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# **brainconn**

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brainconn is a Python package for graph theoretic analysis of neuroimaging data.



## 1.1 What is graph theory?

Graph theory refers to methods for measures graphs.

## 1.2 What is brainconn?

brainconn is a Python package for the calculation of graph theoretic metrics from neuroimaging data.

## 1.3 API Reference

### 1.3.1 `brainconn centrality`: Centrality

Metrics which identify the most important nodes in graphs.

<code>brainconn.centrality</code>	Metrics which identify the most important nodes in graphs.
<code>brainconn.centrality.betweenness_bin(G)</code>	Node betweenness centrality is the fraction of all shortest paths in the network that contain a given node.
<code>brainconn.centrality.betweenness_wei(G)</code>	Node betweenness centrality is the fraction of all shortest paths in the network that contain a given node.
<code>brainconn.centrality.diversity_coef_sign(W, ci)</code>	The Shannon entropy-based diversity coefficient measures the diversity of intermodular connections of individual nodes and ranges from 0 to 1.
<code>brainconn.centrality.edge_betweenness_bin(G)</code>	Edge betweenness centrality is the fraction of all shortest paths in the network that contain a given edge.

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Table 1 – continued from previous page

<code>brainconn.centrali- ty.edge_betweenness_wei(G)</code>	Edge betweenness centrality is the fraction of all shortest paths in the network that contain a given edge.
<code>brainconn.centrali- ty.eigenvector_centrality_und(CIJ)</code>	Eigenvector centrality is a self-referential measure of centrality: nodes have high eigenvector centrality if they connect to other nodes that have high eigenvector centrality.
<code>brainconn.centrali- ty.erange(CIJ)</code>	Shortcuts are central edges which significantly reduce the characteristic path length in the network.
<code>brainconn.centrali- ty.flow_coef_bd(CIJ)</code>	Computes the flow coefficient for each node and averaged over the network, as described in Honey et al.
<code>brainconn.centrali- ty.gateway_coef_sign(W, ci)</code>	The gateway coefficient is a variant of participation coefficient.
<code>brainconn.centrali- ty.kcoreness_centrality_bd(CIJ)</code>	The k-core is the largest subgraph comprising nodes of degree at least k.
<code>brainconn.centrali- ty.kcoreness_centrality_bu(CIJ)</code>	The k-core is the largest subgraph comprising nodes of degree at least k.
<code>brainconn.centrali- ty.module_degree_zscore(W, ci)</code>	The within-module degree z-score is a within-module version of degree centrality.
<code>brainconn.centrali- ty.pagerank_centrality(A, d)</code>	The PageRank centrality is a variant of eigenvector centrality.
<code>brainconn.centrali- ty.participation_coef(W, ci)</code>	Participation coefficient is a measure of diversity of intermodular connections of individual nodes.
<code>brainconn.centrali- ty.participation_coef_sign(W, ci)</code>	Participation coefficient is a measure of diversity of intermodular connections of individual nodes.
<code>brainconn.centrali- ty.subgraph_centrality(CIJ)</code>	The subgraph centrality of a node is a weighted sum of closed walks of different lengths in the network starting and ending at the node.

## brainconn.centrali- ty.betweenness\_bin

### betweenness\_bin (G)

Node betweenness centrality is the fraction of all shortest paths in the network that contain a given node. Nodes with high values of betweenness centrality participate in a large number of shortest paths.

#### Parameters

- **A** (NxN `numpy.ndarray`) – binary directed/undirected connection matrix
- **BC** (Nx1 `numpy.ndarray`) – node betweenness centrality vector

#### Notes

Betweenness centrality may be normalised to the range [0,1] as  $BC/[(N-1)(N-2)]$ , where N is the number of nodes in the network.

## Examples using brainconn.centrali- ty.betweenness\_bin

- *Calculate centrality measures*



**brainconn.centraliity.betweenness\_wei****betweenness\_wei** (*G*)

Node betweenness centrality is the fraction of all shortest paths in the network that contain a given node. Nodes with high values of betweenness centrality participate in a large number of shortest paths.

