**(*adjacency: scipy.sparse.csr.csr_matrix*, *query: Union[int, Iterable, Tuple]*) → Union[bool, numpy.ndarray]

Given a query, return whether each edge is actually in the adjacency.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **query** (*int, Iterable or Tuple*) –
  - If int i, queries (i, j) for all j.
  - If Iterable of integers, return queries (i, j) for i in query, for all j.
  - If tuple (i, j), queries (i, j).
  - If list of tuples or array of shape (n_queries, 2), queries (i, j) in for each line in query.

Returns **y_true** – For each element in the query, returns `True` if the edge exists in the adjacency and `False` otherwise.

Return type Union[bool, np.ndarray]

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> is_edge(adjacency, 0)
array([False,  True, False, False,  True])
>>> is_edge(adjacency, [0, 1])
array([[False,  True, False, False,  True],
       [ True, False,  True, False,  True]])
>>> is_edge(adjacency, (0, 1))
True
>>> is_edge(adjacency, [(0, 1), (0, 2)])
array([ True, False])
```

sknetwork.linkpred.**whitened_sigmoid**(*scores: numpy.ndarray*)

Map the entries of a score array to probabilities through

$$\frac{1}{1+\exp(-(x-\mu)/\sigma)},$$

where μ and σ are respectively the mean and standard deviation of x.

Parameters **scores** (*np.ndarray*) – The input array

Returns **probas** – Array with entries between 0 and 1.

Return type np.ndarray

Examples

```
>>> probas = whitened_sigmoid(np.array([1, 5, 0.25]))
>>> probas.round(2)
array([0.37, 0.8 , 0.29])
>>> probas = whitened_sigmoid(np.array([2, 2, 2]))
>>> probas
array([1, 1, 1])
```

3.2.11 Linear algebra

Tools of linear algebra.

Polynomes

class sknetwork.linalg.**Polynome**(**args*, ***kwargs*)

Polynome of an adjacency matrix as a linear operator

$P(A) = \alpha_k A^k + ... + \alpha_1 A + \alpha_0$.

Parameters

- **adjacency** – Adjacency matrix of the graph
- **coeffs** (*np.ndarray*) – Coefficients of the polynome by increasing order of power.

Examples

```
>>> from scipy import sparse
>>> from sknetwork.linalg import Polynome
>>> adjacency = sparse.eye(2, format='csr')
>>> polynome = Polynome(adjacency, np.arange(3))
>>> x = np.ones(2)
>>> polynome.dot(x)
array([3., 3.])
>>> polynome.T.dot(x)
array([3., 3.])
```

Notes

The polynome is evaluated using the Ruffini-Horner method.

property H

Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

property T
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

adjoint()
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

dot(*x*)
Matrix-matrix or matrix-vector multiplication.

Parameters **x** (*array_like*) – 1-d or 2-d array, representing a vector or matrix.

Returns **Ax** – 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

Return type array

matmat(*X*)
Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters **X** (*{matrix, ndarray}*) – An array with shape (N,K).

Returns **Y** – A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Return type {matrix, ndarray}

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

matvec(*x*)
Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** (*{matrix, ndarray}*) – An array with shape (N,) or (N,1).

Returns **y** – A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

rmatmat(X)
Adjoint matrix-matrix multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array, or 2-d array. The default implementation defers to the adjoint.

Parameters **X** (*{matrix, ndarray}*) – A matrix or 2D array.

Returns **Y** – A matrix or 2D array depending on the type of the input.

Return type {matrix, ndarray}

Notes

This rmatmat wraps the user-specified rmatmat routine.

rmatvec(x)
Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** (*{matrix, ndarray}*) – An array with shape (M,) or (M,1).

Returns **y** – A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

transpose()
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

Sparse + Low Rank

class sknetwork.linalg.**SparseLR**(**args*, ***kwargs*)
Class for matrices with "sparse + low rank" structure. Example:

$A + xy^T$

Parameters

- **sparse_mat** (*scipy.spmatrix*) – Sparse component. Is converted to csr format automatically.
- **low_rank_tuples** (*list*) – Single tuple of arrays of list of tuples, representing the low rank components [(x1, y1), (x2, y2),...]. Each low rank component is of the form xy^T.

Examples

```
>>> from scipy import sparse
>>> from sknetwork.linalg import SparseLR
>>> adjacency = sparse.eye(2, format='csr')
>>> slr = SparseLR(adjacency, (np.ones(2), np.ones(2)))
>>> x = np.ones(2)
>>> slr.dot(x)
array([3., 3.])
>>> slr.sum(axis=0)
array([3., 3.])
>>> slr.sum(axis=1)
array([3., 3.])
>>> slr.sum()
6.0
```

References

De Lara (2019). The Sparse + Low Rank trick for Matrix Factorization-Based Graph Algorithms. Proceedings of the 15th International Workshop on Mining and Learning with Graphs (MLG).

property H
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

property T
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

adjoint()
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

astype(*dtype: Union[str, numpy.dtype]*)
Change dtype of the object.

dot(*x*)
Matrix-matrix or matrix-vector multiplication.

Parameters **x** (*array_like*) – 1-d or 2-d array, representing a vector or matrix.

Returns **Ax** – 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

Return type array

left_sparse_dot(*matrix: scipy.sparse.csr.csr_matrix*)
Left dot product with a sparse matrix.

matmat(*X*)
Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters **X** ({*matrix, ndarray*}) – An array with shape (N,K).

Returns **Y** – A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Return type {matrix, ndarray}

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

matvec(*x*)
Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** ({*matrix, ndarray*}) – An array with shape (N,) or (N,1).

Returns **y** – A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

right_sparse_dot(*matrix: scipy.sparse.csr.csr_matrix*)
Right dot product with a sparse matrix.

rmatmat(*X*)
Adjoint matrix-matrix multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array, or 2-d array. The default implementation defers to the adjoint.

Parameters **X** ({*matrix, ndarray*}) – A matrix or 2D array.

Returns **Y** – A matrix or 2D array depending on the type of the input.

Return type {matrix, ndarray}

Notes

This rmatmat wraps the user-specified rmatmat routine.

rmatvec(*x*)
Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** (*{matrix, ndarray}*) – An array with shape (M,) or (M,1).

Returns **y** – A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

sum(*axis=None*)
Row-wise, column-wise or total sum of operator's coefficients.

Parameters **axis** – If 0, return column-wise sum. If 1, return row-wise sum. Otherwise, return total sum.

transpose()
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

Operators

class sknetwork.linalg.**RegularizedAdjacency**(**args*, ***kwargs*)
Regularized adjacency matrix as a Scipy LinearOperator.

The regularized adjacency is formally defined as $A_\alpha = A + \alpha 1 1^T$, or $A_\alpha = A + \alpha d^+ (d^-)^T$ where α is the regularization parameter.

Parameters

- **adjacency** – *Adjacency* matrix of the graph.
- **regularization** (*float*) – Constant implicitly added to all entries of the adjacency matrix.
- **degree_mode** (*bool*) – If *True*, the regularization parameter for entry (i, j) is scaled by out-degree of node i and in-degree of node j. If *False*, the regularization parameter is applied to all entries.

Examples

```
>>> from sknetwork.data import star_wars
>>> biadjacency = star_wars(metadata=False)
>>> biadj_reg = RegularizedAdjacency(biadjacency, 0.1, degree_mode=True)
>>> biadj_reg.dot(np.ones(3))
array([3.6, 1.8, 5.4, 3.6])
```

property H
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

property T
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

adjoint()
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

astype(*dtype: Union[str, numpy.dtype]*)
Change dtype of the object.

dot(*x*)
Matrix-matrix or matrix-vector multiplication.

Parameters **x** (*array_like*) – 1-d or 2-d array, representing a vector or matrix.

Returns **Ax** – 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

Return type array

left_sparse_dot(*matrix: scipy.sparse.csr.csr_matrix*)
Left dot product with a sparse matrix.

matmat(*X*)
Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters **X** (*{matrix, ndarray}*) – An array with shape (N,K).

Returns **Y** – A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Return type {matrix, ndarray}

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

matvec(*x*)
Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** ({*matrix, ndarray*}) – An array with shape (N,) or (N,1).

Returns **y** – A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

right_sparse_dot(*matrix: scipy.sparse.csr.csr_matrix*)
Right dot product with a sparse matrix.

rmatmat(*X*)
Adjoint matrix-matrix multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array, or 2-d array. The default implementation defers to the adjoint.

Parameters **X** ({*matrix, ndarray*}) – A matrix or 2D array.

Returns **Y** – A matrix or 2D array depending on the type of the input.

Return type {matrix, ndarray}

Notes

This rmatmat wraps the user-specified rmatmat routine.

rmatvec(*x*)
Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** ({*matrix, ndarray*}) – An array with shape (M,) or (M,1).

Returns **y** – A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

sum(*axis=None*)
Row-wise, column-wise or total sum of operator's coefficients.

Parameters **axis** – If 0, return column-wise sum. If 1, return row-wise sum. Otherwise, return total sum.

transpose()
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

class sknetwork.linalg.**LaplacianOperator**(**args*, ***kwargs*)
Regularized Laplacian matrix as a Scipy LinearOperator.

The Laplacian operator is then defined as $L = D - A$.

Parameters

- **adjacency** – *Adjacency* matrix of the graph.
- **regularization** (*float*) – Constant implicitly added to all entries of the adjacency matrix.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> laplacian = LaplacianOperator(adjacency, 0.1)
>>> laplacian.dot(np.ones(adjacency.shape[1]))
array([0., 0., 0., 0., 0.])
```

property H
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

property T
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

adjoint()
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

astype(*dtype: Union[str, numpy.dtype]*)
Change dtype of the object.

dot(*x*)
Matrix-matrix or matrix-vector multiplication.

Parameters **x** (*array_like*) – 1-d or 2-d array, representing a vector or matrix.

Returns **Ax** – 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

Return type array

matmat(*X*)
Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters **X** (*{matrix, ndarray}*) – An array with shape (N,K).

Returns **Y** – A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Return type {matrix, ndarray}

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

matvec(*x*)
Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** (*{matrix, ndarray}*) – An array with shape (N,) or (N,1).

Returns **y** – A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

rmatmat(*X*)
Adjoint matrix-matrix multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array, or 2-d array. The default implementation defers to the adjoint.

Parameters **X** (*{matrix, ndarray}*) – A matrix or 2D array.

Returns **Y** – A matrix or 2D array depending on the type of the input.

Return type {matrix, ndarray}

Notes

This rmatmat wraps the user-specified rmatmat routine.

rmatvec(*x*)

Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** (*{matrix, ndarray}*) – An array with shape (M,) or (M,1).

Returns **y** – A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

transpose()

Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

class sknetwork.linalg.**NormalizedAdjacencyOperator**(**args*, ***kwargs*)

Regularized normalized adjacency matrix as a Scipy LinearOperator.

The normalized adjacency operator is then defined as $\bar{A} = D^{-1/2}AD^{-1/2}$.

Parameters

- **adjacency** – *Adjacency* matrix of the graph.
- **regularization** (*float*) – Constant implicitly added to all entries of the adjacency matrix.

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> adj_norm = NormalizedAdjacencyOperator(adjacency, 0.)
>>> x = np.sqrt(adjacency.dot(np.ones(5)))
>>> np.allclose(x, adj_norm.dot(x))
True
```

property H

Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

property T
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

adjoint()
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

astype(*dtype: Union[str, numpy.dtype]*)
Change dtype of the object.

dot(*x*)
Matrix-matrix or matrix-vector multiplication.

Parameters **x** (*array_like*) – 1-d or 2-d array, representing a vector or matrix.

Returns **Ax** – 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

Return type array

matmat(*X*)
Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters **X** (*{matrix, ndarray}*) – An array with shape (N,K).

Returns **Y** – A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Return type {matrix, ndarray}

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

matvec(*x*)
Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** (*{matrix, ndarray}*) – An array with shape (N,) or (N,1).

Returns **y** – A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

rmatmat(*X*)

Adjoint matrix-matrix multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array, or 2-d array. The default implementation defers to the adjoint.

Parameters **X** ({*matrix, ndarray*}) – A matrix or 2D array.

Returns **Y** – A matrix or 2D array depending on the type of the input.

Return type {matrix, ndarray}

Notes

This rmatmat wraps the user-specified rmatmat routine.

rmatvec(*x*)

Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** ({*matrix, ndarray*}) – An array with shape (M,) or (M,1).

Returns **y** – A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

transpose()

Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

class sknetwork.linalg.**CoNeighborOperator**(**args*, ***kwargs*)

Co-neighborhood adjacency as a LinearOperator.

- Graphs
- Digraphs
- Bigraphs

$\tilde{A} = AF^{-1}A^T$, or $\tilde{B} = BF^{-1}B^T$.

where F is a weight matrix.

Parameters

- **adjacency** – Adjacency or biadjacency of the input graph.

- **normalized** – If `True`, F is the diagonal in-degree matrix $F = \text{diag}(A^T 1)$. Otherwise, F is the identity matrix.

Examples

```
>>> from sknetwork.data import star_wars
>>> biadjacency = star_wars(metadata=False)
>>> d_out = biadjacency.dot(np.ones(3))
>>> coneigh = CoNeighborOperator(biadjacency)
>>> np.allclose(d_out, coneigh.dot(np.ones(4)))
True
```

property H
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

property T
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

adjoint()
Hermitian adjoint.

Returns the Hermitian adjoint of self, aka the Hermitian conjugate or Hermitian transpose. For a complex matrix, the Hermitian adjoint is equal to the conjugate transpose.

Can be abbreviated self.H instead of self.adjoint().

Returns **A_H** – Hermitian adjoint of self.

Return type LinearOperator

astype(*dtype: Union[str, numpy.dtype]*)
Change dtype of the object.

dot(*x*)
Matrix-matrix or matrix-vector multiplication.

Parameters **x** (*array_like*) – 1-d or 2-d array, representing a vector or matrix.

Returns **Ax** – 1-d or 2-d array (depending on the shape of x) that represents the result of applying this linear operator on x.

Return type array

left_sparse_dot(*matrix: scipy.sparse.csr.csr_matrix*)
Left dot product with a sparse matrix

matmat(*X*)
Matrix-matrix multiplication.

Performs the operation y=A*X where A is an MxN linear operator and X dense N*K matrix or ndarray.

Parameters **X** ({*matrix, ndarray*}) – An array with shape (N,K).

Returns **Y** – A matrix or ndarray with shape (M,K) depending on the type of the X argument.

Return type {matrix, ndarray}

Notes

This matmat wraps any user-specified matmat routine or overridden _matmat method to ensure that y has the correct type.

matvec(*x*)

Matrix-vector multiplication.

Performs the operation y=A*x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** ({*matrix, ndarray*}) – An array with shape (N,) or (N,1).

Returns **y** – A matrix or ndarray with shape (M,) or (M,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This matvec wraps the user-specified matvec routine or overridden _matvec method to ensure that y has the correct shape and type.

right_sparse_dot(*matrix: scipy.sparse.csr.csr_matrix*)

Right dot product with a sparse matrix

rmatmat(*X*)

Adjoint matrix-matrix multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array, or 2-d array. The default implementation defers to the adjoint.

Parameters **X** ({*matrix, ndarray*}) – A matrix or 2D array.

Returns **Y** – A matrix or 2D array depending on the type of the input.

Return type {matrix, ndarray}

Notes

This rmatmat wraps the user-specified rmatmat routine.

rmatvec(*x*)

Adjoint matrix-vector multiplication.

Performs the operation y = A^H * x where A is an MxN linear operator and x is a column vector or 1-d array.

Parameters **x** ({*matrix, ndarray*}) – An array with shape (M,) or (M,1).

Returns **y** – A matrix or ndarray with shape (N,) or (N,1) depending on the type and shape of the x argument.

Return type {matrix, ndarray}

Notes

This rmatvec wraps the user-specified rmatvec routine or overridden _rmatvec method to ensure that y has the correct shape and type.

transpose()
Transpose this linear operator.

Returns a LinearOperator that represents the transpose of this one. Can be abbreviated self.T instead of self.transpose().

Solvers

class sknetwork.linalg.**LanczosEig**(*which='LM'*, *maxiter: int = None*, *tol: float = 0.0*)
Eigenvalue solver using Lanczos method.

Parameters

- **which** (*str*) – Which eigenvectors and eigenvalues to find:
  - 'LM' : Largest (in magnitude) eigenvalues.
  - 'SM' : Smallest (in magnitude) eigenvalues.
- **maxiter** (*int*) – Maximum number of Arnoldi update iterations allowed. Default: n*10.
- **tol** (*float*) – Relative accuracy for eigenvalues (stopping criterion). The default value of 0 implies machine precision.

Variables

- **eigenvectors_** (*np.ndarray*) – Two-dimensional array, each column is an eigenvector of the input.
- **eigenvalues_** (*np.ndarray*) – Eigenvalues associated to each eigenvector.

See also:

scipy.sparse.linalg.eigsh

fit(*matrix: Union[scipy.sparse.csr.csr_matrix, scipy.sparse.linalg.interface.LinearOperator]*, *n_components: int*, *v0: numpy.ndarray = None*)
Perform eigenvalue decomposition on symmetric input matrix.

Parameters

- **matrix** – Matrix to decompose.
- **n_components** (*int*) – Number of eigenvectors to compute
- **v0** (*np.ndarray*) – Starting vector for iteration. Default: random.

Returns self

Return type EigSolver

class sknetwork.linalg.**HalkoEig**(*which='LM'*, *n_oversamples: int = 10*, *n_iter='auto'*, *power_iteration_normalizer: Optional[str] = 'auto'*, *random_state=None*, *one_pass: bool = False*)
Eigenvalue solver using Halko's randomized method.

Parameters

- **which** (*str*) – Which eigenvectors and eigenvalues to find:
  - 'LM' : Largest (in magnitude) eigenvalues.

  - `'SM'` : Smallest (in magnitude) eigenvalues.

- **n_oversamples** (*int (default=10)*) – Additional number of random vectors to sample the range of `matrix` so as to ensure proper conditioning. The total number of random vectors used to find the range of `matrix` is `n_components + n_oversamples`. Smaller number can improve speed but can negatively impact the quality of approximation of singular vectors and singular values.
- **n_iter** (*int or 'auto' (default is 'auto')*) – See `randomized_range_finder()`
- **power_iteration_normalizer** (`'auto'` (default), `'QR'`, `'LU'`, `None`) – See `randomized_range_finder()`
- **random_state** (*int, RandomState instance or None, optional (default=None)*) – See `randomized_range_finder()`
- **one_pass** (*bool (default=False)*) – whether to use algorithm 5.6 instead of 5.3. 5.6 requires less access to the original matrix, while 5.3 is more accurate.

fit(*matrix: Union[scipy.sparse.csr.csr_matrix, scipy.sparse.linalg.interface.LinearOperator, sknetwork.linalg.sparse_lowrank.SparseLR]*, *n_components: int*)
Perform eigenvalue decomposition on input matrix.

Parameters

- **matrix** – Matrix to decompose.
- **n_components** (*int*) – Number of eigenvectors to compute

Returns self

Return type `EigSolver`

class `sknetwork.linalg.`**LanczosSVD**(*maxiter: int = None*, *tol: float = 0.0*)
SVD solver using Lanczos method on AA^T or A^TA.

Parameters

- **maxiter** (*int*) – Maximum number of Arnoldi update iterations allowed. Default: n*10.
- **tol** (*float*) – Relative accuracy for eigenvalues (stopping criterion). The default value of 0 implies machine precision.

Variables

- **singular_vectors_left_** (*np.ndarray*) – Two-dimensional array, each column is a left singular vector of the input.
- **singular_vectors_right_** (*np.ndarray*) – Two-dimensional array, each column is a right singular vector of the input.
- **singular_values_** (*np.ndarray*) – Singular values.

See also:

`scipy.sparse.linalg.svds`

fit(*matrix: Union[scipy.sparse.csr.csr_matrix, scipy.sparse.linalg.interface.LinearOperator]*, *n_components: int*, *v0: numpy.ndarray = None*)
Perform singular value decomposition on input matrix.

Parameters

- **matrix** – Matrix to decompose.
- **n_components** (*int*) – Number of singular values to compute

- **v0** (*np.ndarray*) – Starting vector for iteration. Default: random.

Returns self

Return type SVDSolver

class sknetwork.linalg.**HalkoSVD**(*n_oversamples: int = 10*, *n_iter='auto'*, *transpose='auto'*, *power_iteration_normalizer: Optional[str] = 'auto'*, *flip_sign: bool = True*, *random_state=None*)

SVD solver using Halko's randomized method.

Parameters

- **n_oversamples** (*int (default=10)*) – Additional number of random vectors to sample the range of M so as to ensure proper conditioning. The total number of random vectors used to find the range of M is n_components + n_oversamples. Smaller number can improve speed but can negatively impact the quality of approximation of singular vectors and singular values.
- **n_iter** (*int or 'auto' (default is 'auto')*) – See randomized_range_finder()
- **power_iteration_normalizer** ('auto' (default), 'QR', 'LU', None) – See randomized_range_finder()
- **transpose** (*True, False or 'auto' (default)*) – Whether the algorithm should be applied to matrix.T instead of matrix. The result should approximately be the same. The 'auto' mode will trigger the transposition if matrix.shape[1] > matrix.shape[0] since this implementation of randomized SVD tends to be a little faster in that case.
- **flip_sign** (*boolean, (default=True)*) – The output of a singular value decomposition is only unique up to a permutation of the signs of the singular vectors. If *flip_sign* is set to *True*, the sign ambiguity is resolved by making the largest loadings for each component in the left singular vectors positive.
- **random_state** (*int, RandomState instance or None, optional (default=None)*) – See randomized_range_finder()

Variables

- **singular_vectors_left_** (*np.ndarray*) – Two-dimensional array, each column is a left singular vector of the input.
- **singular_vectors_right_** (*np.ndarray*) – Two-dimensional array, each column is a right singular vector of the input.
- **singular_values_** (*np.ndarray*) – Singular values.

fit(*matrix: Union[scipy.sparse.csr.csr_matrix, scipy.sparse.linalg.interface.LinearOperator, sknetwork.linalg.sparse_lowrank.SparseLR]*, *n_components: int*)

Perform singular value decomposition on input matrix.

Parameters

- **matrix** – Matrix to decompose.
- **n_components** (*int*) – Number of singular values to compute

Returns self

Return type SVDSolver

sknetwork.linalg.ppr_solver.**get_pagerank**(*adjacency: Union[scipy.sparse.csr.csr_matrix, scipy.sparse.linalg.interface.LinearOperator], seeds: numpy.ndarray, damping_factor: float, n_iter: int, tol: float = 1e-06, solver: str = 'piteration'*) → numpy.ndarray

Solve the Pagerank problem. Formally,

$x = \alpha P x + (1 - \alpha) y$,

where $P = (D^{-1}A)^T$ is the transition matrix and y is the personalization probability vector.

Parameters

- **adjacency** (*sparse.csr_matrix*) – Adjacency matrix of the graph.
- **seeds** (*np.ndarray*) – Personalization array. Must be a valid probability vector.
- **damping_factor** (*float*) – Probability to continue the random walk.
- **n_iter** (*int*) – Number of iterations for some of the solvers such as `'piteration'` or `'diteration'`.
- **tol** (*float*) – Tolerance for the convergence of some solvers such as `'bicgstab'` or `'lanczos'`.
- **solver** (str) – Which solver to use: `'piteration'`, `'diteration'`, `'bicgstab'`, `'lanczos'`, *'RH'*`.

Returns **pagerank** – Probability vector.

Return type np.ndarray

Examples