**Parameters** **L** (NxN `numpy.ndarray`) – directed/undirected weighted connection matrix

**Returns** **BC** – node betweenness centrality vector

**Return type** Nx1 `numpy.ndarray`

**Notes**

The input matrix must be a connection-length matrix, typically obtained via a mapping from weight to length. For instance, in a weighted correlation network higher correlations are more naturally interpreted as shorter distances and the input matrix should consequently be some inverse of the connectivity matrix.

Betweenness centrality may be normalised to the range [0,1] as  $BC/[(N-1)(N-2)]$ , where *N* is the number of nodes in the network.

**Examples using brainconn.centraliity.betweenness\_wei**

- *Calculate centrality measures*

**brainconn.centraliity.diversity\_coef\_sign****diversity\_coef\_sign** (*W*, *ci*)

The Shannon entropy-based diversity coefficient measures the diversity of intermodular connections of individual nodes and ranges from 0 to 1.

**Parameters**

- **W** (NxN `numpy.ndarray`) – undirected connection matrix with positive and negative weights
- **ci** (Nx1 `numpy.ndarray`) – community affiliation vector

**Returns**

- **Hpos** (Nx1 `numpy.ndarray`) – diversity coefficient based on positive connections
- **Hneg** (Nx1 `numpy.ndarray`) – diversity coefficient based on negative connections

**brainconn.centraliity.edge\_betweenness\_bin****edge\_betweenness\_bin** (*G*)

Edge betweenness centrality is the fraction of all shortest paths in the network that contain a given edge. Edges with high values of betweenness centrality participate in a large number of shortest paths.

**Parameters** **A** (NxN `numpy.ndarray`) – binary directed/undirected connection matrix

**Returns**

- **EBC** (NxN `numpy.ndarray`) – edge betweenness centrality matrix
- **BC** (Nx1 `numpy.ndarray`) – node betweenness centrality vector

## Notes

Betweenness centrality may be normalised to the range [0,1] as  $BC/[(N-1)(N-2)]$ , where  $N$  is the number of nodes in the network.

### Examples using `brainconn.centralities.edge_betweenness_bin`

- *Calculate centrality measures*

### `brainconn.centralities.edge_betweenness_wei`

#### `edge_betweenness_wei` ( $G$ )

Edge betweenness centrality is the fraction of all shortest paths in the network that contain a given edge. Edges with high values of betweenness centrality participate in a large number of shortest paths.

**Parameters**  $L$  ( $N \times N$  `numpy.ndarray`) – directed/undirected weighted connection matrix

#### Returns

- **EBC** ( $N \times N$  `numpy.ndarray`) – edge betweenness centrality matrix
- **BC** ( $N \times 1$  `numpy.ndarray`) – nodal betweenness centrality vector

## Notes

**The input matrix must be a connection-length matrix, typically** obtained via a mapping from weight to length. For instance, in a weighted correlation network higher correlations are more naturally interpreted as shorter distances and the input matrix should consequently be some inverse of the connectivity matrix.

**Betweenness centrality may be normalised to the range [0,1] as**  $BC/[(N-1)(N-2)]$ , where  $N$  is the number of nodes in the network.

### Examples using `brainconn.centralities.edge_betweenness_wei`

- *Calculate centrality measures*

### `brainconn.centralities.eigenvector centrality_und`

#### `eigenvector centrality_und` ( $C_{IJ}$ )

Eigenvector centrality is a self-referential measure of centrality: nodes have high eigenvector centrality if they connect to other nodes that have high eigenvector centrality. The eigenvector centrality of node  $i$  is equivalent to the  $i$ th element in the eigenvector corresponding to the largest eigenvalue of the adjacency matrix.

#### Parameters

- **$C_{IJ}$**  ( $N \times N$  `numpy.ndarray`) – binary/weighted undirected adjacency matrix
- **$v$**  ( $N \times 1$  `numpy.ndarray`) – eigenvector associated with the largest eigenvalue of the matrix

**brainconn.centralities.erange****erange** (*CIJ*)

Shortcuts are central edges which significantly reduce the characteristic path length in the network.