```
>>> from sknetwork.data import house
>>> adjacency = house()
>>> seeds = np.array([1, 0, 0, 0, 0])
>>> scores = get_pagerank(adjacency, seeds, damping_factor=0.85, n_iter=10)
>>> np.round(scores, 2)
array([0.29, 0.24, 0.12, 0.12, 0.24])
```

References

- Hong, D. (2012). Optimized on-line computation of pagerank algorithm. arXiv preprint arXiv:1202.6158.
- Van der Vorst, H. A. (1992). Bi-CGSTAB: A fast and smoothly converging variant of Bi-CG for the solution of nonsymmetric linear systems. SIAM Journal on scientific and Statistical Computing, 13(2), 631-644.
- Lanczos, C. (1950). An iteration method for the solution of the eigenvalue problem of linear differential and integral operators. Los Angeles, CA: United States Governm. Press Office.

Randomized methods

sknetwork.linalg.randomized_methods.**randomized_range_finder**(*matrix: numpy.ndarray*, *size: int*, *n_iter: int*, *power_iteration_normalizer='auto'*, *random_state=None*, *return_all: bool = False*) → Union[numpy.ndarray, Tuple[numpy.ndarray, numpy.ndarray, numpy.ndarray]]

Compute an orthonormal matrix Q, whose range approximates the range of the input matrix.

$A \approx QQ^*A$.

Parameters

- **matrix** – Input matrix
- **size** – Size of the return array
- **n_iter** – Number of power iterations. It can be used to deal with very noisy problems. When 'auto', it is set to 4, unless `size` is small (< .1 * min(matrix.shape)) in which case `n_iter` is set to 7. This improves precision with few components.
- **power_iteration_normalizer** (`'auto'` (default), `'QR'`, `'LU'`, `None`) – Whether the power iterations are normalized with step-by-step QR factorization (the slowest but most accurate), `None` (the fastest but numerically unstable when `n_iter` is large, e.g. typically 5 or larger), or `'LU'` factorization (numerically stable but can lose slightly in accuracy). The `'auto'` mode applies no normalization if `n_iter` <= 2 and switches to `'LU'` otherwise.
- **random_state** (int, RandomState instance or `None`, optional (default= `None`)) – The seed of the pseudo random number generator to use when shuffling the data. If int, random_state is the seed used by the random number generator; If RandomState instance, random_state is the random number generator; If `None`, the random number generator is the RandomState instance used by *np.random*.
- **return_all** (*if True, returns (range_matrix, random_matrix, random_proj)*) – else returns range_matrix.

Returns

- **range_matrix** (*np.ndarray*) – matrix (size x size) projection matrix, the range of which approximates well the range of the input matrix.
- **random_matrix** (*np.ndarray, optional*) – projection matrix
- **projected_matrix** (*np.ndarray, optional*) – product between the data and the projection matrix

Notes

Follows Algorithm 4.3 of Finding structure with randomness: Stochastic algorithms for constructing approximate matrix decompositions Halko, et al., 2009 (arXiv:909)

sknetwork.linalg.**randomized_svd**(*matrix*, *n_components: int*, *n_oversamples: int = 10*, *n_iter='auto'*, *transpose='auto'*, *power_iteration_normalizer: Optional[str] = 'auto'*, *flip_sign: bool = True*, *random_state=None*)

Truncated randomized SVD

Parameters

- **matrix** (*ndarray or sparse matrix*) – Matrix to decompose
- **n_components** (*int*) – Number of singular values and vectors to extract.
- **n_oversamples** (*int (default=10)*) – Additional number of random vectors to sample the range of M so as to ensure proper conditioning. The total number of random vectors used to find the range of M is n_components + n_oversamples. Smaller number can improve speed but can negatively impact the quality of approximation of singular vectors and singular values.
- **n_iter** (*int or 'auto' (default is 'auto')*) – See `randomized_range_finder()`
- **power_iteration_normalizer** (`'auto'` (default), `'QR'`, `'LU'`, `None`) – See `randomized_range_finder()`
- **transpose** (*True, False or 'auto' (default)*) – Whether the algorithm should be applied to `matrix.T` instead of `matrix`. The result should approximately be the same. The 'auto' mode will trigger the transposition if `matrix.shape[1] > matrix.shape[0]` since this implementation of randomized SVD tends to be a little faster in that case.
- **flip_sign** (*boolean, (default=True)*) – The output of a singular value decomposition is only unique up to a permutation of the signs of the singular vectors. If *flip_sign* is set to *True*, the sign ambiguity is resolved by making the largest loadings for each component in the left singular vectors positive.
- **random_state** (*int, RandomState instance or None, optional (default=None)*) – See `randomized_range_finder()`

Returns

- **left_singular_vectors** (*np.ndarray*)
- **singular_values** (*np.ndarray*)
- **right_singular_vectors** (*np.ndarray*)

Notes

This algorithm finds a (usually very good) approximate truncated singular value decomposition using randomization to speed up the computations. It is particularly fast on large matrices on which you wish to extract only a small number of components. In order to obtain further speed up, `n_iter` can be set <=2 (at the cost of loss of precision).

References

- Finding structure with randomness: Stochastic algorithms for constructing approximate matrix decompositions Halko, et al., 2009 http://arxiv.org/abs/arXiv:0909.4061 (algorithm 5.1)
- A randomized algorithm for the decomposition of matrices Per-Gunnar Martinsson, Vladimir Rokhlin and Mark Tygert
- An implementation of a randomized algorithm for principal component analysis A. Szlam et al. 2014

`sknetwork.linalg.`**`randomized_eig`**(*matrix*, *n_components: int*, *which='LM'*, *n_oversamples: int = 10*, *n_iter='auto'*, *power_iteration_normalizer: Optional[str] = 'auto'*, *random_state=None*, *one_pass: bool = False*)

Truncated randomized eigenvalue decomposition.

Parameters

- **`matrix`** (*ndarray or sparse matrix*) – Matrix to decompose
- **`n_components`** (*int*) – Number of singular values and vectors to extract.
- **`which`** (*str*) – which eigenvalues to compute. `'LM'` for Largest Magnitude and `'SM'` for Smallest Magnitude. Any other entry will result in Largest Magnitude.
- **`n_oversamples`** (*int (default=10)*) – Additional number of random vectors to sample the range of `matrix` so as to ensure proper conditioning. The total number of random vectors used to find the range of `matrix` is `n_components + n_oversamples`. Smaller number can improve speed but can negatively impact the quality of approximation of singular vectors and singular values.
- **`n_iter`** (*int or 'auto' (default is 'auto')*) – See `randomized_range_finder()`
- **`power_iteration_normalizer`** (`'auto'` (default), `'QR'`, `'LU'`, `None`) – See `randomized_range_finder()`
- **`random_state`** (*int, RandomState instance or None, optional (default=None)*) – See `randomized_range_finder()`
- **`one_pass`** (*bool (default=False)*) – whether to use algorithm 5.6 instead of 5.3. 5.6 requires less access to the original matrix, while 5.3 is more accurate.

Returns

- **eigenvalues** (*np.ndarray*)
- **eigenvectors** (*np.ndarray*)

References

Finding structure with randomness: Stochastic algorithms for constructing approximate matrix decompositions Halko, et al., 2009 http://arxiv.org/abs/arXiv:0909.4061

Miscellaneous

sknetwork.linalg.**diag_pinv**(*weights: numpy.ndarray*) → scipy.sparse.csr.csr_matrix

Compute $W^+ = \text{diag}(w)^+$, the pseudo inverse of the diagonal matrix with diagonal the weights w.

Parameters **weights** – The weights to invert.

Returns W^+

Return type sparse.csr_matrix

sknetwork.linalg.**normalize**(*matrix: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray, scipy.sparse.linalg.interface.LinearOperator]*, *p=1*)

Normalize rows of a matrix. Null rows remain null.

Parameters

- **matrix** – Input matrix.
- **p** – Order of the norm

Returns **normalized matrix**

Return type same as input

3.2.12 Utils

Various tools.

Build graphs

sknetwork.utils.**edgelist2adjacency**(*edgelist: list*, *undirected: bool = False*) → scipy.sparse.csr.csr_matrix

Build an adjacency matrix from a list of edges.

Parameters

- **edgelist** (*list*) – List of edges as pairs (i, j) or triplets (i, j, w) for weighted edges.
- **undirected** (*bool*) – If `True`, return a symmetric adjacency.

Returns **adjacency**

Return type sparse.csr_matrix

Examples

```
>>> edgelist = [(0, 1), (1, 2), (2, 0)]
>>> adjacency = edgelist2adjacency(edgelist)
>>> adjacency.shape, adjacency.nnz
((3, 3), 3)
>>> adjacency = edgelist2adjacency(edgelist, undirected=True)
>>> adjacency.shape, adjacency.nnz
((3, 3), 6)
>>> weighted_edgelist = [(0, 1, 0.2), (1, 2, 4), (2, 0, 1.3)]
>>> adjacency = edgelist2adjacency(weighted_edgelist)
>>> adjacency.dtype
dtype('float64')
```

sknetwork.utils.**edgelist2biadjacency**(*edgelist: list*) → scipy.sparse.csr.csr_matrix

Build a biadjacency matrix from a list of edges.

Parameters **edgelist** (*list*) – List of edges as pairs (i, j) or triplets (i, j, w) for weighted edges.

Returns **biadjacency**

Return type sparse.csr_matrix

Examples

```
>>> edgelist = [(0, 0), (1, 0), (1, 1), (2, 1)]
>>> biadjacency = edgelist2biadjacency(edgelist)
>>> biadjacency.shape, biadjacency.nnz
((3, 2), 4)
>>> weighted_edgelist = [(0, 0, 0.5), (1, 0, 1), (1, 1, 1), (2, 1, 2)]
>>> biadjacency = edgelist2biadjacency(weighted_edgelist)
>>> biadjacency.dtype
dtype('float64')
```

Convert graphs

sknetwork.utils.**bipartite2directed**(*biadjacency: Union[scipy.sparse.csr.csr_matrix, sknetwork.linalg.sparse_lowrank.SparseLR]*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.linalg.sparse_lowrank.SparseLR]

Adjacency matrix of the directed graph associated with a bipartite graph (with edges from one part to the other).

The returned adjacency matrix is:

$$A = \begin{bmatrix} 0 & B \\ 0 & 0 \end{bmatrix}$$

where B is the biadjacency matrix.

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns Adjacency matrix (same format as input).

Return type adjacency

sknetwork.utils.**bipartite2undirected**(*biadjacency: Union[scipy.sparse.csr.csr_matrix, sknetwork.linalg.sparse_lowrank.SparseLR]*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.linalg.sparse_lowrank.SparseLR]

Adjacency matrix of a bigraph defined by its biadjacency matrix.

The returned adjacency matrix is:

$$A = \begin{bmatrix} 0 & B \\ B^T & 0 \end{bmatrix}$$

where B is the biadjacency matrix of the bipartite graph.

Parameters **biadjacency** – Biadjacency matrix of the graph.

Returns Adjacency matrix (same format as input).

Return type adjacency

sknetwork.utils.**directed2undirected**(*adjacency: Union[scipy.sparse.csr.csr_matrix, sknetwork.linalg.sparse_lowrank.SparseLR]*, *weighted: bool = True*) → Union[scipy.sparse.csr.csr_matrix, sknetwork.linalg.sparse_lowrank.SparseLR]

Adjacency matrix of the undirected graph associated with some directed graph.

The new adjacency matrix becomes either:

$A + A^T$ (default)

or

$\max(A, A^T)$

If the initial adjacency matrix A is binary, bidirectional edges have weight 2 (first method, default) or 1 (second method).

Parameters

- **adjacency** – Adjacency matrix.
- **weighted** – If `True`, return the sum of the weights in both directions of each edge.

Returns New adjacency matrix (same format as input).

Return type new_adjacency

Clustering

sknetwork.utils.**membership_matrix**(*labels: numpy.ndarray*, *dtype=<class 'bool'>*, *n_labels: Optional[int] = None*) → scipy.sparse.csr.csr_matrix

Build a n x k matrix of the label assignments, with k the number of labels. Negative labels are ignored.

Parameters

- **labels** – Label of each node.
- **dtype** – Type of the entries. Boolean by default.
- **n_labels** (*int*) – Number of labels.

Returns **membership** – Binary matrix of label assignments.

Return type sparse.csr_matrix

Notes

The inverse operation is simply `labels = membership.indices`.

class sknetwork.utils.**KMeansDense**(*n_clusters: int = 8*, *init: str = '++'*, *n_init: int = 10*, *tol: float = 0.0001*)

Standard KMeansDense clustering based on SciPy function `kmeans2`.

Parameters

- **n_clusters** – Number of desired clusters.
- **init** – Method for initialization. Available methods are 'random', 'points', '++' and 'matrix': * 'random': generate k centroids from a Gaussian with mean and variance estimated from the data. * 'points': choose k observations (rows) at random from data for the initial centroids. * '++': choose k observations accordingly to the kmeans++ method (careful seeding) * 'matrix': interpret the k parameter as a k by M (or length k array for one-dimensional data) array of initial centroids.
- **n_init** – Number of iterations of the k-means algorithm to run.
- **tol** – Relative tolerance with regards to inertia to declare convergence.

Variables

- **labels_** – Label of each sample.
- **cluster_centers_** – A 'k' by 'N' array of centroids found at the last iteration of k-means.

References

- MacQueen, J. (1967, June). Some methods for classification and analysis of multivariate observations. In Proceedings of the fifth Berkeley symposium on mathematical statistics and probability (Vol. 1, No. 14, pp. 281-297).
- Arthur, D., & Vassilvitskii, S. (2007, January). k-means++: The advantages of careful seeding. In Proceedings of the eighteenth annual ACM-SIAM symposium on Discrete algorithms (pp. 1027-1035). Society for Industrial and Applied Mathematics.

fit(*x: numpy.ndarray*) → sknetwork.utils.kmeans.KMeansDense

Fit algorithm to the data.

Parameters **x** – Data to cluster.

Returns **self**

Return type *KMeansDense*

fit_transform(*x: numpy.ndarray*) → numpy.ndarray

Fit algorithm to the data and return the labels.

Parameters **x** – Data to cluster.

Returns **labels**

Return type np.ndarray

class sknetwork.utils.**WardDense**

Hierarchical clustering by the Ward method based on SciPy.

Variables **dendrogram_** (*np.ndarray (n - 1, 4)*) – Dendrogram.

References

- Ward, J. H., Jr. (1963). Hierarchical grouping to optimize an objective function. Journal of the American Statistical Association, 58, 236–244.
- Murtagh, F., & Contreras, P. (2012). Algorithms for hierarchical clustering: an overview. Wiley Interdisciplinary Reviews: Data Mining and Knowledge Discovery, 2(1), 86-97.

fit (*x: numpy.ndarray*) → sknetwork.utils.ward.WardDense
Apply algorithm to a dense matrix.

Parameters **x** – Data to cluster.

Returns **self**

Return type *WardDense*

fit_transform (*x: numpy.ndarray*) → numpy.ndarray
Apply algorithm to a dense matrix and return the dendrogram.

Parameters **x** – Data to cluster.

Returns **dendrogram**

Return type np.ndarray

Nearest-neighbors

class sknetwork.utils.**KNNDense**(*n_neighbors: int = 5*, *undirected: bool = False*, *leaf_size: int = 16*, *p=2*, *eps: float = 0.01*, *n_jobs=1*)
Extract adjacency from vector data through k-nearest-neighbor search with KD-Tree.

Parameters

- **n_neighbors** – Number of neighbors for each sample in the transformed sparse graph.
- **undirected** – As the nearest neighbor relationship is not symmetric, the graph is directed by default. Setting this parameter to `True` forces the algorithm to return undirected graphs.
- **leaf_size** – Leaf size passed to KDTree. This can affect the speed of the construction and query, as well as the memory required to store the tree.
- **p** – Which Minkowski p-norm to use. 1 is the sum-of-absolute-values "Manhattan" distance, 2 is the usual Euclidean distance infinity is the maximum-coordinate-difference distance. A finite large p may cause a ValueError if overflow can occur.
- **eps** – Return approximate nearest neighbors; the k-th returned value is guaranteed to be no further than (1+tol_nn) times the distance to the real k-th nearest neighbor.
- **n_jobs** – Number of jobs to schedule for parallel processing. If -1 is given all processors are used.

Variables **adjacency_** – Adjacency matrix of the graph.

References

Maneewongvatana, S., & Mount, D. M. (1999, December). It's okay to be skinny, if your friends are fat. In Center for Geometric Computing 4th Annual Workshop on Computational Geometry (Vol. 2, pp. 1-8).

fit(*x: numpy.ndarray*) → sknetwork.utils.knn.KNNDense
Fit algorithm to the data.

Parameters **x** – Data to transform into adjacency.

Returns self

Return type *KNNDense*

fit_transform(*x: numpy.ndarray*) → scipy.sparse.csr.csr_matrix
Fit algorithm to the data and return the computed adjacency.

Parameters **x** (*np.ndarray*) – Input data.

Returns adjacency

Return type sparse.csr_matrix

make_undirected()
Modifies the adjacency to match desired constrains.

class sknetwork.utils.**CNNDense**(*n_neighbors: int = 1*, *undirected: bool = False*)
Extract adjacency from vector data through component-wise k-nearest-neighbor search. KNN is applied independently on each column of the input matrix.

Parameters

- **n_neighbors** – Number of neighbors per dimension.
- **undirected** – As the nearest neighbor relationship is not symmetric, the graph is directed by default. Setting this parameter to `True` forces the algorithm to return undirected graphs.

Variables **adjacency_** – Adjacency matrix of the graph.

fit(*x: numpy.ndarray*) → sknetwork.utils.knn.CNNDense
Fit algorithm to the data.

Parameters **x** – Data to transform into adjacency.

Returns self

Return type *CNNDense*

fit_transform(*x: numpy.ndarray*) → scipy.sparse.csr.csr_matrix
Fit algorithm to the data and return the computed adjacency.

Parameters **x** (*np.ndarray*) – Input data.

Returns adjacency

Return type sparse.csr_matrix

make_undirected()
Modifies the adjacency to match desired constrains.

Co-Neighborhood

sknetwork.utils.**co_neighbor_graph**(*adjacency: Union[scipy.sparse.csr.csr_matrix, numpy.ndarray]*, *normalized: bool = True*, *method='knn'*, *n_neighbors: int = 5*, *n_components: int = 8*) → scipy.sparse.csr.csr_matrix

Compute the co-neighborhood adjacency.

- Graphs
- Digraphs
- Bigraphs

$\tilde{A} = AF^{-1}A^T$,

where F is a weight matrix.

Parameters

- **adjacency** – Adjacency of the input graph.
- **normalized** – If `True`, F is the diagonal in-degree matrix $F = \text{diag}(A^T 1)$. Otherwise, F is the identity matrix.
- **method** – Either `'exact'` or `'knn'`. If 'exact' the output is computed with matrix multiplication. However, the density can be much higher than in the input graph and this can trigger Memory errors. If `'knn'`, the co-neighborhood is approximated through KNNDense-search in an appropriate spectral embedding space.
- **n_neighbors** – Number of neighbors for the KNNDense search. Only useful if `method='knn'`.
- **n_components** – Dimension of the embedding space. Only useful if `method='knn'`.

Returns **adjacency** – Adjacency of the co-neighborhood.

Return type sparse.csr_matrix

Projection

sknetwork.utils.**projection_simplex**(*x: Union[numpy.ndarray, scipy.sparse.csr.csr_matrix]*, *scale: float = 1.0*)

Project each line of the input onto the Euclidean simplex i.e. solve

$\min_w ||w - x_i||_2^2$ s.t. $\sum w_j = z, w_j \geq 0$.

Parameters

- **x** – Data to project. Either one or two dimensional. Can be sparse or dense.
- **scale** (*float*) – Scale of the simplex i.e. sums of the projected coefficients.

Returns **projection** – Array with the same type and shape as the input.

Return type np.ndarray or sparse.csr_matrix

Example