**Parameters** *CIJ* (NxN `numpy.ndarray`) – binary directed connection matrix

**Returns**

- **Erange** (NxN `numpy.ndarray`) – range for each edge, i.e. the length of the shortest path from *i* to *j* for edge *c(i,j)* after the edge has been removed from the graph
- **eta** (*float*) – average range for the entire graph
- **Eshort** (NxN `numpy.ndarray`) – entries are ones for shortcut edges
- **fs** (*float*) – fractions of shortcuts in the graph

**Notes**

Follows the treatment of ‘shortcuts’ by Duncan Watts

**brainconn.centralities.flow\_coef\_bd****flow\_coef\_bd** (*CIJ*)

Computes the flow coefficient for each node and averaged over the network, as described in Honey et al. (2007) PNAS. The flow coefficient is similar to betweenness centrality, but works on a local neighborhood. It is mathematically related to the clustering coefficient (*cc*) at each node as,  $fc+cc \leq 1$ .

**Parameters** *CIJ* (NxN `numpy.ndarray`) – binary directed connection matrix

**Returns**

- **fc** (Nx1 `numpy.ndarray`) – flow coefficient for each node
- **FC** (*float*) – average flow coefficient over the network
- **total\_flo** (*int*) – number of paths that “flow” across the central node

**brainconn.centralities.gateway\_coef\_sign****gateway\_coef\_sign** (*W, ci, centrality\_type='degree'*)

The gateway coefficient is a variant of participation coefficient. It is weighted by how critical the connections are to intermodular connectivity (e.g. if a node is the only connection between its module and another module, it will have a higher gateway coefficient, unlike participation coefficient).

**Parameters**

- **W** (NxN `numpy.ndarray`) – undirected signed connection matrix
- **ci** (Nx1 `numpy.ndarray`) – community affiliation vector
- **centrality\_type** (*enum*) – ‘degree’ - uses the weighted degree (i.e. node strength)  
‘betweenness’ - uses the betweenness centrality

**Returns**

- **Gpos** (Nx1 `numpy.ndarray`) – gateway coefficient for positive weights
- **Gneg** (Nx1 `numpy.ndarray`) – gateway coefficient for negative weights

## References

### `brainconn.centralities.kcoreness_centrality_bd`

#### `kcoreness_centrality_bd` (*CIJ*)

The k-core is the largest subgraph comprising nodes of degree at least k. The coreness of a node is k if the node belongs to the k-core but not to the (k+1)-core. This function computes k-coreness of all nodes for a given binary directed connection matrix.

**Parameters** *CIJ* (NxN `numpy.ndarray`) – binary directed connection matrix

#### Returns

- **coreness** ((N,) `numpy.ndarray`) – node coreness
- **kn** ((N,) `numpy.ndarray`) – size of k-core

### `brainconn.centralities.kcoreness_centrality_bu`

#### `kcoreness_centrality_bu` (*CIJ*)

The k-core is the largest subgraph comprising nodes of degree at least k. The coreness of a node is k if the node belongs to the k-core but not to the (k+1)-core. This function computes the coreness of all nodes for a given binary undirected connection matrix.

**Parameters** *CIJ* (NxN `numpy.ndarray`) – binary undirected connection matrix

#### Returns

- **coreness** ((N,) `numpy.ndarray`) – node coreness
- **kn** ((N,) `numpy.ndarray`) – size of k-core

### `brainconn.centralities.module_degree_zscore`

#### `module_degree_zscore` (*W, ci, flag=0*)

The within-module degree z-score is a within-module version of degree centrality.

#### Parameters

- **W** (NxN `numpy.ndarray`) – binary/weighted directed/undirected connection matrix
- **ci** (Nx1 `np.array_like`) – community affiliation vector
- **flag** (*int*) –

**Graph type. 0: undirected graph (default)** 1: directed graph in degree 2: directed graph out degree 3: directed graph in and out degree

**Returns** *Z* – within-module degree Z-score

**Return type** Nx1 `numpy.ndarray`

### `brainconn.centralities.pagerank_centrality`

#### `pagerank_centrality` (*A, d, falff=None*)

The PageRank centrality is a variant of eigenvector centrality. This function computes the PageRank centrality of each vertex in a graph.

Formally, PageRank is defined as the stationary distribution achieved by instantiating a Markov chain on a graph. The PageRank centrality of a given vertex, then, is proportional to the number of steps (or amount of time) spent at that vertex as a result of such a process.