```
>>> X = np.array([[2, 2], [-0.75, 0.25]])
>>> projection_simplex(X)
array([[0.5, 0.5],
       [0. , 1. ]])
>>> X_csr = sparse.csr_matrix(X)
>>> X_proj = projection_simplex(X_csr)
>>> X_proj.nnz
3
>>> X_proj.toarray()
array([[0.5, 0.5],
       [0. , 1. ]])
```

References

Duchi, J., Shalev-Shwartz, S., Singer, Y., & Chandra, T. (2008, July). Efficient projections onto the l 1-ball for learning in high dimensions. In Proceedings of the 25th international conference on Machine learning (pp. 272-279). ACM.

sknetwork.utils.**projection_simplex_array**(*array: numpy.ndarray*, *scale: float = 1*) → numpy.ndarray

Project each line of the input onto the Euclidean simplex i.e. solve

$\min_w ||w - x_i||_2^2$ s.t. $\sum w_j = z, w_j \geq 0$.

Parameters

- **array** (*np.ndarray*) – Data to project. Either one or two dimensional.
- **scale** (*float*) – Scale of the simplex i.e. sums of the projected coefficients.

Returns **projection** – Array with the same shape as the input.

Return type np.ndarray

Example

```
>>> X = np.array([[2, 2], [-0.75, 0.25]])
>>> projection_simplex_array(X)
array([[0.5, 0.5],
       [0. , 1. ]])
```

sknetwork.utils.**projection_simplex_csr**(*matrix: scipy.sparse.csr.csr_matrix*, *scale: float = 1*)

Project each line of the input onto the Euclidean simplex i.e. solve

$\min_w ||w - x_i||_2^2$ s.t. $\sum w_j = z, w_j \geq 0$.

Parameters

- **matrix** (*sparse.csr_matrix*) – Matrix whose rows must be projected.
- **scale** (*float*) – Scale of the simplex i.e. sums of the projected coefficients.

Returns **projection** – Matrix with the same shape as the input.

Return type sparse.csr_matrix

Examples

```
>>> X = sparse.csr_matrix(np.array([[2, 2], [-0.75, 0.25]]))
>>> X_proj = projection_simplex_csr(X)
>>> X_proj.nnz
3
>>> X_proj.toarray()
array([[0.5, 0.5],
       [0. , 1. ]])
```

3.2.13 Visualization

Visualization tools.

Graphs

sknetwork.visualization.graphs.**svg_graph**(*adjacency: Optional[scipy.sparse.csr.csr_matrix] = None*, *position: Optional[numpy.ndarray] = None*, *names: Optional[numpy.ndarray] = None*, *labels: Optional[Iterable] = None*, *scores: Optional[Iterable] = None*, *membership: Optional[scipy.sparse.csr.csr_matrix] = None*, *seeds: Union[list, dict] = None*, *width: Optional[float] = 400*, *height: Optional[float] = 300*, *margin: float = 20*, *margin_text: float = 3*, *scale: float = 1*, *node_order: Optional[numpy.ndarray] = None*, *node_size: float = 7*, *node_size_min: float = 1*, *node_size_max: float = 20*, *display_node_weight: bool = False*, *node_weights: Optional[numpy.ndarray] = None*, *node_width: float = 1*, *node_width_max: float = 3*, *node_color: str = 'gray'*, *display_edges: bool = True*, *edge_labels: Optional[list] = None*, *edge_width: float = 1*, *edge_width_min: float = 0.5*, *edge_width_max: float = 20*, *display_edge_weight: bool = True*, *edge_color: Optional[str] = None*, *label_colors: Optional[Iterable] = None*, *font_size: int = 12*, *directed: bool = False*, *filename: Optional[str] = None*) → str

Return SVG image of a graph.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **position** – Positions of the nodes.
- **names** – Names of the nodes.
- **labels** – Labels of the nodes (negative values mean no label).
- **scores** – Scores of the nodes (measure of importance).
- **membership** – Membership of the nodes (label distribution).

- **seeds** – Nodes to be highlighted (if dict, only keys are considered).
- **width** – Width of the image.
- **height** – Height of the image.
- **margin** – Margin of the image.
- **margin_text** – Margin between node and text.
- **scale** – Multiplicative factor on the dimensions of the image.
- **node_order** – Order in which nodes are displayed.
- **node_size** – Size of nodes.
- **node_size_min** – Minimum size of a node.
- **node_size_max** – Maximum size of a node.
- **node_width** – Width of node circle.
- **node_width_max** – Maximum width of node circle.
- **node_color** – Default color of nodes (svg color).
- **display_node_weight** – If `True`, display node weights through node size.
- **node_weights** – Node weights (used only if **display_node_weight** is `True`).
- **display_edges** – If `True`, display edges.
- **edge_labels** – Labels of the edges, as a list of tuples (source, destination, label)
- **edge_width** – Width of edges.
- **edge_width_min** – Minimum width of edges.
- **edge_width_max** – Maximum width of edges.
- **display_edge_weight** – If `True`, display edge weights through edge widths.
- **edge_color** – Default color of edges (svg color).
- **label_colors** – Colors of the labels (svg colors).
- **font_size** – Font size.
- **directed** – If `True`, considers the graph as directed.
- **filename** – Filename for saving image (optional).

Returns **image** – SVG image.

Return type str

Example

```
>>> from sknetwork.data import karate_club
>>> graph = karate_club(True)
>>> adjacency = graph.adjacency
>>> position = graph.position
>>> from sknetwork.visualization import svg_graph
>>> image = svg_graph(adjacency, position)
>>> image[1:4]
'svg'
```

sknetwork.visualization.graphs.**svg_digraph**(*adjacency: Optional[scipy.sparse.csr.csr_matrix] = None*, *position: Optional[numpy.ndarray] = None*, *names: Optional[numpy.ndarray] = None*, *labels: Optional[Iterable] = None*, *scores: Optional[Iterable] = None*, *membership: Optional[scipy.sparse.csr.csr_matrix] = None*, *seeds: Union[list, dict] = None*, *width: Optional[float] = 400*, *height: Optional[float] = 300*, *margin: float = 20*, *margin_text: float = 10*, *scale: float = 1*, *node_order: Optional[numpy.ndarray] = None*, *node_size: float = 7*, *node_size_min: float = 1*, *node_size_max: float = 20*, *display_node_weight: bool = False*, *node_weights: Optional[numpy.ndarray] = None*, *node_width: float = 1*, *node_width_max: float = 3*, *node_color: str = 'gray'*, *display_edges: bool = True*, *edge_labels: Optional[list] = None*, *edge_width: float = 1*, *edge_width_min: float = 0.5*, *edge_width_max: float = 5*, *display_edge_weight: bool = True*, *edge_color: Optional[str] = None*, *label_colors: Optional[Iterable] = None*, *font_size: int = 12*, *filename: Optional[str] = None*) → str

Return SVG image of a digraph.

Parameters

- **adjacency** – Adjacency matrix of the graph.
- **position** – Positions of the nodes.
- **names** – Names of the nodes.
- **labels** – Labels of the nodes (negative values mean no label).
- **scores** – Scores of the nodes (measure of importance).
- **membership** – Membership of the nodes (label distribution).
- **seeds** – Nodes to be highlighted (if dict, only keys are considered).
- **width** – Width of the image.
- **height** – Height of the image.
- **margin** – Margin of the image.
- **margin_text** – Margin between node and text.
- **scale** – Multiplicative factor on the dimensions of the image.
- **node_order** – Order in which nodes are displayed.
- **node_size** – Size of nodes.
- **node_size_min** – Minimum size of a node.
- **node_size_max** – Maximum size of a node.
- **display_node_weight** – If `True`, display node in-weights through node size.

- **node_weights** – Node weights (used only if **display_node_weight** is `True`).
- **node_width** – Width of node circle.
- **node_width_max** – Maximum width of node circle.
- **node_color** – Default color of nodes (svg color).
- **display_edges** – If `True`, display edges.
- **edge_labels** – Labels of the edges, as a list of tuples (source, destination, label)
- **edge_width** – Width of edges.
- **edge_width_min** – Minimum width of edges.
- **edge_width_max** – Maximum width of edges.
- **display_edge_weight** – If `True`, display edge weights through edge widths.
- **edge_color** – Default color of edges (svg color).
- **label_colors** – Colors of the labels (svg color).
- **font_size** – Font size.
- **filename** – Filename for saving image (optional).

Returns **image** – SVG image.

Return type str

Example

```
>>> from sknetwork.data import painters
>>> graph = painters(True)
>>> adjacency = graph.adjacency
>>> position = graph.position
>>> from sknetwork.visualization import svg_digraph
>>> image = svg_graph(adjacency, position)
>>> image[1:4]
'svg'
```

sknetwork.visualization.graphs.**svg_bigraph**(*biadjacency: scipy.sparse.csr.csr_matrix*, *names_row: Optional[numpy.ndarray] = None*, *names_col: Optional[numpy.ndarray] = None*, *labels_row: Optional[Union[numpy.ndarray, dict]] = None*, *labels_col: Optional[Union[numpy.ndarray, dict]] = None*, *scores_row: Optional[Union[numpy.ndarray, dict]] = None*, *scores_col: Optional[Union[numpy.ndarray, dict]] = None*, *membership_row: Optional[scipy.sparse.csr.csr_matrix] = None*, *membership_col: Optional[scipy.sparse.csr.csr_matrix] = None*, *seeds_row: Union[list, dict] = None*, *seeds_col: Union[list, dict] = None*, *position_row: Optional[numpy.ndarray] = None*, *position_col: Optional[numpy.ndarray] = None*, *reorder: bool = True*, *width: Optional[float] = 400*, *height: Optional[float] = 300*, *margin: float = 20*, *margin_text: float = 3*, *scale: float = 1*, *node_size: float = 7*, *node_size_min: float = 1*, *node_size_max: float = 20*, *display_node_weight: bool = False*, *node_weights_row: Optional[numpy.ndarray] = None*, *node_weights_col: Optional[numpy.ndarray] = None*, *node_width: float = 1*, *node_width_max: float = 3*, *color_row: str = 'gray'*, *color_col: str = 'gray'*, *label_colors: Optional[Iterable] = None*, *display_edges: bool = True*, *edge_labels: Optional[list] = None*, *edge_width: float = 1*, *edge_width_min: float = 0.5*, *edge_width_max: float = 10*, *edge_color: str = 'black'*, *display_edge_weight: bool = True*, *font_size: int = 12*, *filename: Optional[str] = None*) → str

Return SVG image of a bigraph.

Parameters

- **biadjacency** – Biadjacency matrix of the graph.
- **names_row** – Names of the rows.
- **names_col** – Names of the columns.
- **labels_row** – Labels of the rows (negative values mean no label).
- **labels_col** – Labels of the columns (negative values mean no label).
- **scores_row** – Scores of the rows (measure of importance).
- **scores_col** – Scores of the columns (measure of importance).
- **membership_row** – Membership of the rows (label distribution).
- **membership_col** – Membership of the columns (label distribution).
- **seeds_row** – Rows to be highlighted (if dict, only keys are considered).

- **seeds_col** – Columns to be highlighted (if dict, only keys are considered).
- **position_row** – Positions of the rows.
- **position_col** – Positions of the columns.
- **reorder** – Use clustering to order nodes.
- **width** – Width of the image.
- **height** – Height of the image.
- **margin** – Margin of the image.
- **margin_text** – Margin between node and text.
- **scale** – Multiplicative factor on the dimensions of the image.
- **node_size** – Size of nodes.
- **node_size_min** – Minimum size of nodes.
- **node_size_max** – Maximum size of nodes.
- **display_node_weight** – If `True`, display node weights through node size.
- **node_weights_row** – Weights of rows (used only if **display_node_weight** is `True`).
- **node_weights_col** – Weights of columns (used only if **display_node_weight** is `True`).
- **node_width** – Width of node circle.
- **node_width_max** – Maximum width of node circle.
- **color_row** – Default color of rows (svg color).
- **color_col** – Default color of cols (svg color).
- **label_colors** – Colors of the labels (svg color).
- **display_edges** – If `True`, display edges.
- **edge_labels** – Labels of the edges, as a list of tuples (source, destination, label)
- **edge_width** – Width of edges.
- **edge_width_min** – Minimum width of edges.
- **edge_width_max** – Maximum width of edges.
- **display_edge_weight** – If `True`, display edge weights through edge widths.
- **edge_color** – Default color of edges (svg color).
- **font_size** – Font size.
- **filename** – Filename for saving image (optional).

Returns **image** – SVG image.

Return type str

Example

```
>>> from sknetwork.data import movie_actor
>>> biadjacency = movie_actor()
>>> from sknetwork.visualization import svg_bigraph
>>> image = svg_bigraph(biadjacency)
>>> image[1:4]
'svg'
```

Dendrograms

sknetwork.visualization.dendrograms.**svg_dendrogram**(*dendrogram: numpy.ndarray*, *names: Optional[numpy.ndarray] = None*, *rotate: bool = False*, *width: float = 400*, *height: float = 300*, *margin: float = 10*, *margin_text: float = 5*, *scale: float = 1*, *line_width: float = 2*, *n_clusters: int = 2*, *color: str = 'black'*, *colors: Optional[Iterable] = None*, *font_size: int = 12*, *reorder: bool = False*, *rotate_names: bool = True*, *filename: Optional[str] = None*)

Return SVG image of a dendrogram.

Parameters

- **dendrogram** – Dendrogram to display.
- **names** – Names of leaves.
- **rotate** – If `True`, rotate the tree so that the root is on the left.
- **width** – Width of the image (margins excluded).
- **height** – Height of the image (margins excluded).
- **margin** – Margin.
- **margin_text** – Margin between leaves and their names, if any.
- **scale** – Scaling factor.
- **line_width** – Line width.
- **n_clusters** – Number of coloured clusters to display.
- **color** – Default SVG color for the dendrogram.
- **colors** – SVG colors of the clusters of the dendrogram (optional).
- **font_size** – Font size.
- **reorder** – If `True`, reorder leaves so that left subtree has more leaves than right subtree.
- **rotate_names** – If `True`, rotate names of leaves (only valid if **rotate** is `False`).
- **filename** – Filename for saving image (optional).

Example

```
>>> dendrogram = np.array([[0, 1, 1, 2], [2, 3, 2, 3]])
>>> from sknetwork.visualization import svg_dendrogram
>>> image = svg_dendrogram(dendrogram)
>>> image[1:4]
'svg'
```

3.3 Getting started

In scikit-network, graphs are represented by their adjacency matrix in the Compressed Sparse Row format of SciPy.

In this tutorial, we present a few methods to instantiate such inputs.

[1]:
```
from IPython.display import SVG

import numpy as np
from scipy import sparse

from sknetwork.utils import edgelist2adjacency, edgelist2biadjacency
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

3.3.1 From a NumPy array

For small graphs, you can instantiate the adjacency matrix as a dense NumPy array and convert it into a sparse matrix in CSR format.

[2]:
```
adjacency = np.array([[0, 1, 1, 0], [1, 0, 1, 1], [1, 1, 0, 0], [0, 1, 0, 0]])
adjacency = sparse.csr_matrix(adjacency)

image = svg_graph(adjacency)
SVG(image)
```

[2]:

3.3.2 From an edge list

Another natural way to build a graph is from a list of edges.

[3]:
```
edgelist = [(0, 1), (1, 2), (2, 3), (3, 0), (0, 2)]
adjacency = edgelist2adjacency(edgelist)

image = svg_digraph(adjacency)
SVG(image)
```

[3]:

By default, the graph is treated as directed, but you can easily make it undirected.

[4]:
```
adjacency = edgelist2adjacency(edgelist, undirected=True)

image = svg_graph(adjacency)
SVG(image)
```

[4]:

You might also want to add weights to your edges. Just use triplets instead of pairs!

[5]:
```
edgelist = [(0, 1, 1), (1, 2, 0.5), (2, 3, 1), (3, 0, 0.5), (0, 2, 2)]
adjacency = edgelist2adjacency(edgelist)

image = svg_digraph(adjacency)
SVG(image)
```

[5]:

You can instantiate a bipartite graph as well.

[6]:
```
edgelist = [(0, 0), (1, 0), (1, 1), (2, 1)]
biadjacency = edgelist2biadjacency(edgelist)

image = svg_bigraph(biadjacency)
SVG(image)
```

[6]:

3.3.3 From a NetworkX object

NetworkX has import and export functions from and towards the CSR format.

3.3.4 Other options

- You have a TSV file containing a list of edges
- You have a GraphML file
- You want to test our toy graphs
- You want to generate a graph from a model
- You want to load a graph from one of our referenced repositories (see NetSets and KONECT)

Take a look at the tutorials of the **data** section !

3.4 Data

3.4.1 Toy graphs

This notebook shows how to load some toy graphs.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import house, bow_tie, karate_club, miserables, painters,␣
↪hourglass, star_wars, movie_actor
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

House graph

[4]:
```
graph = house(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[5]:
```
image = svg_graph(adjacency, position, scale=0.5)
```

[6]:
```
SVG(image)
```

[6]:

[7]:
```
# adjacency matrix only
adjacency = house()
```

Bow tie

[8]:
```
graph = bow_tie(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[9]:
```
image = svg_graph(adjacency, position, scale=0.5)
```

[10]:
```
SVG(image)
```

[10]:

Karate club

[11]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels = graph.labels
```

[12]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[13]:
```
SVG(image)
```

[13]:

Les Miserables

[14]:
```
graph = miserables(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

[15]:
```
image = svg_graph(adjacency, position, names, scale=2)
```

[16]:
```
SVG(image)
```

[16]:

Digraphs

[17]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[18]:
```
image = svg_digraph(adjacency, position, names)
```

[19]:
```
SVG(image)
```

[19]:

Bigraphs

Star wars

[20]:
```
graph = star_wars(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[21]:
```
image = svg_bigraph(biadjacency, names_row, names_col)
```

[22]:
```
SVG(image)
```

[22]:

[23]:
```
# biadjacency matrix only
biadjacency = star_wars()
```

Movie-actor

[24]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[25]:
```
image = svg_bigraph(biadjacency, names_row, names_col)
```

[26]:
```
SVG(image)
```

[26]:

3.4.2 Models

This notebook shows how to load some graphs based on simple models.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import erdos_renyi, block_model, linear_graph, cyclic_graph,␣
↪linear_digraph, cyclic_digraph, grid, albert_barabasi, watts_strogatz
from sknetwork.visualization import svg_graph, svg_digraph
```

Graphs

Erdos-Renyi model

[4]:
```
adjacency = erdos_renyi(20, 0.2)
```

[5]:
```
image = svg_graph(adjacency)
```

[6]:
```
SVG(image)
```

[6]:

Stochastic block model

[7]:
```
graph = block_model([20,25,30], p_in=[0.5,0.4,0.3], p_out=0.02, metadata=True)
adjacency = graph.adjacency
labels = graph.labels
```

[8]:
```
image = svg_graph(adjacency, labels=labels)
```

[9]:
```
SVG(image)
```

[9]:

Linear graph

[10]:
```
graph = linear_graph(8, metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[11]:
```
image = svg_graph(adjacency, position)
```

[12]:
```
SVG(image)
```

[12]:

[13]:
```
# adjacency matrix only
adjacency = linear_graph(8)
```

Cyclic graph

[14]:
```
graph = cyclic_graph(8, metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[15]:
```
image = svg_graph(adjacency, position, width=200, height=200)
```

[16]:
```
SVG(image)
```

[16]:

Grid

[17]:
```
graph = grid(6, 4, metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[18]:
```
image = svg_graph(adjacency, position)
```

[19]:
```
SVG(image)
```
[19]:

Albert-Barabasi model

[20]:
```
adjacency = albert_barabasi(n=100, degree=3)
```

[21]:
```
image = svg_graph(adjacency, labels={i:0 for i in range(3)}, display_node_weight=True,
↪ node_order=np.flip(np.arange(100)))
```

[22]:
```
SVG(image)
```
[22]:

Watts-Strogatz model

[23]:
```
adjacency = watts_strogatz(n=100, degree=6, prob=0.2)
```

[24]:
```
image = svg_graph(adjacency, display_node_weight=True, node_size_max=10)
```

[25]:
```
SVG(image)
```
[25]:

Digraphs

Linear graph

[26]:
```
graph = linear_digraph(8, metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[27]:
```
image = svg_digraph(adjacency, position)
```

[28]:
```
SVG(image)
```
[28]:

Cyclic graph

[29]:
```
graph = cyclic_digraph(8, metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[30]:
```
image = svg_digraph(adjacency, position, width=200, height=200)
```

[31]:
```
SVG(image)
```

[31]:

3.4.3 Load

This tutorial shows how to load graphs from files in various formats and from existing collections of datasets, NetSets and Konect.

[1]:
```
from sknetwork.data import load_edge_list, load_graphml, load_netset, load_konect
```

TSV files

Loading a graph from a TSV file (list of edges).

[2]:
```
graph = load_edge_list('miserables.tsv')
adjacency = graph.adjacency
names = graph.names
```

[3]:
```
# Digraph
graph = load_edge_list('painters.tsv', directed=True)
adjacency = graph.adjacency
names = graph.names
```

[4]:
```
# Bigraph
graph = load_edge_list('movie_actor.tsv', bipartite=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

GraphML files

Loading a graph from a GraphML file.

[5]:
```
graph = load_graphml('miserables.graphml')
adjacency = graph.adjacency
names = graph.names
```

[6]:
```
# Digraph
graph = load_graphml('painters.graphml')
adjacency = graph.adjacency
names = graph.names
```

NetSet

Loading a graph from the NetSets collection.

[7]:
```
graph = load_netset('openflights')
adjacency = graph.adjacency
names = graph.names
```

[8]:
```
# to get all fields
graph
```

[8]:
```
{'adjacency': <3097x3097 sparse matrix of type '<class 'numpy.int64'>'
        with 36386 stored elements in Compressed Sparse Row format>,
 'names': array(['Goroka Airport', 'Madang Airport', 'Mount Hagen Kagamuga Airport',
        ..., 'Saumlaki/Olilit Airport', 'Tarko-Sale Airport',
        'Alashankou Bole (Bortala) airport'], dtype='<U65'),
 'meta': {'name': 'openflights',
  'description': 'Airports with daily number of flights between them.',
  'source': 'https://openflights.org'},
 'position': array([[145.39199829,  -6.08168983],
        [145.78900147,  -5.20707989],
        [144.29600525,  -5.82678986],
        ...,
        [131.30599976,  -7.98860979],
        [ 77.81809998,  64.93080139],
        [ 82.3       ,  44.895     ]])}
```

[9]:
```
# Digraph
graph = load_netset('wikivitals')
adjacency = graph.adjacency
names = graph.names
labels = graph.labels
```

[10]:
```
# Bigraph
graph = load_netset('cinema')
biadjacency = graph.biadjacency
```

Konect

Loading a graph from the Konect collection.

[11]:
```
# first check server availability!
# graph = load_konect('dolphins')
# adjacency = graph.adjacency
```

3.4.4 Save

This notebooks shows how to save and load graphs.

[1]:
```
import numpy as np
from scipy import sparse
```

[2]:
```
from sknetwork.data import Bunch, load, save
```

[3]:
```
# random graph
adjacency = sparse.csr_matrix(np.random.random((10, 10)) < 0.2)
```

[4]:
```
# names
names = list('abcdefghij')
```

[5]:
```
graph = Bunch()
graph.adjacency = adjacency
graph.names = np.array(names)
```

[6]:
```
save('mygraph', graph)
```

[7]:
```
graph = load('mygraph')
```

[8]:
```
graph
```

[8]:
```
{'adjacency': <10x10 sparse matrix of type '<class 'numpy.bool_'>'
        with 17 stored elements in Compressed Sparse Row format>,
 'names': array(['a', 'b', 'c', 'd', 'e', 'f', 'g', 'h', 'i', 'j'], dtype='<U1')}
```

3.5 Topology

3.5.1 Connected components

This notebook illustrates the search for connected components in graphs.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.topology import connected_components
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
from sknetwork.utils.format import bipartite2undirected
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[5]:
```
# subgraph
k = 15
adjacency = adjacency[:k][:,:k]
position = position[:k]
```

[6]:
```
labels = connected_components(adjacency)
```

[7]:
```
image = svg_graph(adjacency, position, labels=labels)
SVG(image)
```

[7]:

Digraphs

[8]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[9]:
```
labels = connected_components(adjacency)
```

[10]:
```
image = svg_digraph(adjacency, position, names, labels)
SVG(image)
```

[10]:

[11]:
```
labels = connected_components(adjacency, connection='strong')
```

[12]:
```
image = svg_digraph(adjacency, position, names, labels)
SVG(image)
```

[12]:

Bigraphs

[13]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[14]:
```
# subgraph
k = 5
biadjacency = biadjacency[k:]
names_row = names_row[k:]
```

[15]:
```
adjacency = bipartite2undirected(biadjacency)
```

[16]:
```
labels = connected_components(adjacency)
```

[17]:
```
n_row, _ = biadjacency.shape
labels_row = labels[:n_row]
labels_col = labels[n_row:]
```

[18]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col)
```

[19]:
```
SVG(image)
```

[19]:

3.5.2 Core decomposition

This notebook illustrates the k-core decomposition of graphs.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters
from sknetwork.topology import CoreDecomposition
from sknetwork.visualization import svg_graph, svg_digraph
from sknetwork.utils import directed2undirected
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[5]:
```
core = CoreDecomposition()
```

[6]:
```
labels = core.fit_transform(adjacency)
```

[7]:
```
image = svg_graph(adjacency, position, scores=labels)
SVG(image)
```

[7]:

Digraphs

[8]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[9]:
```
labels = core.fit_transform(directed2undirected(adjacency))
```

[10]:
```
image = svg_digraph(adjacency, position, names, scores=labels)
SVG(image)
```

[10]:

3.5.3 Triangles and cliques

This notebook illustrates clique counting and evaluation of the clustering coefficient of a graph.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club
from sknetwork.topology import Triangles, Cliques
from sknetwork.visualization import svg_graph
```

Triangles

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[5]:
```
image = svg_graph(adjacency, position)
SVG(image)
```

[5]:

[6]:
```
triangles = Triangles()
```

[7]:
```
triangles.fit_transform(adjacency)
```

[7]:
```
45
```

[8]:
```
np.round(triangles.clustering_coef_, 2)
```

[8]:
```
0.26
```

Cliques

[9]:
```
cliques = Cliques(4)
```

[10]:
```
cliques.fit_transform(adjacency)
```

[10]:
```
11
```

3.5.4 Graph isomorphism

This notebook illustrates the Weisfeiler-Lehman test of isomorphism.

[1]:
```
from IPython.display import SVG

from sknetwork.data import house
from sknetwork.topology import WeisfeilerLehman, are_isomorphic
from sknetwork.visualization import svg_graph
```

Graph labeling

[2]:
```
graph = house(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[3]:
```
weisfeiler_lehman = WeisfeilerLehman()
labels = weisfeiler_lehman.fit_transform(adjacency)
```

[4]:
```
image = svg_graph(adjacency, position, labels=labels)
SVG(image)
```

[4]:

[5]:
```
# first iteration
weisfeiler_lehman = WeisfeilerLehman(max_iter=1)
labels = weisfeiler_lehman.fit_transform(adjacency)
```

[6]:
```
image = svg_graph(adjacency, position, labels=labels)
SVG(image)
```

[6]:

Weisfeiler-Lehman test

[7]:
```
adjacency_1 = house()
adjacency_2 = house()

are_isomorphic(adjacency_1, adjacency_2)
```

[7]:
```
True
```

3.6 Path

3.6.1 Distance

This notebook illustrates the computation of distances between nodes in graphs (in number of hops).

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import miserables, painters, movie_actor
from sknetwork.path import distance
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
from sknetwork.utils import bipartite2undirected
```

Graphs

[4]:
```
graph = miserables(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[5]:
```
napoleon = 1
```

[6]:
```
dist = distance(adjacency, sources=napoleon)
```

[7]:
```
image = svg_graph(adjacency, position, names, scores = -dist, seeds=[napoleon], scale
↪= 1.5)
```

[8]:
```
SVG(image)
```

[8]:

Digraphs

[9]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[10]:
```
cezanne = 11
```

[11]:
```
dist = distance(adjacency, sources=cezanne)
```

[12]:
```
dist_neg= {i: -d for i, d in enumerate(dist) if d < np.inf}
```

[13]:
```
image = svg_digraph(adjacency, position, names, scores=dist_neg , seeds=[cezanne])
```

[14]:
```
SVG(image)
```

[14]:

Bigraphs

[15]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[16]:
```
adjacency = bipartite2undirected(biadjacency)
```

[17]:
```
n_row, _ = biadjacency.shape
```

[18]:
```
seydoux = 9
```

[19]:
```
dist = distance(adjacency, sources=seydoux + n_row)
```

[20]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_col=-dist[n_row:],␣
↪seeds_col=seydoux)
```

[21]:
```
SVG(image)
```

[21]:

3.6.2 Shortest paths

This notebook illustrates the search for shortest paths in graphs.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import miserables, painters, movie_actor
from sknetwork.path import shortest_path
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
from sknetwork.utils import bipartite2undirected
```

Graphs

[4]:
```
graph = miserables(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[5]:
```
napoleon = 1
jondrette = 46
```

[6]:
```
path = shortest_path(adjacency, sources=napoleon, targets=jondrette)
```

[7]:
```
edge_labels = [(path[k], path[k + 1], 0) for k in range(len(path) - 1)]
```

[8]:
```
image = svg_graph(adjacency, position, names, edge_labels=edge_labels, edge_width=3,␣
↪display_edge_weight=False, scale = 1.5)
```

[9]:
```
SVG(image)
```

[9]:

Digraphs

[10]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[11]:
```
klimt = 6
vinci = 9
```

[12]:
```
path = shortest_path(adjacency, sources=klimt, targets=vinci)
```

[13]:
```
edge_labels = [(path[k], path[k + 1], 0) for k in range(len(path) - 1)]
```

[14]:
```
image = svg_digraph(adjacency, position, names, edge_labels=edge_labels, edge_width=2)
```

[15]:
```
SVG(image)
```

[15]:

Bigraphs

[16]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[17]:
```
adjacency = bipartite2undirected(biadjacency)
```

[18]:
```
n_row, _ = biadjacency.shape
```

[19]:
```
seydoux = 9
lewitt = 2
```

[20]:
```
path = shortest_path(adjacency, sources=seydoux + n_row, targets=lewitt + n_row)
```

[21]:
```
edge_labels = []
labels_row = {}
labels_col = {}
for k in range(len(path) - 1):
    i = path[k]
    j = path[k + 1]
    # row first
    if i > j:
        i, j = j, i
    j -= n_row
    labels_row[i] = 0
    labels_col[j] = 0
    edge_labels.append((i, j, 0))
```

[22]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col,
                    edge_labels=edge_labels, edge_color='gray', edge_width=3)
```

[23]:
```
SVG(image)
```

[23]:

3.7 Clustering

3.7.1 Louvain

This notebook illustrates the clustering of a graph by the Louvain algorithm.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.clustering import Louvain, BiLouvain, modularity, bimodularity
from sknetwork.linalg import normalize
from sknetwork.utils import bipartite2undirected, membership_matrix
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

Clustering

[5]:
```
louvain = Louvain()
labels = louvain.fit_transform(adjacency)
```

[6]:
```
labels_unique, counts = np.unique(labels, return_counts=True)
print(labels_unique, counts)
```

```
[0 1 2 3] [12 11  6  5]
```

[7]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[8]:
```
SVG(image)
```

[8]:

Metrics

[9]:
```
modularity(adjacency, labels)
```

[9]:
```
0.4188034188034188
```

Aggregate graph

[10]:
```
adjacency_aggregate = louvain.adjacency_
```

[11]:
```
average = normalize(membership_matrix(labels).T)
position_aggregate = average.dot(position)
labels_unique, counts = np.unique(labels, return_counts=True)
```

[12]:
```
image = svg_graph(adjacency_aggregate, position_aggregate, counts, labels=labels_
↪unique,
                  display_node_weight=True, node_weights=counts, scale=0.5)
```

[13]:
```
SVG(image)
```

[13]:

Soft clustering

[14]:
```
scores = louvain.membership_[:,1].toarray().ravel()
```

[15]:
```
image = svg_graph(adjacency, position, scores=scores)
```

[16]:
```
SVG(image)
```

[16]:

Digraphs

[17]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

Clustering

[18]:
```
louvain = Louvain()
labels = louvain.fit_transform(adjacency)
```

[19]:
```
labels_unique, counts = np.unique(labels, return_counts=True)
print(labels_unique, counts)
```

```
[0 1 2] [5 5 4]
```

[20]:
```
image = svg_digraph(adjacency, position, names, labels)
```

[21]:
```
SVG(image)
```

[21]:

Metrics

[22]:
```
modularity(adjacency, labels)
```

[22]:
```
0.32480000000000003
```

Aggregate graph

[23]:
```
adjacency_aggregate = louvain.adjacency_
```

[24]:
```
average = normalize(membership_matrix(labels).T)
position_aggregate = average.dot(position)
labels_unique, counts = np.unique(labels, return_counts=True)
```

[25]:
```
image = svg_digraph(adjacency_aggregate, position_aggregate, counts, labels=labels_
↪unique,
                    display_node_weight=True, node_weights=counts, scale=0.5)
```

[26]:
```
SVG(image)
```

[26]:

Soft clustering

[27]:
```
scores = louvain.membership_[:,1].toarray().ravel()
```

[28]:
```
image = svg_graph(adjacency, position, scores=scores)
```

[29]:
```
SVG(image)
```

[29]:

Bigraphs

[30]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Clustering by BiLouvain

[31]:
```
bilouvain = BiLouvain()
bilouvain.fit(biadjacency)
labels_row = bilouvain.labels_row_
labels_col = bilouvain.labels_col_
```

[32]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col)
```

[33]:
```
SVG(image)
```

[33]:

Metrics

[34]:
```
bimodularity(biadjacency, labels_row, labels_col)
```

[34]:
```
0.5742630385487529
```

Aggregate graph

[35]:
```
biadjacency_aggregate = bilouvain.biadjacency_
```

[36]:
```
labels_unique_row, counts_row = np.unique(labels_row, return_counts=True)
labels_unique_col, counts_col = np.unique(labels_col, return_counts=True)
```

[37]:
```
image = svg_bigraph(biadjacency_aggregate, counts_row, counts_col, labels_unique_row,␣
↪labels_unique_col,
                    display_node_weight=True, node_weights_row=counts_row, node_
↪weights_col=counts_col,
                    scale=0.5)
```

[38]:
```
SVG(image)
```

[38]:

Soft clustering

[39]:
```
scores_row = bilouvain.membership_row_[:,1].toarray().ravel()
scores_col = bilouvain.membership_col_[:,1].toarray().ravel()
```

[40]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col)
```

[41]:
```
SVG(image)
```

[41]:

Clustering by Louvain

[42]:
```
louvain = Louvain()
adjacency = bipartite2undirected(biadjacency)
labels = louvain.fit_transform(adjacency)
```

[43]:
```
n_row = biadjacency.shape[0]
labels_row = louvain.labels_[:n_row]
labels_col = louvain.labels_[n_row:]
```

[44]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col)
```

[45]:
```
SVG(image)
```

[45]:

Aggregate graph

[46]:
```
biadjacency_aggregate = louvain.adjacency_[:n_row][:n_row]
```

[47]:
```
labels_unique_row, counts_row = np.unique(labels_row, return_counts=True)
labels_unique_col, counts_col = np.unique(labels_col, return_counts=True)
```

[48]:
```
image = svg_bigraph(biadjacency_aggregate, counts_row, counts_col, labels_unique_row,␣
↪labels_unique_col,
                    display_node_weight=True, node_weights_row=counts_row, node_
↪weights_col=counts_col,
                    scale=0.5)
```

[49]:
```
SVG(image)
```

[49]:

3.7.2 Propagation

This notebook illustrates the clustering of a graph by label propagation.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.clustering import PropagationClustering, BiPropagationClustering,␣
↪modularity, bimodularity
from sknetwork.linalg import normalize
from sknetwork.utils import bipartite2undirected, membership_matrix
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