The PageRank index gets modified by the addition of a damping factor,  $d$ . In terms of a Markov chain, the damping factor specifies the fraction of the time that a random walker will transition to one of its current state's neighbors. The remaining fraction of the time the walker is restarted at a random vertex. A common value for the damping factor is  $d = 0.85$ .

#### Parameters

- **A** ( $N \times N$  `numpy.ndarray`) – adjacency matrix
- **d** (`float`) – damping factor (see description)
- **fa1ff** ( $N \times 1$  `numpy.ndarray` or `None`) – Initial page rank probability, non-negative values. Default value is `None`. If not specified, a naive bayesian prior is used.

**Returns** **r** – vectors of page rankings

**Return type**  $N \times 1$  `numpy.ndarray`

#### Notes

The algorithm will work well for smaller matrices (number of nodes around 1000 or less)

### `brainconn.centraliry.participation_coef`

**participation\_coef** ( $W, ci, degree='undirected'$ )

Participation coefficient is a measure of diversity of intermodular connections of individual nodes.

#### Parameters

- **W** ( $N \times N$  `numpy.ndarray`) – binary/weighted directed/undirected connection matrix
- **ci** ( $N \times 1$  `numpy.ndarray`) – community affiliation vector
- **degree** (`{'undirected', 'in', 'out'}`, *optional*) – Flag to describe nature of graph. 'undirected': For undirected graphs, 'in': Uses the in-degree, 'out': Uses the out-degree

**Returns** **P** – participation coefficient

**Return type**  $N \times 1$  `numpy.ndarray`

### `brainconn.centraliry.participation_coef_sign`

**participation\_coef\_sign** ( $W, ci$ )

Participation coefficient is a measure of diversity of intermodular connections of individual nodes.

#### Parameters

- **W** ( $N \times N$  `numpy.ndarray`) – undirected connection matrix with positive and negative weights
- **ci** ( $N \times 1$  `numpy.ndarray`) – community affiliation vector

#### Returns

- **Ppos** ( $N \times 1$  `numpy.ndarray`) – participation coefficient from positive weights

- **Pneg** (Nx1 `numpy.ndarray`) – participation coefficient from negative weights

### **brainconn.centraliity.subgraph\_centrality**

#### **subgraph\_centrality** (*CIJ*)

The subgraph centrality of a node is a weighted sum of closed walks of different lengths in the network starting and ending at the node. This function returns a vector of subgraph centralities for each node of the network.

##### **Parameters**

- **CIJ** (NxN `numpy.ndarray`) – binary adjacency matrix
- **Cs** (Nx1 `numpy.ndarray`) – subgraph centrality

## **1.3.2 brainconn.clustering: Clustering**

Metrics which group nodes within graphs into clusters.

<code>brainconn.clustering</code>	Metrics which group nodes within graphs into clusters.
<code>brainconn.clustering.agreement(ci[, buffsz])</code>	Takes as input a set of vertex partitions CI of dimensions [vertex x partition].
<code>brainconn.clustering. agreement_weighted(ci, wts)</code>	$D = \text{AGREEMENT\_WEIGHTED}(CI, WTS)$ is identical to AGREEMENT, with the exception that each partitions contribution is weighted according to the corresponding scalar value stored in the vector WTS.
<code>brainconn.clustering. clustering_coef_bd(A)</code>	The clustering coefficient is the fraction of triangles around a node (equiv.
<code>brainconn.clustering. clustering_coef_bu(G)</code>	The clustering coefficient is the fraction of triangles around a node (equiv.
<code>brainconn.clustering. clustering_coef_wd(W)</code>	The weighted clustering coefficient is the average “intensity” of triangles around a node.
<code>brainconn.clustering. clustering_coef_wu(W)</code>	The weighted clustering coefficient is the average “intensity” of triangles around a node.
<code>brainconn.clustering. clustering_coef_wu_sign(W)</code>	Returns the weighted clustering coefficient generalized or separated for positive and negative weights.
<code>brainconn.clustering.consensus_und(D, tau[, ...])</code>	This algorithm seeks a consensus partition of the agreement matrix D.
<code>brainconn.clustering. get_components(A[, ...])</code>	Returns the components of an undirected graph specified by the binary and undirected adjacency matrix adj.
<code>brainconn.clustering. get_components_old(A[, ...])</code>	Returns the components of an undirected graph specified by the binary and undirected adjacency matrix adj.
<code>brainconn.clustering. number_of_components(A)</code>	
<code>brainconn.clustering. transitivity_bd(A)</code>	Transitivity is the ratio of ‘triangles to triplets’ in the network.
<code>brainconn.clustering. transitivity_bu(A)</code>	Transitivity is the ratio of ‘triangles to triplets’ in the network.
<code>brainconn.clustering. transitivity_wd(W)</code>	Transitivity is the ratio of ‘triangles to triplets’ in the network.
<code>brainconn.clustering. transitivity_wu(W)</code>	Transitivity is the ratio of ‘triangles to triplets’ in the network.