Clustering

[5]:
```
propagation = PropagationClustering()
labels = propagation.fit_transform(adjacency)
```

[6]:
```
labels_unique, counts = np.unique(labels, return_counts=True)
print(labels_unique, counts)
```

```
[0 1] [19 15]
```

[7]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[8]:
```
SVG(image)
```

[8]:

Metrics

[9]:
```
modularity(adjacency, labels)
```

[9]:
```
0.35231755424063116
```

Aggregate graph

[10]:
```
adjacency_aggregate = propagation.adjacency_
```

[11]:
```
average = normalize(membership_matrix(labels).T)
position_aggregate = average.dot(position)
labels_unique, counts = np.unique(labels, return_counts=True)
```

[12]:
```
image = svg_graph(adjacency_aggregate, position_aggregate, counts, labels=labels_
↪unique,
                  display_node_weight=True, node_weights=counts, scale=0.5)
```

[13]:
```
SVG(image)
```

[13]:

Soft clustering

[14]:
```
scores = propagation.membership_[:,1].toarray().ravel()
```

[15]:
```
image = svg_graph(adjacency, position, scores=scores)
```

[16]:
```
SVG(image)
```

[16]:

Digraphs

[17]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

Clustering

[18]:
```
propagation = PropagationClustering()
labels = propagation.fit_transform(adjacency)
```

[19]:
```
labels_unique, counts = np.unique(labels, return_counts=True)
print(labels_unique, counts)
```

```
[0 1] [10  4]
```

[20]:
```
image = svg_digraph(adjacency, position, names, labels)
```

[21]:
```
SVG(image)
```

[21]:

Metrics

[22]:
```
modularity(adjacency, labels)
```

[22]:
```
0.256
```

Aggregate graph

[23]:
```
adjacency_aggregate = propagation.adjacency_
```

[24]:
```
average = normalize(membership_matrix(labels).T)
position_aggregate = average.dot(position)
labels_unique, counts = np.unique(labels, return_counts=True)
```

[25]:
```
image = svg_digraph(adjacency_aggregate, position_aggregate, counts, labels=labels_
↪unique,
                    display_node_weight=True, node_weights=counts, scale=0.5)
```

[26]:
```
SVG(image)
```
[26]:

Soft clustering

[27]:
```
scores = propagation.membership_[:,0].toarray().ravel()
```

[28]:
```
image = svg_graph(adjacency, position, scores=scores)
```

[29]:
```
SVG(image)
```
[29]:

Bigraphs

[30]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Clustering

[31]:
```
bipropagation = BiPropagationClustering()
bipropagation.fit(biadjacency)
labels_row = bipropagation.labels_row_
labels_col = bipropagation.labels_col_
```

[32]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col)
```

[33]:
```
SVG(image)
```
[33]:

Metrics

[34]:
```
bimodularity(biadjacency, labels_row, labels_col)
```
[34]:
```
0.41496598639455773
```

Aggregate graph

[35]:
```
biadjacency_aggregate = bipropagation.biadjacency_
```

[36]:
```
labels_unique_row, counts_row = np.unique(labels_row, return_counts=True)
labels_unique_col, counts_col = np.unique(labels_col, return_counts=True)
```

[37]:
```
image = svg_bigraph(biadjacency_aggregate, counts_row, counts_col, labels_unique_row,␣
↪labels_unique_col,
                    display_node_weight=True, node_weights_row=counts_row, node_
↪weights_col=counts_col,
                    scale=0.5)
```

[38]:
```
SVG(image)
```
[38]:

Soft clustering

[39]:
```
scores_row = bipropagation.membership_row_[:,1].toarray().ravel()
scores_col = bipropagation.membership_col_[:,1].toarray().ravel()
```

[40]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col)
```

[41]:
```
SVG(image)
```

[41]:

3.7.3 K-means

This notebook illustrates the clustering of a graph by k-means. This clustering involves the embedding of the graph in a space of low dimension.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.clustering import KMeans, BiKMeans, modularity, bimodularity
from sknetwork.linalg import normalize
from sknetwork.embedding import GSVD
from sknetwork.utils import membership_matrix
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

Clustering

[5]:
```
kmeans = KMeans(n_clusters = 2, embedding_method=GSVD(3))
labels = kmeans.fit_transform(adjacency)
```

[6]:
```
unique_labels, counts = np.unique(labels, return_counts=True)
print(unique_labels, counts)
```

```
[0 1] [25  9]
```

[7]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[8]:
```
SVG(image)
```

[8]:

Metrics

[9]:
```
modularity(adjacency, labels)
```

[9]:
```
-0.26923076923076933
```

Aggregate graph

[10]:
```
adjacency_aggregate = kmeans.adjacency_
```

[11]:
```
average = normalize(membership_matrix(labels).T)
position_aggregate = average.dot(position)
labels_unique, counts = np.unique(labels, return_counts=True)
```

[12]:
```
image = svg_graph(adjacency_aggregate, position_aggregate, counts, labels=labels_
↪unique,
                  display_node_weight=True, node_weights=counts, scale=0.5)
```

[13]:
```
SVG(image)
```

[13]:

Soft clustering

[14]:
```
scores = kmeans.membership_[:,1].toarray().ravel()
```

[15]:
```
image = svg_graph(adjacency, position, scores=scores)
```

[16]:
```
SVG(image)
```

[16]:

Digraphs

[17]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Clustering

[18]:
```
kmeans = KMeans(3, GSVD(3))
labels = kmeans.fit_transform(adjacency)
```

[19]:
```
image = svg_digraph(adjacency, position, names=names, labels=labels)
```

[20]:
```
SVG(image)
```

[20]:

Metrics

[21]:
```
modularity(adjacency, labels)
```

[21]:
```
0.16639999999999994
```

Aggregate graph

[22]:
```
adjacency_aggregate = kmeans.adjacency_
```

[23]:
```
average = normalize(membership_matrix(labels).T)
position_aggregate = average.dot(position)
labels_unique, counts = np.unique(labels, return_counts=True)
```

[24]:
```
image = svg_digraph(adjacency_aggregate, position_aggregate, counts, labels=labels_
↪unique,
                    display_node_weight=True, node_weights=counts, scale=0.5)
```

[25]:
```
SVG(image)
```

[25]:

Soft clustering

[26]:
```
scores = kmeans.membership_[:,1].toarray().ravel()
```

[27]:
```
image = svg_digraph(adjacency, position, scores=scores)
```

[28]:
```
SVG(image)
```

[28]:

Bigraphs

[29]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Clustering

[30]:
```
bikmeans = BiKMeans(3, GSVD(3), co_cluster=True)
bikmeans.fit(biadjacency)
labels_row = bikmeans.labels_row_
labels_col = bikmeans.labels_col_
```

[31]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col)
```

[32]:
```
SVG(image)
```

[32]:

Metrics

[33]:
```
bimodularity(biadjacency, labels_row, labels_col)
```

[33]:
```
0.4943310657596373
```

Aggregate graph

[34]:
```
biadjacency_aggregate = bikmeans.biadjacency_
```

[35]:
```
labels_unique_row, counts_row = np.unique(labels_row, return_counts=True)
labels_unique_col, counts_col = np.unique(labels_col, return_counts=True)
```

[36]:
```
image = svg_bigraph(biadjacency_aggregate, counts_row, counts_col, labels_unique_row,␣
↪labels_unique_col,
                    display_node_weight=True, node_weights_row=counts_row, node_
↪weights_col=counts_col,
                    scale=0.5)
```

[37]:
```
SVG(image)
```
[37]:

Soft clustering

[38]:
```
scores_row = bikmeans.membership_row_[:,1].toarray().ravel()
scores_col = bikmeans.membership_col_[:,1].toarray().ravel()
```

[39]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col)
```

[40]:
```
SVG(image)
```
[40]:

3.8 Hierarchy

3.8.1 Paris

This notebook illustrates the hierarchical clustering of graphs by the Paris algorithm.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.hierarchy import Paris, BiParis, cut_straight, dasgupta_score, tree_
↪sampling_divergence
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph, svg_
↪dendrogram
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

Hierarchy

[5]:
```
paris = Paris()
dendrogram = paris.fit_transform(adjacency)
```

[6]:
```
image = svg_dendrogram(dendrogram)
```

[7]:
```
SVG(image)
```
[7]:

Cuts of the dendrogram

[8]:
```
labels = cut_straight(dendrogram)
print(labels)
```

```
[1 1 1 1 1 1 1 1 0 1 1 1 1 1 0 0 1 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0]
```

[9]:
```
n_clusters = 4
labels, dendrogram_aggregate = cut_straight(dendrogram, n_clusters, return_
↪dendrogram=True)
print(labels)
```

```
[0 0 0 0 3 3 3 0 1 0 3 0 0 0 1 1 3 0 1 0 1 0 1 2 2 2 2 2 2 2 1 2 1 1]
```

[10]:
```
_, counts = np.unique(labels, return_counts=True)
```

[11]:
```
image = svg_dendrogram(dendrogram_aggregate, names=counts, rotate_names=False)
```

[12]:
```
SVG(image)
```

[12]:

[13]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[14]:
```
SVG(image)
```

[14]:

Metrics

[15]:
```
dasgupta_score(adjacency, dendrogram)
```

[15]:
```
0.6655354449472097
```

[16]:
```
tree_sampling_divergence(adjacency, dendrogram)
```

[16]:
```
0.4867262842323475
```

Digraphs

[17]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Hierarchy

[18]:
```
paris = Paris()
dendrogram = paris.fit_transform(adjacency)
```

[19]:
```
image = svg_dendrogram(dendrogram, names, n_clusters=3, rotate=True)
```

[20]:
```
SVG(image)
```

[20]:

Cuts of the dendrogram

[21]:
```
# cut with 3 clusters
labels = cut_straight(dendrogram, n_clusters = 3)
print(labels)
```

```
[0 0 1 0 1 1 2 0 0 1 0 0 0 2]
```

[22]:
```
image = svg_digraph(adjacency, position, names=names, labels=labels)
```

[23]:
```
SVG(image)
```

[23]:

Metrics

[24]:
```
dasgupta_score(adjacency, dendrogram)
```

[24]:
```
0.5842857142857143
```

[25]:
```
tree_sampling_divergence(adjacency, dendrogram)
```

[25]:
```
0.4685697020629489
```

Bigraphs

[26]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Hierarchy

[27]:
```
biparis = BiParis()
biparis.fit(biadjacency)
dendrogram_row = biparis.dendrogram_row_
dendrogram_col = biparis.dendrogram_col_
dendrogram_full = biparis.dendrogram_full_
```

[28]:
```
image = svg_dendrogram(dendrogram_row, names_row, n_clusters=4, rotate=True)
```

[29]:
```
SVG(image)
```

[29]:

[30]:
```
image = svg_dendrogram(dendrogram_col, names_col, n_clusters=4, rotate=True)
```

[31]:
```
SVG(image)
```

[31]:

Cuts of the dendrogram

[32]:
```
labels = cut_straight(dendrogram_full, n_clusters = 4)
n_row = biadjacency.shape[0]
labels_row = labels[:n_row]
labels_col = labels[n_row:]
```

[33]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col)
```

[34]:
```
SVG(image)
```

[34]:

3.8.2 Ward

This notebook illustrates the hierarchical clustering of graphs by the Ward method, after embedding in a space of low dimension.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.embedding import Spectral
from sknetwork.hierarchy import Ward, BiWard, cut_straight, dasgupta_score, tree_
↪sampling_divergence
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph, svg_
↪dendrogram
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

Hierarchy

[5]:
```
ward = Ward()
dendrogram = ward.fit_transform(adjacency)
```

[6]:
```
image = svg_dendrogram(dendrogram)
```

[7]:
```
SVG(image)
```

[7]:

Cuts of the dendrogram

[8]:
```
labels = cut_straight(dendrogram)
print(labels)
```

```
[1 1 1 1 1 1 1 1 0 0 1 1 1 1 0 0 1 1 0 1 0 1 0 0 0 0 0 0 0 0 0 0 0 0]
```

[9]:
```
n_clusters = 4
labels, dendrogram_aggregate = cut_straight(dendrogram, n_clusters, return_
↪dendrogram=True)
print(labels)
```

```
[1 1 1 1 3 3 3 1 0 0 3 1 1 1 2 2 3 1 2 1 2 1 2 0 0 0 0 0 0 2 2 0 0 0]
```

[10]:
```
_, counts = np.unique(labels, return_counts=True)
```

[11]:
```
image = svg_dendrogram(dendrogram_aggregate, names=counts, rotate_names=False)
```

[12]:
```
SVG(image)
```

[12]:

[13]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[14]:
```
SVG(image)
```

[14]:

Metrics

[15]:
```
dasgupta_score(adjacency, dendrogram)
```

[15]:
```
0.583710407239819
```

[16]:
```
tree_sampling_divergence(adjacency, dendrogram)
```

[16]:
```
0.4342993247923879
```

Other embedding

[17]:
```
ward = Ward(embedding_method=Spectral(4))
```

Digraphs

[18]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Hierarchy

[19]:
```
biward = BiWard()
dendrogram = biward.fit_transform(adjacency)
```

[20]:
```
image = svg_dendrogram(dendrogram, names, n_clusters=3, rotate=True)
```

[21]:
```
SVG(image)
```

[21]:

Cuts of the dendrogram

[22]:
```
# cut with 3 clusters
labels = cut_straight(dendrogram, n_clusters = 3)
print(labels)
```

```
[0 0 1 0 1 1 2 0 0 1 0 0 0 2]
```

[23]:
```
image = svg_digraph(adjacency, position, names=names, labels=labels)
```

[24]:
```
SVG(image)
```

[24]:

Metrics

[25]:
```
dasgupta_score(adjacency, dendrogram)
```

[25]:
```
0.49857142857142855
```

[26]:
```
tree_sampling_divergence(adjacency, dendrogram)
```

[26]:
```
0.48729193280825467
```

Bigraphs

[27]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Hierarchy

[28]:
```
biward = BiWard(cluster_col = True, cluster_both = True)
biward.fit(biadjacency)
```

[28]:
```
BiWard(embedding_method=GSVD(n_components=10, regularization=None, relative_
↪regularization=True, factor_row=0.5, factor_col=0.5, factor_singular=0.0,␣
↪normalized=True, solver=LanczosSVD(maxiter=None, tol=0.0)), cluster_col=True,␣
↪cluster_both=True)
```

[29]:
```
dendrogram_row = biward.dendrogram_row_
dendrogram_col = biward.dendrogram_col_
dendrogram_full = biward.dendrogram_full_
```

[30]:
```
image = svg_dendrogram(dendrogram_row, names_row, n_clusters=4, rotate=True)
```

[31]:
```
SVG(image)
```

[31]:

[32]:
```
image = svg_dendrogram(dendrogram_col, names_col, n_clusters=4, rotate=True)
```

[33]:
```
SVG(image)
```

[33]:

Cuts of the dendrogram

[34]:
```
labels = cut_straight(dendrogram_full, n_clusters = 4)
n_row = biadjacency.shape[0]
labels_row = labels[:n_row]
labels_col = labels[n_row:]
```

[35]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col)
```

[36]:
```
SVG(image)
```

[36]:

3.8.3 Louvain

This notebook illustrates the hierarchical clustering of graphs by the Louvain hierarchical algorithm.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.hierarchy import LouvainHierarchy, BiLouvainHierarchy
from sknetwork.hierarchy import cut_straight, dasgupta_score, tree_sampling_divergence
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph, svg_
↪dendrogram
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

Hierarchy

[5]:
```
louvain_hierarchy = LouvainHierarchy()
dendrogram = louvain_hierarchy.fit_transform(adjacency)
```

[6]:
```
image = svg_dendrogram(dendrogram)
```

[7]:
```
SVG(image)
```

[7]:

Cuts of the dendrogram

[8]:
```
labels = cut_straight(dendrogram)
print(labels)
```

```
[0 0 0 0 3 3 3 0 1 0 3 0 0 0 1 1 3 0 1 0 1 0 1 2 2 2 1 2 2 1 1 2 1 1]
```

[9]:
```
labels, dendrogram_aggregate = cut_straight(dendrogram, n_clusters=4, return_
↪dendrogram=True)
print(labels)
```

```
[0 0 0 0 3 3 3 0 1 0 3 0 0 0 1 1 3 0 1 0 1 0 1 2 2 2 1 2 2 1 1 2 1 1]
```

[10]:
```
_, counts = np.unique(labels, return_counts=True)
```

[11]:
```
image = svg_dendrogram(dendrogram_aggregate, names=counts, rotate_names=False)
```

[12]:
```
SVG(image)
```

[12]:

[13]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[14]:
```
SVG(image)
```

[14]:

Metrics

[15]:
```
dasgupta_score(adjacency, dendrogram)
```

[15]:
```
0.5878582202111614
```

[16]:
```
tree_sampling_divergence(adjacency, dendrogram)
```

[16]:
```
0.4484780069854286
```

Digraphs

[17]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Hierarchy

[18]:
```
louvain_hierarchy = LouvainHierarchy()
dendrogram = louvain_hierarchy.fit_transform(adjacency)
```

[19]:
```
image = svg_dendrogram(dendrogram, names, rotate=True)
```

[20]:
```
SVG(image)
```

[20]:

Cuts of the dendrogram

[21]:
```
# cut with 3 clusters
labels = cut_straight(dendrogram, n_clusters = 3)
print(labels)
```

```
[1 0 2 0 2 2 1 0 1 2 1 0 0 1]
```

[22]:
```
image = svg_digraph(adjacency, position, names=names, labels=labels)
```

[23]:
```
SVG(image)
```

[23]:

Metrics

[24]:
```
dasgupta_score(adjacency, dendrogram)
```

[24]:
```
0.4842857142857143
```

[25]:
```
tree_sampling_divergence(adjacency, dendrogram)
```

[25]:
```
0.42595079927794577
```

Bigraphs

[26]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Hierarchy

[27]:
```
bilouvain = BiLouvainHierarchy()
bilouvain.fit(biadjacency)
dendrogram_row = bilouvain.dendrogram_row_
dendrogram_col = bilouvain.dendrogram_col_
dendrogram_full = bilouvain.dendrogram_full_
```

[28]:
```
image = svg_dendrogram(dendrogram_row, names_row, n_clusters=4, rotate=True)
```

[29]:
```
SVG(image)
```

[29]:

[30]:
```
image = svg_dendrogram(dendrogram_col, names_col, n_clusters=4, rotate=True)
```

[31]:
```
SVG(image)
```

[31]:

Cuts of the dendrogram

[32]:
```
labels = cut_straight(dendrogram_full, n_clusters = 4)
n_row = biadjacency.shape[0]
labels_row = labels[:n_row]
labels_col = labels[n_row:]
```

[33]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col)
```

[34]:
```
SVG(image)
```

[34]:

3.9 Ranking

3.9.1 PageRank

This notebook illustrates the ranking of the nodes of a graph by PageRank.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.ranking import PageRank, BiPageRank
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

Ranking

[5]:
```
pagerank = PageRank()
scores = pagerank.fit_transform(adjacency)
```

[6]:
```
image = svg_graph(adjacency, position, scores=np.log(scores))
```

[7]:
```
SVG(image)
```

[7]:

Ranking with personalization

[8]:
```
seeds = {1: 1, 10: 1}
```

[9]:
```
scores = pagerank.fit_transform(adjacency, seeds)
```

[10]:
```
image = svg_graph(adjacency, position, scores=np.log(scores), seeds=seeds)
```

[11]:
```
SVG(image)
```

[11]:

Digraphs

[12]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

Ranking

[13]:
```
pagerank = PageRank()
scores = pagerank.fit_transform(adjacency)
```

[14]:
```
image = svg_digraph(adjacency, position, scores=np.log(scores), names=names)
```

[15]:
```
SVG(image)
```

[15]:

Ranking with personalization

[16]:
```
cezanne = 11
seeds = {cezanne:1}
```

[17]:
```
scores = pagerank.fit_transform(adjacency, seeds)
```

[18]:
```
image = svg_digraph(adjacency, position, names, scores=np.log(scores + 1e-6),␣
↪seeds=seeds)
```

[19]:
```
SVG(image)
```
[19]:

Bigraphs

[20]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Ranking

[21]:
```
bipagerank = BiPageRank()
```

[22]:
```
drive = 3
aviator = 9
seeds_row={drive: 1, aviator: 1}
```

[23]:
```
bipagerank.fit(biadjacency, seeds_row)
scores_row = bipagerank.scores_row_
scores_col = bipagerank.scores_col_
```

[24]:
```
image = svg_bigraph(biadjacency, names_row, names_col,
                    scores_row=np.log(scores_row), scores_col=np.log(scores_col),␣
↪seeds_row=seeds_row)
```

[25]:
```
SVG(image)
```
[25]:

3.9.2 Diffusion

This notebook illustrates the ranking of the nodes of a graph by heat diffusion.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.ranking import Diffusion, BiDiffusion
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels_true = graph.labels
```

[5]:
```
diffusion = Diffusion()
seeds = {0: 0, 33: 1}
scores = diffusion.fit_transform(adjacency, seeds)
```

[6]:
```
image = svg_graph(adjacency, position, scores=scores, seeds=seeds)
```

[7]:
```
SVG(image)
```

[7]:

Digraphs

[8]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

[9]:
```
picasso = 0
manet = 3
```

[10]:
```
diffusion = Diffusion()
seeds = {picasso: 1, manet: 1}
scores = diffusion.fit_transform(adjacency, seeds, init=0)
```

[11]:
```
image = svg_digraph(adjacency, position, names, scores=scores, seeds=seeds)
```

[12]:
```
SVG(image)
```

[12]:

Bigraphs

[13]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[14]:
```
drive = 3
aviator = 9
```

[15]:
```
bidiffusion = BiDiffusion()
seeds_row = {drive: 0, aviator: 1}
bidiffusion.fit(biadjacency, seeds_row=seeds_row)
scores_row = bidiffusion.scores_row_
scores_col = bidiffusion.scores_col_
```

[16]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col,
                    seeds_row=seeds_row)
```

[17]:
```
SVG(image)
```

[17]:

3.9.3 Dirichlet

This notebook illustrates the ranking of the nodes of a graph through the Dirichlet problem (heat diffusion with constraints).

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.ranking import Dirichlet, BiDirichlet
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels_true = graph.labels
```

[5]:
```
diffusion = Dirichlet()
seeds = {0: 0, 33: 1}
scores = diffusion.fit_transform(adjacency, seeds)
```

[6]:
```
image = svg_graph(adjacency, position, scores=scores, seeds=seeds)
```

[7]:
```
SVG(image)
```

[7]:

Digraphs

[8]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

[9]:
```
picasso = 0
monet = 1
```

[10]:
```
diffusion = Dirichlet()
seeds = {picasso: 0, monet: 1}
scores = diffusion.fit_transform(adjacency, seeds)
```

[11]:
```
image = svg_digraph(adjacency, position, names, scores=scores, seeds=seeds)
```

[12]:
```
SVG(image)
```

[12]:

Bigraphs

[13]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[14]:
```
bidiffusion = BiDirichlet()
```

[15]:
```
drive = 3
aviator = 9
```

[16]:
```
seeds_row = {drive: 0, aviator: 1}
bidiffusion.fit(biadjacency, seeds_row)
scores_row = bidiffusion.scores_row_
scores_col = bidiffusion.scores_col_
```

[17]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col,
                    seeds_row=seeds_row)
```

[18]:
```
SVG(image)
```

[18]:

3.9.4 Katz centrality

This notebook illustrates the ranking of the nodes of a graph by Katz centrality, a weighted average of number of paths of different lengths to each node.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.ranking import Katz, BiKatz
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[5]:
```
katz = Katz()
scores = katz.fit_transform(adjacency)
```

[6]:
```
image = svg_graph(adjacency, position, scores=scores)
SVG(image)
```

[6]:

Digraphs

[7]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[8]:
```
katz = Katz()
scores = katz.fit_transform(adjacency)
```

[9]:
```
image = svg_digraph(adjacency, position, scores=scores, names=names)
SVG(image)
```

[9]:

Bigraphs

[10]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[11]:
```
bikatz = BiKatz()
bikatz.fit(biadjacency)
scores_row = bikatz.scores_row_
scores_col = bikatz.scores_col_
```

[12]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col)
SVG(image)
```

[12]:

3.10 Classification

3.10.1 PageRank

This notebook illustrates the classification of the nodes of a graph by PageRank, based on the labels of a few nodes.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.classification import PageRankClassifier, BiPageRankClassifier
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels_true = graph.labels
```

Classification

[5]:
```
seeds = {i: labels_true[i] for i in [0, 33]}
```

[6]:
```
pagerank = PageRankClassifier()
labels_pred = pagerank.fit_transform(adjacency, seeds)
```

[7]:
```
precision = np.round(np.mean(labels_pred == labels_true), 2)
precision
```

[7]:
```
0.97
```

[8]:
```
image = svg_graph(adjacency, position, labels=labels_pred, seeds=seeds)
```

[9]:
```
SVG(image)
```

[9]:

Soft classification

[10]:
```
membership = pagerank.membership_
```

[11]:
```
scores = membership[:,1].toarray().ravel()
```

[12]:
```
image = svg_graph(adjacency, position, scores=scores, seeds=seeds)
```

[13]:
```
SVG(image)
```

[13]:

Digraphs

[14]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Classification

[15]:
```
rembrandt = 5
klimt = 6
cezanne = 11
seeds = {cezanne: 0, rembrandt: 1, klimt: 2}
```

[16]:
```
pagerank = PageRankClassifier()
labels = pagerank.fit_transform(adjacency, seeds)
```

[17]:
```
image = svg_digraph(adjacency, position, names, labels, seeds=seeds)
```

[18]:
```
SVG(image)
```

[18]:

Soft classification

[19]:
```
membership = pagerank.membership_
```

[20]:
```
scores = membership[:,0].toarray().ravel()
```

[21]:
```
image = svg_digraph(adjacency, position, names, scores=scores, seeds=[cezanne])
```

[22]:
```
SVG(image)
```

[22]:

Bigraphs

[23]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Classification

[24]:
```
inception = 0
drive = 3
budapest = 8
```

[25]:
```
seeds_row = {inception: 0, drive: 1, budapest: 2}
```

[26]:
```
bipagerank = BiPageRankClassifier()
bipagerank.fit(biadjacency, seeds_row)
labels_row = bipagerank.labels_row_
labels_col = bipagerank.labels_col_
```

[27]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col, seeds_
↪row=seeds_row)
```

[28]:
```
SVG(image)
```

[28]:

Soft classification

[29]:
```
membership_row = bipagerank.membership_row_
membership_col = bipagerank.membership_col_
```

[30]:
```
scores_row = membership_row[:,1].toarray().ravel()
scores_col = membership_col[:,1].toarray().ravel()
```

[31]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col,
                    seeds_row=seeds_row)
```

[32]:
```
SVG(image)
```
[32]:

3.10.2 Diffusion

This notebook illustrates the classification of the nodes of a graph by diffusion, based on the labels of a few nodes.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.classification import DiffusionClassifier, BiDiffusionClassifier
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels_true = graph.labels
```

Classification

[5]:
```
seeds = {i: labels_true[i] for i in [0, 33]}
```

[6]:
```
diffusion = DiffusionClassifier()
labels_pred = diffusion.fit_transform(adjacency, seeds)
```

[7]:
```
precision = np.round(np.mean(labels_pred == labels_true), 2)
precision
```
[7]:
```
0.94
```

[8]:
```
image = svg_graph(adjacency, position, labels=labels_pred, seeds=seeds)
```

[9]:
```
SVG(image)
```
[9]:

Soft classification

[10]:
```
scores = diffusion.score(1)
```

[11]:
```
image = svg_graph(adjacency, position, scores=scores, seeds=seeds)
```

[12]:
```
SVG(image)
```
[12]:

Digraphs

[13]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Classification

[14]:
```
rembrandt = 5
klimt = 6
cezanne = 11
seeds = {cezanne: 0, rembrandt: 1}
```

[15]:
```
diffusion = DiffusionClassifier()
labels = diffusion.fit_transform(adjacency, seeds)
```

[16]:
```
image = svg_digraph(adjacency, position, names, labels, seeds=seeds)
```

[17]:
```
SVG(image)
```

[17]:

Soft classification

[18]:
```
scores = diffusion.score(0)
```

[19]:
```
image = svg_digraph(adjacency, position, names=names, scores=scores, seeds=[cezanne])
```

[20]:
```
SVG(image)
```

[20]:

Bigraphs

[21]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Classification

[22]:
```
inception = 0
drive = 3
```

[23]:
```
seeds_row = {inception: 0, drive: 1}
```

[24]:
```
bidiffusion = BiDiffusionClassifier()
bidiffusion.fit(biadjacency, seeds_row)
labels_row = bidiffusion.labels_row_
labels_col = bidiffusion.labels_col_
```

[25]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col, seeds_
↪row=seeds_row)
```

[26]:
```
SVG(image)
```
[26]:

Soft classification

[27]:
```
membership_row = bidiffusion.membership_row_
membership_col = bidiffusion.membership_col_
```

[28]:
```
scores_row = membership_row[:,1].toarray().ravel()
scores_col = membership_col[:,1].toarray().ravel()
```

[29]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col,
                    seeds_row=seeds_row)
```

[30]:
```
SVG(image)
```
[30]:

3.10.3 Dirichlet

This notebook illustrates the classification of the nodes of a graph by the Dirichlet problem, based on the labels of a few nodes.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.classification import DirichletClassifier, BiDirichletClassifier
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels_true = graph.labels
```

Classification

[5]:
```
seeds = {i: labels_true[i] for i in [0, 33]}
```

[6]:
```
diffusion = DirichletClassifier()
labels_pred = diffusion.fit_transform(adjacency, seeds)
```

[7]:
```
precision = np.round(np.mean(labels_pred == labels_true), 2)
precision
```
[7]:
```
0.97
```

[8]:
```
image = svg_graph(adjacency, position, labels=labels_pred, seeds=seeds)
```

[9]:
```
SVG(image)
```
[9]:

Soft classification

[10]:
```
membership = diffusion.membership_
```

[11]:
```
scores = membership[:,1].toarray().ravel()
```

[12]:
```
image = svg_graph(adjacency, position, scores=scores, seeds=seeds)
```

[13]:
```
SVG(image)
```
[13]:

Digraphs

[14]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Classification

[15]:
```
rembrandt = 5
klimt = 6
cezanne = 11
seeds = {cezanne: 0, rembrandt: 1, klimt: 2}
```

[16]:
```
diffusion = DirichletClassifier()
labels = diffusion.fit_transform(adjacency, seeds)
```

[17]:
```
image = svg_digraph(adjacency, position, names, labels, seeds=seeds)
```

[18]:
```
SVG(image)
```
[18]:

Soft classification

[19]:
```
membership = diffusion.membership_
```

[20]:
```
scores = membership[:,0].toarray().ravel()
```

[21]:
```
image = svg_digraph(adjacency, position, names=names, scores=scores, seeds=[cezanne])
```

[22]:
```
SVG(image)
```
[22]:

Bigraphs

[23]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Classification

[24]:
```
inception = 0
drive = 3
budapest = 8
```

[25]:
```
seeds_row = {inception: 0, drive: 1, budapest: 2}
```

[26]:
```
bidiffusion = BiDirichletClassifier()
bidiffusion.fit(biadjacency, seeds_row)
labels_row = bidiffusion.labels_row_
labels_col = bidiffusion.labels_col_
```

[27]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col, seeds_
↪row=seeds_row)
```

[28]:
```
SVG(image)
```

[28]:

Soft classification

[29]:
```
membership_row = bidiffusion.membership_row_
membership_col = bidiffusion.membership_col_
```

[30]:
```
scores_row = membership_row[:,1].toarray().ravel()
scores_col = membership_col[:,1].toarray().ravel()
```

[31]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col,
                    seeds_row=seeds_row)
```

[32]:
```
SVG(image)
```

[32]:

3.10.4 Propagation

This notebook illustrates the classification of the nodes of a graph by label propagation.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.classification import BiPropagation, Propagation
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels_true = graph.labels
```

Classification

[5]:
```
seeds = {i: labels_true[i] for i in [0, 33]}
```

[6]:
```
propagation = Propagation()
labels_pred = propagation.fit_transform(adjacency, seeds)
```

[7]:
```
image = svg_graph(adjacency, position, labels=labels_pred, seeds=seeds)
```

[8]:
```
SVG(image)
```

[8]:

Soft classification

[9]:
```
membership = propagation.membership_
```

[10]:
```
scores = membership[:,1].toarray().ravel()
```

[11]:
```
image = svg_graph(adjacency, position, scores=scores, seeds=seeds)
```

[12]:
```
SVG(image)
```

[12]:

Digraphs

[13]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Classification

[14]:
```
rembrandt = 5
klimt = 6
cezanne = 11
seeds = {cezanne: 0, rembrandt: 1, klimt: 2}
```

[15]:
```
propagation = Propagation()
labels = propagation.fit_transform(adjacency, seeds)
```

[16]:
```
image = svg_digraph(adjacency, position, names, labels, seeds=seeds)
```

[17]:
```
SVG(image)
```

[17]:

Soft classification

[18]:
```
membership = propagation.membership_
```

[19]:
```
scores = membership[:,0].toarray().ravel()
```

[20]:
```
image = svg_digraph(adjacency, position, names, scores=scores, seeds=[cezanne])
```

[21]:
```
SVG(image)
```

[21]:

Bipartite graphs

[22]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Classification

[23]:
```
inception = 0
drive = 3
budapest = 8
```

[24]:
```
seeds_row = {inception: 0, drive: 1, budapest: 2}
```

[25]:
```
bipropagation = BiPropagation()
labels_row = bipropagation.fit_transform(biadjacency, seeds_row)
labels_col = bipropagation.labels_col_
```

[26]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col, seeds_
↪row=seeds_row)
```

[27]:
```
SVG(image)
```

[27]:

Soft classification

[28]:
```
membership_row = bipropagation.membership_row_
membership_col = bipropagation.membership_col_
```

[29]:
```
scores_row = membership_row[:,1].toarray().ravel()
scores_col = membership_col[:,1].toarray().ravel()
```

[30]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col,
                    seeds_row=seeds_row)
```

[31]:
```
SVG(image)
```

[31]:

3.10.5 Nearest neighbors

This notebook illustrates the classification of the nodes of a graph by the k-nearest neighbors algorithm, based on the labels of a few nodes.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.classification import KNN, BiKNN
from sknetwork.embedding import GSVD
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels_true = graph.labels
```

Classification

[5]:
```
seeds = {i: labels_true[i] for i in [0, 33]}
```

[6]:
```
knn = KNN(GSVD(3), n_neighbors=1)
labels_pred = knn.fit_transform(adjacency, seeds)
```

[7]:
```
precision = np.round(np.mean(labels_pred == labels_true), 2)
precision
```

[7]:
```
0.97
```

[8]:
```
image = svg_graph(adjacency, position, labels=labels_pred, seeds=seeds)
```

[9]:
```
SVG(image)
```

[9]:

Soft classification

[10]:
```
knn = KNN(GSVD(3), n_neighbors=2)
knn.fit(adjacency, seeds)
membership = knn.membership_
```

[11]:
```
scores = membership[:,1].toarray().ravel()
```

[12]:
```
image = svg_graph(adjacency, position, scores=scores, seeds=seeds)
```

[13]:
```
SVG(image)
```

[13]:

Digraphs

[14]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Classification

[15]:
```
rembrandt = 5
klimt = 6
cezanne = 11
seeds = {cezanne: 0, rembrandt: 1, klimt: 2}
```

[16]:
```
knn = KNN(GSVD(3), n_neighbors=2)
labels = knn.fit_transform(adjacency, seeds)
```

[17]:
```
image = svg_digraph(adjacency, position, names, labels, seeds=seeds)
```

[18]:
```
SVG(image)
```

[18]:

Soft classification

[19]:
```
membership = knn.membership_
```

[20]:
```
scores = membership[:,0].toarray().ravel()
```

[21]:
```
image = svg_digraph(adjacency, position, names, scores=scores, seeds=[cezanne])
```

[22]:
```
SVG(image)
```

[22]:

Bipartite graphs

[23]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Classification

[24]:
```
inception = 0
drive = 3
budapest = 8
```

[25]:
```
seeds_row = {inception: 0, drive: 1, budapest: 2}
```

[26]:
```
biknn = BiKNN(GSVD(3), n_neighbors=2)
labels_row = biknn.fit_transform(biadjacency, seeds_row)
labels_col = biknn.labels_col_
```

[27]:
```
image = svg_bigraph(biadjacency, names_row, names_col, labels_row, labels_col, seeds_
↪row=seeds_row)
```

[28]:
```
SVG(image)
```

[28]:

Soft classification

[29]:
```
membership_row = biknn.membership_row_
membership_col = biknn.membership_col_
```

[30]:
```
scores_row = membership_row[:,1].toarray().ravel()
scores_col = membership_col[:,1].toarray().ravel()
```

[31]:
```
image = svg_bigraph(biadjacency, names_row, names_col, scores_row=scores_row, scores_
↪col=scores_col,
                    seeds_row=seeds_row)
```

[32]:
```
SVG(image)
```

[32]:

3.11 Embedding

3.11.1 Spectral

This notebook illustrates the spectral embedding of a graph through the spectral decomposition of the Laplacian matrix.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.embedding import Spectral, BiSpectral, cosine_modularity
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
labels = graph.labels
```

Embedding

[5]:
```
spectral = Spectral(2, normalized=False)
embedding = spectral.fit_transform(adjacency)
embedding.shape
```

[5]:
```
(34, 2)
```

[6]:
```
image = svg_graph(adjacency, embedding, labels=labels)
```

[7]:
```
SVG(image)
```

[7]:

Predict

[8]:
```
# find the embedding of a new node
adjacency_vector = np.zeros(adjacency.shape[0], dtype = int)
adjacency_vector[:5] = np.ones(5, dtype = int)
```

[9]:
```
embedding_vector = spectral.predict(adjacency_vector)
```

Metrics

[10]:
```
cosine_modularity(adjacency, embedding)
```

[10]:
```
0.3802862736382374
```

Digraphs

[11]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Embedding

[12]:
```
bispectral = BiSpectral(2, normalized=False)
embedding = bispectral.fit_transform(adjacency)
embedding.shape
```

[12]:
```
(14, 2)
```

[13]:
```
image = svg_digraph(adjacency, embedding, names=names)
```

[14]:
```
SVG(image)
```

[14]:

Metrics

[15]:
```
cosine_modularity(adjacency, embedding)
```

[15]:
```
0.2068899883033235
```

Bigraphs

[16]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Embedding

[17]:
```
bispectral = BiSpectral(normalized=False)
bispectral.fit(biadjacency)
```

[17]:
```
BiSpectral(n_components=2, regularization=0.01, relative_regularization=True,␣
↪scaling=0.5, normalized=False, solver='auto')
```

[18]:
```
embedding_row = bispectral.embedding_row_
embedding_row.shape
```

[18]:
```
(15, 2)
```

[19]:
```
embedding_col = bispectral.embedding_col_
embedding_col.shape
```

[19]:
```
(16, 2)
```

[20]:
```
image = svg_bigraph(biadjacency, names_row, names_col,
                    position_row=embedding_row, position_col=embedding_col,
                    color_row='blue', color_col='red')
```

[21]:
```
SVG(image)
```

[21]:

3.11.2 SVD

This notebook illustrates the embedding of a graph through the singular value decomposition of the adjacency matrix.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.embedding import SVD, cosine_modularity
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
labels = graph.labels
```

Embedding

[5]:
```
svd = SVD(3)
embedding = svd.fit_transform(adjacency)
embedding.shape
```

[5]:
```
(34, 3)
```

[6]:
```
# skip first component
position = embedding[:,1:]
```

[7]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[8]:
```
SVG(image)
```

[8]:

Metrics

[9]:
```
cosine_modularity(adjacency, embedding)
```

[9]:
```
-0.7621328461686108
```

Digraphs

[10]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Embedding

[11]:
```
svd = SVD(3)
embedding = svd.fit_transform(adjacency)
embedding.shape
```

[11]:
```
(14, 3)
```

[12]:
```
# skip first component
position = embedding[:,1:]
```

[13]:
```
image = svg_digraph(adjacency, position, names=names)
```

[14]:
```
SVG(image)
```

[14]:

Metrics

[15]:
```
cosine_modularity(adjacency, embedding)
```

[15]:
```
-0.41509320559034557
```

Bigraphs

Loading

[16]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Embedding

[17]:
```
svd = SVD(3, normalized=False)
svd.fit(biadjacency)
```

[17]:
```
SVD(n_components=3, regularization=None, relative_regularization=True, factor_
↪singular=0.0, normalized=False, solver=LanczosSVD(maxiter=None, tol=0.0))
```

[18]:
```
embedding_row = svd.embedding_row_
embedding_row.shape
```

[18]:
```
(15, 3)
```

[19]:
```
embedding_col = svd.embedding_col_
embedding_col.shape
```

[19]:
```
(16, 3)
```

[20]:
```
# skip first component
position_row = embedding_row[:,1:]
position_col = embedding_col[:,1:]
```

[21]:
```
image = svg_bigraph(biadjacency, names_row, names_col,
                    position_row=embedding_row, position_col=embedding_col,
                    color_row='blue', color_col='red')
```

[22]:
```
SVG(image)
```

[22]:

3.11.3 GSVD

This notebook illustrates the embedding of a graph through the generalized singular value decomposition of the adjacency matrix.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.embedding import GSVD, cosine_modularity
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
labels = graph.labels
```

Embedding

[5]:
```
gsvd = GSVD(3, normalized=False)
embedding = gsvd.fit_transform(adjacency)
embedding.shape
```

[5]:
```
(34, 3)
```

[6]:
```
# skip first component
position = embedding[:,1:]
```

[7]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[8]:
```
SVG(image)
```

[8]:

Metrics

[9]:
```
cosine_modularity(adjacency, embedding)
```

[9]:
```
0.293795138937445
```

Digraphs

[10]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Embedding

[11]:
```
gsvd = GSVD(3, normalized=False)
embedding = gsvd.fit_transform(adjacency)
embedding.shape
```

[11]:
```
(14, 3)
```

[12]:
```
# skip first component
position = embedding[:,1:]
```

[13]:
```
image = svg_digraph(adjacency, position, names=names)
```

[14]:
```
SVG(image)
```

[14]:

Metrics

[15]:
```
cosine_modularity(adjacency, embedding)
```

[15]:
```
0.3903213346351039
```

Bigraphs

Loading

[16]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Embedding

[17]:
```
gsvd = GSVD(3, normalized=False)
gsvd.fit(biadjacency)
```

[17]:
```
GSVD(n_components=3, regularization=None, relative_regularization=True, factor_row=0.
↪5, factor_col=0.5, factor_singular=0.0, normalized=False,␣
↪solver=LanczosSVD(maxiter=None, tol=0.0))
```

[18]:
```
embedding_row = gsvd.embedding_row_
embedding_row.shape
```

[18]:
```
(15, 3)
```

[19]:
```
embedding_col = gsvd.embedding_col_
embedding_col.shape
```

[19]:
```
(16, 3)
```

[20]:
```
# skip first component
position_row = embedding_row[:,1:]
position_col = embedding_col[:,1:]
```

[21]:
```
image = svg_bigraph(biadjacency, names_row, names_col,
                    position_row=embedding_row, position_col=embedding_col,
                    color_row='blue', color_col='red')
```

[22]:
```
SVG(image)
```

[22]:

3.11.4 Louvain embedding

This notebook illustrates the spectral embedding of a graph obtained by looking at the edges between a node and each cluster in a clustering obtained by using the Louvain method for bipartite graphs.

[1]:
```
import numpy as np
```

[2]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.embedding import LouvainEmbedding, BiLouvainEmbedding, cosine_
↪modularity
```

Graphs

[3]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
labels = graph.labels
```

Embedding

[4]:
```
louvain = LouvainEmbedding()
embedding = louvain.fit_transform(adjacency)
embedding.shape
```

[4]:
```
(34, 7)
```

Predict

[5]:
```
# find the embedding of a new node
adjacency_vector = np.zeros(adjacency.shape[0], dtype = int)
adjacency_vector[:5] = np.ones(5, dtype = int)
```

[6]:
```
embedding_vector = louvain.predict(adjacency_vector)
```

Metrics

[7]:
```
embedding
```

[7]:
```
<34x7 sparse matrix of type '<class 'numpy.float64'>'
        with 75 stored elements in Compressed Sparse Row format>
```

[8]:
```
adjacency
```

[8]:
```
<34x34 sparse matrix of type '<class 'numpy.bool_'>'
        with 156 stored elements in Compressed Sparse Row format>
```

[9]:
```
cosine_modularity(adjacency, embedding)
```

[9]:
```
0.15385367663099692
```

Digraphs

[10]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
position = graph.position
names = graph.names
```

Embedding

[11]:
```
louvain = LouvainEmbedding()
embedding = louvain.fit_transform(adjacency)
embedding.shape
```

[11]:
```
(14, 5)
```

Metrics

[12]:
```
cosine_modularity(adjacency, embedding)
```

[12]:
```
0.1690350595626824
```

Bigraphs

[13]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

Embedding

[14]:
```
bilouvain = BiLouvainEmbedding()
bilouvain.fit(biadjacency)
```

[14]:
```
BiLouvainEmbedding(resolution=1.0, merge_isolated=True, modularity='dugue', tol_
↪optimization=0.001, tol_aggregation=0.001, n_aggregations=-1, shuffle_nodes=False)
```

[15]:
```
embedding_row = bilouvain.embedding_row_
embedding_row.shape
```

[15]:
```
(15, 5)
```

[16]:
```
embedding_col = bilouvain.embedding_col_
embedding_col.shape
```

[16]:
```
(16, 5)
```

3.11.5 Spring

This notebook illustrates the 2D embedding of a graph through the force-directed algorithm.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters
from sknetwork.embedding import Spring
from sknetwork.visualization import svg_graph, svg_digraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
labels = graph.labels
```

Embedding

[5]:
```
spring = Spring()
embedding = spring.fit_transform(adjacency)
embedding.shape
```

[5]:
```
(34, 2)
```

[6]:
```
image = svg_graph(adjacency, embedding, labels=labels)
```

[7]:
```
SVG(image)
```

[7]:

Digraphs

[8]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
```

Embedding

[9]:
```
spring = Spring()
embedding = spring.fit_transform(adjacency)
embedding.shape
```

[9]:
```
(14, 2)
```

[10]:
```
image = svg_digraph(adjacency, embedding, names=names)
```

[11]:
```
SVG(image)
```

[11]:

3.11.6 ForceAtlas2

This notebook illustrates the embedding of a graph through the force-directed algorithm Force Atlas 2.

[1]:
```
from IPython.display import SVG
```

[2]:
```
from sknetwork.data import karate_club
from sknetwork.embedding.force_atlas import ForceAtlas2
from sknetwork.visualization import svg_graph
```

Graphs

[3]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
labels = graph.labels
```

Embedding

[4]:
```
forceatlas2 = ForceAtlas2()
embedding = forceatlas2.fit_transform(adjacency)
image = svg_graph(adjacency, embedding, labels=labels)
SVG(image)
```

[4]:

Settings

Here we illustrate the influences of the different settings offered to the user.

LinLog

Replace the linear attraction force with a logarithmic attraction force.

[5]:
```
forceatlas2 = ForceAtlas2(lin_log = True)
embedding = forceatlas2.fit_transform(adjacency)
image = svg_graph(adjacency, embedding, labels=labels)
SVG(image)
```

[5]:

Scalling : repulsive and gravity force

Set the gravity and repulsion force constants (`gravity_factor` and `repulsion_factor`) to set the importance of each force in the layout. Keep values between 0.01 and 0.1.

[6]:
```
forceatlas2 = ForceAtlas2(gravity_factor = 0.1)
embedding = forceatlas2.fit_transform(adjacency)
image = svg_graph(adjacency, embedding, labels=labels)
SVG(image)
```

[6]:

Tolerance

Set the amount of swinging tolerated. Lower swinging yields less speed and more precision.

[7]:
```
forceatlas2 = ForceAtlas2(tolerance=1.5)
embedding = forceatlas2.fit_transform(adjacency)
image = svg_graph(adjacency, embedding, labels=labels)
SVG(image)
```

[7]:

KDTree Approximation

[8]:
```
forceatlas2 = ForceAtlas2(approx_radius=2)
embedding = forceatlas2.fit_transform(adjacency)
image = svg_graph(adjacency, embedding, labels=labels)
SVG(image)
```

[8]:

3.12 Link prediction

3.12.1 First-order methods

[1]:
```
from numpy import argsort

from sknetwork.classification import accuracy_score
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.linkpred import JaccardIndex, AdamicAdar, is_edge, whitened_sigmoid
```

Adamic-Adar

Graph

[2]:
```
adjacency = karate_club()
```

[3]:
```
aa = AdamicAdar()
aa.fit(adjacency)
```

[3]:
```
AdamicAdar()
```

[4]:
```
edges = [(0, 5), (4, 7), (15, 23), (17, 30)]
y_true = is_edge(adjacency, edges)

scores = aa.predict(edges)
y_pred = whitened_sigmoid(scores) > 0.75

accuracy_score(y_true, y_pred)
```

[4]:
```
1.0
```

DiGraph

[5]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
```

[6]:
```
picasso = 0
```

[7]:
```
aa.fit(adjacency)
```

[7]:
```
AdamicAdar()
```

[8]:
```
scores = aa.predict(picasso)

names[argsort(-scores)]
```

[8]:
```
array(['Pablo Picasso', 'Paul Cezanne', 'Claude Monet', 'Edgar Degas',
       'Vincent van Gogh', 'Henri Matisse', 'Pierre-Auguste Renoir',
       'Michel Angelo', 'Edouard Manet', 'Peter Paul Rubens', 'Rembrandt',
       'Gustav Klimt', 'Leonardo da Vinci', 'Egon Schiele'], dtype='<U21')
```

BiGraph

[9]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names = graph.names
```

[10]:
```
inception = 0
```

[11]:
```
aa.fit(biadjacency)
```

[11]:
```
AdamicAdar()
```

[12]:
```
scores = aa.predict(inception)

names[argsort(-scores)]
```

[12]:
```
array(['Inception', 'The Dark Knight Rises', 'The Great Gatsby',
       'Aviator', 'Midnight In Paris', 'The Big Short', 'Drive',
       'La La Land', 'Crazy Stupid Love', 'Vice',
       'The Grand Budapest Hotel', '007 Spectre', 'Inglourious Basterds',
       'Murder on the Orient Express', 'Fantastic Beasts 2'], dtype='<U28')
```

Jaccard Index

Graph

[13]:
```
adjacency = karate_club()
```

[14]:
```
ji = JaccardIndex()
ji.fit(adjacency)
```

[14]:
```
JaccardIndex()
```

[15]:
```
edges = [(0, 5), (4, 7), (15, 23), (17, 30)]
y_true = is_edge(adjacency, edges)

scores = ji.predict(edges)
y_pred = whitened_sigmoid(scores) > 0.75

accuracy_score(y_true, y_pred)
```

[15]:
```
0.5
```

DiGraph

[16]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
```

[17]:
```
picasso = 0
```

[18]:
```
ji.fit(adjacency)
```

[18]:
```
JaccardIndex()
```

[19]:
```
scores = ji.predict(picasso)

names[argsort(-scores)]
```

[19]:
```
array(['Pablo Picasso', 'Paul Cezanne', 'Claude Monet',
       'Pierre-Auguste Renoir', 'Henri Matisse', 'Edgar Degas',
       'Vincent van Gogh', 'Michel Angelo', 'Edouard Manet',
       'Peter Paul Rubens', 'Rembrandt', 'Gustav Klimt',
       'Leonardo da Vinci', 'Egon Schiele'], dtype='<U21')
```

BiGraph

[20]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names = graph.names
```

[21]:
```
inception = 0
```

[22]:
```
ji.fit(biadjacency)
```

[22]:
```
JaccardIndex()
```

[23]:
```
scores = ji.predict(inception)

names[argsort(-scores)]
```

[23]:
```
array(['Inception', 'The Dark Knight Rises', 'The Great Gatsby',
       'Aviator', 'Midnight In Paris', 'The Big Short', 'Drive',
       'La La Land', 'Crazy Stupid Love', 'Vice',
       'The Grand Budapest Hotel', '007 Spectre', 'Inglourious Basterds',
       'Murder on the Orient Express', 'Fantastic Beasts 2'], dtype='<U28')
```

3.13 Utils

3.13.1 Build graphs

Building graphs from the Iris dataset using nearest neighbors.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import pickle
```

[3]:
```
from sknetwork.embedding import Spring
from sknetwork.utils import KNNDense, CNNDense
from sknetwork.visualization import svg_graph
```

Nearest neighbors

[4]:
```
iris = pickle.load(open('iris.p', 'rb'))
```

[5]:
```
data = iris['data']
```

[6]:
```
labels = iris['labels']
```

[7]:
```
knn = KNNDense(n_neighbors=3, undirected=True)
adjacency = knn.fit_transform(data)
```

[8]:
```
image = svg_graph(adjacency, labels=labels, display_edge_weight=False)
```

[9]:
```
SVG(image)
```

[9]:

Component-wise nearest neighbors

[10]:
```
cnn = CNNDense(n_neighbors=2, undirected=True)
adjacency = cnn.fit_transform(data)
```

[11]:
```
image = svg_graph(adjacency, labels=labels, display_edge_weight=False)
```

[12]:
```
SVG(image)
```

[12]:

3.14 Visualization

3.14.1 Graphs

Visualization of graphs as SVG images.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor, load_netset
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels = graph.labels
```

Visualization

[5]:
```
image = svg_graph(adjacency, position, labels=labels, scale=3, node_size=30)
```

[6]:
```
SVG(image)
```

[6]:

Export

[7]:
```
svg_graph(adjacency, position, labels=labels, filename='karate_club')
```

[7]:
```
'<svg width="440" height="340" xmlns="http://www.w3.org/2000/svg">\n<path stroke-
↪width="1" stroke="black" d="M 264 200 353 168"/>\n<path stroke-width="1" stroke=
↪"black" d="M 20 116 153 125"/>\n<path stroke-width="1" stroke="black" d="M 28 91␣
↪131 68"/>\n<path stroke-width="1" stroke="black" d="M 28 91 20 116"/>\n<path stroke-
↪width="1" stroke="black" d="M 28 91 153 125"/>\n<path stroke-width="1" stroke="black
↪" d="M 162 20 171 45"/>\n<path stroke-width="1" stroke="black" d="M 162 20 246 82"/>
↪\n<path stroke-width="1" stroke="black" d="M 122 103 251 143"/>\n<path stroke-width=
↪"1" stroke="black" d="M 122 103 131 68"/>\n<path stroke-width="1" stroke="black" d=
↪"M 122 103 20 116"/>\n<path stroke-width="1" stroke="black" d="M 122 103 246 82"/>\n
↪<path stroke-width="1" stroke="black" d="M 197 120 251 143"/>\n<path stroke-width="1
↪" stroke="black" d="M 197 120 153 125"/>\n<path stroke-width="1" stroke="black" d=
↪"M 197 120 246 82"/>\n<path stroke-width="1" stroke="black" d="M 171 45 131 68"/>\n
↪<path stroke-width="1" stroke="black" d="M 171 45 162 20"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 20 116 122 103"/>\n<path stroke-width="1" stroke="black" d="M␣
↪20 116 28 91"/>\n<path stroke-width="1" stroke="black" d="M 131 68 246 82"/>\n<path␣
↪stroke-width="1" stroke="black" d="M 131 68 260 73"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 388 216 264 200"/>\n<path stroke-width="1" stroke="black" d="M␣
↪388 216 353 168"/>\n<path stroke-width="1" stroke="black" d="M 313 34 260 73"/>\n
↪<path stroke-width="1" stroke="black" d="M 313 34 246 82"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 331 143 264 200"/>\n<path stroke-width="1" stroke="black" d="M␣
↪331 143 353 168"/>\n<path stroke-width="1" stroke="black" d="M 331 143 246 82"/>\n
↪<path stroke-width="1" stroke="black" d="M 171 45 260 73"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 366 61 260 73"/>\n<path stroke-width="1" stroke="black" d="M␣
↪420 202 264 200"/>\n<path stroke-width="1" stroke="black" d="M 420 202 353 168"/>\n
↪<path stroke-width="1" stroke="black" d="M 228 32 260 73"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 228 32 246 82"/>\n<path stroke-width="1" stroke="black" d="M␣
↪131 68 28 91"/>\n<path stroke-width="1" stroke="black" d="M 131 68 122 103"/>\n
↪<path stroke-width="1" stroke="black" d="M 131 68 171 45"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 366 61 246 82"/>\n<path stroke-width="1" stroke="black" d="M␣
↪220 320 264 277"/>\n<path stroke-width="1" stroke="black" d="M 171 45 246 82"/>\n
↪<path stroke-width="1" stroke="black" d="M 344 107 282 125"/>\n<path stroke-width="1
↪" stroke="black" d="M 246 82 282 125"/>\n<path stroke-width="1" stroke="black" d="M␣
↪246 82 197 100"/>\n<path stroke-width="1" stroke="black" d="M 246 82 282 153"/>\n
↪<path stroke-width="1" stroke="black" d="M 246 82 348 43"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 246 82 273 27"/>\n<path stroke-width="1" stroke="black" d="M␣
↪246 82 313 34"/>\n<path stroke-width="1" stroke="black" d="M 246 82 331 143"/>\n
↪<path stroke-width="1" stroke="black" d="M 246 82 366 61"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 246 82 228 32"/>\n<path stroke-width="1" stroke="black" d="M␣
↪246 82 131 68"/>\n<path stroke-width="1" stroke="black" d="M 246 82 162 20"/>\n
↪<path stroke-width="1" stroke="black" d="M 246 82 122 103"/>\n<path stroke-width="1
↪" stroke="black" d="M 246 82 197 120"/>\n<path stroke-width="1" stroke="black" d="M␣
↪246 82 171 45"/>\n<path stroke-width="1" stroke="black" d="M 246 82 344 107"/>\n
↪<path stroke-width="1" stroke="black" d="M 260 73 246 82"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 260 73 153 125"/>\n<path stroke-width="1" stroke="black" d="M␣
↪260 73 344 107"/>\n<path stroke-width="1" stroke="black" d="M 260 73 171 45"/>\n
↪<path stroke-width="1" stroke="black" d="M 344 107 260 73"/>\n<path stroke-width="1
↪" stroke="black" d="M 344 107 246 82"/>\n<path stroke-width="1" stroke="black" d="M␣
↪153 125 264 200"/>\n<path stroke-width="1" stroke="black" d="M 153 125 20 116"/>\n
↪<path stroke-width="1" stroke="black" d="M 153 125 28 91"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 153 125 197 120"/>\n<path stroke-width="1" stroke="black" d="M␣
↪153 125 260 73"/>\n<path stroke-width="1" stroke="black" d="M 344 107 353 168"/>\n
↪<path stroke-width="1" stroke="black" d="M 153 125 246 82"/>\n<path stroke-width="1
↪" stroke="black" d="M 260 73 282 125"/>\n<path stroke-width="1" stroke="black" d="M␣
↪260 73 348 43"/>\n<path stroke-width="1" stroke="black" d="M 260 73 273 27"/>\n
↪<path stroke-width="1" stroke="black" d="M 260 73 313 34"/>\n<path stroke-width="1"␣
↪stroke="black" d="M 260 73 366 61"/>\n<path stroke-width="1" stroke="black" d="M␣
↪260 73 228 32"/>\n<path stroke-width="1" stroke="black" d="M 260 73 131 68"/>\n
```

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Degrees

[8]:
```
image = svg_graph(adjacency, position, labels=labels, display_node_weight=True)
```

[9]:
```
SVG(image)
```

[9]:

Scores

[10]:
```
degrees = adjacency.dot(np.ones(adjacency.shape[0]))
```

[11]:
```
image = svg_graph(adjacency, position, scores=degrees)
```

[12]:
```
SVG(image)
```

[12]:

Seeds

[13]:
```
seeds = list(np.argsort(-degrees)[:2])
```

[14]:
```
image = svg_graph(adjacency, position, labels=labels, seeds=seeds)
```

[15]:
```
SVG(image)
```

[15]:

No edges

[16]:
```
graph = load_netset('openflights')
adjacency = graph.adjacency
position = graph.position
```

[17]:
```
weights = adjacency.dot(np.ones(adjacency.shape[0]))
```

[18]:
```
image = svg_graph(adjacency, position, scores=np.log(weights), node_order=np.
↪argsort(weights),
                  node_size_min=2, node_size_max=10, height=400, width=800,
                  display_node_weight=True, display_edges=False)
```

[19]:
```
SVG(image)
```

[19]:

Digraphs

[20]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[21]:
```
image = svg_digraph(adjacency, position, names)
```

[22]:
```
SVG(image)
```
[22]:

Bigraphs

[23]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[24]:
```
# default layout
image = svg_bigraph(biadjacency, names_row, names_col, color_row='blue', color_col=
↪'red')
```

[25]:
```
SVG(image)
```
[25]:

[26]:
```
# keep original order of rows and columns
image = svg_bigraph(biadjacency, names_row, names_col=names_col, color_row='blue',␣
↪color_col='red',
                    reorder=False)
```

[27]:
```
SVG(image)
```
[27]:

3.14.2 Paths

Visualization of paths.

[1]:
```
from IPython.display import SVG
```

[2]:
```
from sknetwork.data import house, cyclic_digraph, star_wars
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
```

Graphs

[3]:
```
graph = house(True)
adjacency = graph.adjacency
position = graph.position
```

[4]:
```
image = svg_graph(adjacency, position, edge_width=5, edge_labels=[(0, 1, 0), (1, 2,␣
↪0), (2, 3, 0)])
```

[5]:
```
SVG(image)
```
[5]:

[6]:
```
image = svg_graph(None, position, edge_width=5, edge_labels=[(0, 1, 0), (1, 2, 0), (2,
↪ 3, 0)])
```

[7]:
```
SVG(image)
```
[7]:

Digraphs

[8]:
```
graph = cyclic_digraph(10, metadata=True)
adjacency = graph.adjacency
position = graph.position
```

[9]:
```
path1 = [(0, 1, 0), (1, 2, 0), (2, 3, 0)]
path2 = [(6, 7, 1), (7, 8, 1)]
```

[10]:
```
image = svg_digraph(adjacency, position, width = 200, height=None, edge_width=5, edge_
↪labels=path1 + path2)
```

[11]:
```
SVG(image)
```
[11]:

Bigraphs

[12]:
```
graph = star_wars(True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[13]:
```
path = [(0, 1, 0), (2, 1, 0)]
```

[14]:
```
image = svg_bigraph(biadjacency, names_row=names_row, names_col=names_col, edge_
↪width=5, edge_labels=path)
```

[15]:
```
SVG(image)
```
[15]:

3.14.3 Dendrograms

Visualization of dendrograms as SVG images.

[1]:
```
from IPython.display import SVG
```

[2]:
```
import numpy as np
```

[3]:
```
from sknetwork.data import karate_club, painters, movie_actor
from sknetwork.hierarchy import Paris, BiParis
from sknetwork.visualization import svg_graph, svg_digraph, svg_bigraph
from sknetwork.visualization import svg_dendrogram
```

Graphs

[4]:
```
graph = karate_club(metadata=True)
adjacency = graph.adjacency
position = graph.position
labels = graph.labels
```

[5]:
```
image = svg_graph(adjacency, position, labels=labels)
```

[6]:
```
SVG(image)
```

[6]:

Dendrogram

[7]:
```
paris = Paris()
dendrogram = paris.fit_transform(adjacency)
```

[8]:
```
image = svg_dendrogram(dendrogram)
```

[9]:
```
SVG(image)
```

[9]:

[10]:
```
n = adjacency.shape[0]
```

[11]:
```
image = svg_dendrogram(dendrogram, names=np.arange(n), n_clusters=5, color='gray')
```

[12]:
```
SVG(image)
```

[12]:

Export

[13]:
```
svg_dendrogram(dendrogram, filename='dendrogram_karate_club')
```

[13]:
```
'<svg width="420" height="320"  xmlns="http://www.w3.org/2000/svg"><path stroke-width=
↪"2" stroke="red" d="M 351.1764705882353 310 351.1764705882353 306.05522660108716" />
↪<path stroke-width="2" stroke="red" d="M 362.9411764705883 310 362.9411764705883␣
↪306.05522660108716" /><path stroke-width="2" stroke="red" d="M 351.1764705882353␣
↪306.05522660108716 362.9411764705883 306.05522660108716" /><path stroke-width="2"␣
↪stroke="blue" d="M 33.529411764705884 310 33.529411764705884 306.05522660108716" />
↪<path stroke-width="2" stroke="blue" d="M 45.294117647058826 310 45.294117647058826␣
↪306.05522660108716" /><path stroke-width="2" stroke="blue" d="M 33.529411764705884␣
↪306.05522660108716 45.294117647058826 306.05522660108716" /><path stroke-width="2"␣
↪stroke="red" d="M 386.47058823529414 310 386.47058823529414 305.5621300890031" />
↪<path stroke-width="2" stroke="red" d="M 398.2352941176471 310 398.2352941176471␣
↪305.5621300890031" /><path stroke-width="2" stroke="red" d="M 386.47058823529414␣
↪305.5621300890031 398.2352941176471 305.5621300890031" /><path stroke-width="2"␣
↪stroke="blue" d="M 80.58823529411765 310 80.58823529411765 305.5621300890031" />
↪<path stroke-width="2" stroke="blue" d="M 92.3529411764706 310 92.3529411764706 305.
↪5621300890031" /><path stroke-width="2" stroke="blue" d="M 80.58823529411765 305.
↪5621300890031 92.3529411764706 305.5621300890031" /><path stroke-width="2" stroke=
↪"red" d="M 257.05882352941177 310 257.05882352941177 304.0828399016307" /><path␣
↪stroke-width="2" stroke="red" d="M 268.82352941176475 310 268.82352941176475 304.
↪0828399016307" /><path stroke-width="2" stroke="red" d="M 257.05882352941177 304.
↪0828399016307 268.82352941176475 304.0828399016307" /><path stroke-width="2" stroke=
↪"red" d="M 357.0588235294118 306.05522660108716 357.0588235294118 304.0828399016307
↪" /><path stroke-width="2" stroke="red" d="M 374.7058823529412 310 374.
↪7058823529412 304.0828399016307" /><path stroke-width="2" stroke="red" d="M 357.
↪0588235294118 304.0828399016307 374.7058823529412 304.0828399016307" /><path stroke-
↪width="2" stroke="red" d="M 292.3529411764706 310 292.3529411764706 302.
↪11045320217426" /><path stroke-width="2" stroke="red" d="M 304.11764705882354 310␣
↪304.11764705882354 302.11045320217426" /><path stroke-width="2" stroke="red" d="M␣
↪292.3529411764706 302.11045320217426 304.11764705882354 302.11045320217426" /><path␣
↪stroke-width="2" stroke="red" d="M 221.76470588235296 310 221.76470588235296 301.
↪12426017800624" /><path stroke-width="2" stroke="red" d="M 233.5294117647059 310␣
```

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Digraphs

[14]:
```
graph = painters(metadata=True)
adjacency = graph.adjacency
names = graph.names
position = graph.position
```

[15]:
```
image = svg_digraph(adjacency, position, names)
```

[16]:
```
SVG(image)
```

[16]:

Dendrogram

[17]:
```
paris = Paris()
dendrogram = paris.fit_transform(adjacency)
```

[18]:
```
image = svg_dendrogram(dendrogram, names, n_clusters=3, rotate=True)
```

[19]:
```
SVG(image)
```

[19]:

Bigraphs

[20]:
```
graph = movie_actor(metadata=True)
biadjacency = graph.biadjacency
names_row = graph.names_row
names_col = graph.names_col
```

[21]:
```
image = svg_bigraph(biadjacency, names_row, names_col)
```

[22]:
```
SVG(image)
```

[22]:

Dendrograms

[23]:
```
biparis = BiParis()
biparis.fit(biadjacency)
dendrogram_row = biparis.dendrogram_row_
dendrogram_col = biparis.dendrogram_col_
dendrogram_full = biparis.dendrogram_full_
```

[24]:
```
image = svg_dendrogram(dendrogram_row, names_row, n_clusters=3, rotate=True)
```

[25]:
```
SVG(image)
```

[25]:

[26]:
```
image = svg_dendrogram(dendrogram_col, names_col, n_clusters=3, rotate=True)
```

[27]:
```
SVG(image)
```
[27]:

3.14.4 Pie-chart nodes

Visualization of membership matrices with pie-chart nodes.

[1]:
```
from IPython.display import SVG
from scipy import sparse
```

[2]:
```
from sknetwork.data import bow_tie, painters
from sknetwork.visualization import svg_graph
from sknetwork.clustering import Louvain
```

Graphs

[3]:
```
graph = bow_tie(True)
adjacency = graph.adjacency
position = graph.position
```

[4]:
```
image = svg_graph(adjacency, position, membership=sparse.csr_matrix([[.5, .5], [0, 1],
↪ [0, 1], [1, 0], [1, 0]]), node_size=15)
```

[5]:
```
SVG(image)
```
[5]:

Digraphs

[6]:
```
graph = painters(True)
adjacency = graph.adjacency
names = graph.names
```

[7]:
```
louvain = Louvain()
louvain.fit(adjacency)
membership = louvain.membership_
```

[8]:
```
image = svg_graph(adjacency, names=names, membership=membership, node_size=15)
```

[9]:
```
SVG(image)
```
[9]:

3.15 Contributing

Contributions are welcome, and they are greatly appreciated! Every little bit helps, and credit will always be given.

You can contribute in many ways:

3.15.1 Types of Contributions

Report Bugs

Report bugs at https://github.com/sknetwork-team/sknetwork/issues.

If you are reporting a bug, please include:

- Your operating system name and version.
- Any details about your local setup that might be helpful in troubleshooting.
- Detailed steps to reproduce the bug.

Fix Bugs

Look through the GitHub issues for bugs. Anything tagged with "bug" and "help wanted" is open to whoever wants to implement it.

Implement Features

Look through the GitHub projects. Anything listed in the projects is a feature to be implemented.

You can also look through GitHub issues for features. Anything tagged with "enhancement" and "help wanted" is open to whoever wants to implement it.

Write Documentation

scikit-network could always use more documentation, whether as part of the official scikit-network docs, in docstrings, or even on the web in blog posts, articles, and such.

Submit Feedback

The best way to send feedback is to file an issue at https://github.com/sknetwork-team/sknetwork/issues.

If you are proposing a feature:

- Explain in detail how it would work.
- Keep the scope as narrow as possible, to make it easier to implement.
- Remember that this is a volunteer-driven project, and that contributions are welcome :)

3.15.2 Get Started!

Ready to contribute? Here's how to set up *sknetwork* for local development.

1. Fork the *sknetwork* repo on GitHub.
2. Clone your fork locally:

```
$ git clone git@github.com:your_name_here/sknetwork.git
```

3. Install your local copy into a virtualenv. Assuming you have virtualenvwrapper installed, this is how you set up your fork for local development:

```
$ mkvirtualenv sknetwork
$ cd sknetwork/
$ python setup.py develop
```

4. Create a branch for local development:

```
$ git checkout -b name-of-your-bugfix-or-feature
```

   Now you can make your changes locally.

5. When you're done making changes, check that your changes pass flake8 and the tests, including testing other Python versions with tox:

```
$ flake8 sknetwork tests
$ python setup.py test or py.test
$ tox
```

   To get flake8 and tox, just pip install them into your virtualenv.

6. Commit your changes and push your branch to GitHub:

```
$ git add .
$ git commit -m "Your detailed description of your changes."
$ git push origin name-of-your-bugfix-or-feature
```

7. Submit a pull request through the GitHub website.

3.15.3 Pull Request Guidelines

Before you submit a pull request, check that it meets these guidelines:

1. The pull request should include tests.
2. If the pull request adds functionality, the docs should be updated. Put your new functionality into a function with a docstring, and add the feature to the list in README.rst.
3. The pull request should work for Python 3.6, 3.7 and 3.8. Check https://travis-ci.org/sharpenb/sknetwork/pull_requests and make sure that the tests pass for all supported Python versions.

A more complete guide for writing code for the package can be found under "Contributing guide" in the Wiki.

3.15.4 Tips

To run a subset of tests:

```
$ py.test tests.test_sknetwork
```

Do not hesitate to check the Wiki.

3.15.5 Deploying

A reminder for the maintainers on how to deploy. Make sure all your changes are committed (including an entry in HISTORY.rst). Then run:

```
$ bumpversion patch # possible: major / minor / patch
$ git push
$ git push --tags
```

Travis will then deploy to PyPI if tests pass.

3.16 Credits

3.16.1 Development Lead

- Thomas Bonald <thomas.bonald@telecom-paris.fr>
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3.16.2 Contributors

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- Julien Simonnet
- Alexis Barreaux
- Rémi Jaylet
- Victor Manach
- Pierre Pébereau
- Armand Boschin
- Tiphaine Viard

3.17 History

3.17.1 0.20.0 (2020-10-20)

- Added betweenness algorithm by Tiphaine Viard (#444)

3.17.2 0.19.3 (2020-09-17)

- Added Louvain-based embedding
- Fix documentation with new dataset website URLs

3.17.3 0.19.2 (2020-09-14)

- Fix documentation with new dataset website URLs.

3.17.4 0.19.1 (2020-09-09)

- Fix visualization features
- Fix documentation

3.17.5 0.19.0 (2020-09-02)

- Added link prediction module
- Added pie-node visualization of memberships
- Added Weisfeiler-Lehman graph coloring by Pierre Pebereau and Alexis Barreaux (#394)
- Added Force Atlas 2 graph layout by Victor Manach and Rémi Jaylet (#396)
- Added triangle listing algorithm for directed and undirected graph by Julien Simonnet and Yohann Robert (#376)
- Added k-core decomposition algorithm by Julien Simonnet and Yohann Robert (#377)
- Added k-clique listing algorithm by Julien Simonnet and Yohann Robert (#377)
- Added color map option in visualization module
- Updated NetSet URL

3.17.6 0.18.0 (2020-06-08)

- Added Katz centrality
- Refactor connectivity module into paths and topology
- Refactor Diffusion into Dirichlet
- Added parsers for adjacency list TSV and GraphML
- Added shortest paths and distances

3.17.7 0.17.0 (2020-05-07)

- Add clustering by label propagation
- Add models
- Add function to build graph from edge list
- Change a parameter in SVG visualization functions
- Minor corrections

3.17.8 0.16.0 (2020-04-30)

- Refactor basics module into connectivity
- Cython version for label propagation
- Minor corrections

3.17.9 0.15.2 (2020-04-24)

- Clarified requirements
- Minor corrections

3.17.10 0.15.1 (2020-04-21)

- Added OpenMP support for all platforms

3.17.11 0.15.0 (2020-04-20)

- Updated ranking module : new pagerank solver, new HITS params, post-processing
- Polynomes in linear algebra
- Added meta.name attribute for Bunch
- Minor corrections

3.17.12 0.14.0 (2020-04-17)

- Added spring layout in embedding
- Added label propagation in classification
- Added save / load functions in data
- Added display edges parameter in svg graph exports
- Corrected typos in documentation

3.17.13 0.13.3 (2020-04-13)

- Minor bug

3.17.14 0.13.2 (2020-04-13)

- Added wheels for multiple platforms (OSX, Windows (32 & 64 bits) and many Linux) and Python version (3.6/3.7/3.8)
- Documentation update (SVG dendrograms, tutorial updates)

3.17.15 0.13.1a (2020-04-09)

- Minor bug

3.17.16 0.13.0a (2020-04-09)

- Changed from Numba to Cython for better performance
- Added visualization module
- Added k-nearest neighbors classifier
- Added Louvain hierarchy
- Added predict method in embedding
- Added soft clustering to clustering algorithms
- Added soft classification to classification algorithms
- Added graphs in data module
- Various API change

3.17.17 0.12.1 (2020-01-20)

- Added heat kernel based node classifier
- Updated loaders for WikiLinks
- Fixed file-related issues for Windows

3.17.18 0.12.0 (2019-12-10)

- Added VerboseMixin for verbosity features
- Added Loaders for WikiLinks & Konect databases

3.17.19 0.11.0 (2019-11-28)

- sknetwork: new API for bipartite graphs
- new module: Soft node classification
- new module: Node classification
- new module: data (merge toy graphs + loader)
- clustering: Spectral Clustering
- ranking: new algorithms
- utils: K-neighbors
- hierarchy: Spectral WardDense
- data: loader (Vital Wikipedia)

3.17.20 0.10.1 (2019-08-26)

- Minor bug

3.17.21 0.10.0 (2019-08-26)

- Clustering (and related metrics) for directed and bipartite graphs
- Hierarchical clustering (and related metrics) for directed and bipartite graphs
- Fix bugs on embedding algorithms

3.17.22 0.9.0 (2019-07-24)

- Change parser output
- Fix bugs in ranking algorithms (zero-degree nodes)
- Add notebooks
- Import algorithms from scipy (shortest path, connected components, bfs/dfs)
- Change SVD embedding (now in decreasing order of singular values)

3.17.23 0.8.2 (2019-07-19)

- Minor bug

3.17.24 0.8.1 (2019-07-18)

- Added diffusion ranking
- Minor fixes
- Minor doc tweaking

3.17.25 0.8.0 (2019-07-17)

- Changed Louvain, BiLouvain, Paris and PageRank APIs
- Changed PageRank method
- Documentation overhaul
- Improved Jupyter tutorials

3.17.26 0.7.1 (2019-07-04)

- Added Algorithm class for nicer repr of some classes
- Added Jupyter notebooks as tutorials in the docs
- Minor fixes

3.17.27 0.7.0 (2019-06-24)

- Updated PageRank
- Added tests for Numba versioning

3.17.28 0.6.1 (2019-06-19)

- Minor bug

3.17.29 0.6.0 (2019-06-19)

- Largest connected component
- Simplex projection
- Sparse Low Rank Decomposition
- Numba support for Paris
- Various fixes and updates

3.17.30 0.5.0 (2019-04-18)

- Unified Louvain.

3.17.31 0.4.0 (2019-04-03)

- Added Louvain for directed graphs and ComboLouvain for bipartite graphs.

3.17.32 0.3.0 (2019-03-29)

- Updated clustering module and documentation.

3.17.33 0.2.0 (2019-03-21)

- First real release on PyPI.

3.17.34 0.1.1 (2018-05-29)

- First release on PyPI.

3.18 Index

3.19 Glossary

adjacency Square matrix whose entries indicate edges between nodes of a graph, usually denoted by A.

biadjacency Rectangular matrix whose entries indicate edges between nodes of a bipartite graph, usually denoted by B.

co-neighbors Graph defined by $\tilde{A} = AF^{-1}A^T$, or $\tilde{B} = BF^{-1}B^T$, where F is a weight matrix.

degree For an unweighted, undirected graph, the degree of a node is defined as its number of neighbors.

embedding Mapping of the nodes of a graph to points in a vector space.

graph Mathematical object $G = (V, E)$, where V is the set of vertices or nodes and $E \in V \times V$ the set of edges.

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