**brainconn.clustering.agreement****agreement** (*ci*, *buffsz=1000*)

Takes as input a set of vertex partitions CI of dimensions [vertex x partition]. Each column in CI contains the assignments of each vertex to a class/community/module. This function aggregates the partitions in CI into a square [vertex x vertex] agreement matrix D, whose elements indicate the number of times any two vertices were assigned to the same class.

In the case that the number of nodes and partitions in CI is large (greater than ~1000 nodes or greater than ~1000 partitions), the script can be made faster by computing D in pieces. The optional input BUFFSZ determines the size of each piece. Trial and error has found that BUFFSZ ~ 150 works well.

**Parameters**

- **ci** (NxM `numpy.ndarray`) – set of M (possibly degenerate) partitions of N nodes
- **buffsz** (*int* | *None*) – sets buffer size. If not specified, defaults to 1000

**Returns** **D** – agreement matrix

**Return type** NxN `numpy.ndarray`

**brainconn.clustering.agreement\_weighted****agreement\_weighted** (*ci*, *wts*)

D = AGREEMENT\_WEIGHTED(CI,WTS) is identical to AGREEMENT, with the exception that each partitions contribution is weighted according to the corresponding scalar value stored in the vector WTS. As an example, suppose CI contained partitions obtained using some heuristic for maximizing modularity. A possible choice for WTS might be the Q metric (Newman's modularity score). Such a choice would add more weight to higher modularity partitions.

NOTE: Unlike AGREEMENT, this script does not have the input argument BUFFSZ.

**Parameters**

- **ci** (MxN `numpy.ndarray`) – set of M (possibly degenerate) partitions of N nodes
- **wts** (Mx1 `numpy.ndarray`) – relative weight of each partition

**Returns** **D** – weighted agreement matrix

**Return type** NxN `numpy.ndarray`

**brainconn.clustering.clustering\_coef\_bd****clustering\_coef\_bd** (*A*)

The clustering coefficient is the fraction of triangles around a node (equiv. the fraction of nodes neighbors that are neighbors of each other).

**Parameters** **A** (NxN `numpy.ndarray`) – binary directed connection matrix

**Returns** **C** – clustering coefficient vector

**Return type** Nx1 `numpy.ndarray`

**Notes**

Methodological note: In directed graphs, 3 nodes generate up to 8 triangles ( $2 \times 2 \times 2$  edges). The number of existing triangles is the main diagonal of  $S^3/2$ . The number of all (in or out) neighbour pairs is  $K(K-1)/2$ . Each

neighbour pair may generate two triangles. “False pairs” are  $i \leftrightarrow j$  edge pairs (these do not generate triangles). The number of false pairs is the main diagonal of  $A^2$ . Thus the maximum possible number of triangles =

$$= (2 \text{ edges}) * ([\text{ALL PAIRS}] - [\text{FALSE PAIRS}]) = 2 * (K(K-1)/2 - \text{diag}(A^2)) = K(K-1) - 2(\text{diag}(A^2))$$

### **brainconn.clustering.clustering\_coef\_bu**

#### **clustering\_coef\_bu** (*G*)

The clustering coefficient is the fraction of triangles around a node (equiv. the fraction of nodes neighbors that are neighbors of each other).

**Parameters** **A** (NxN `numpy.ndarray`) – binary undirected connection matrix

**Returns** **C** – clustering coefficient vector

**Return type** Nx1 `numpy.ndarray`

### **brainconn.clustering.clustering\_coef\_wd**

#### **clustering\_coef\_wd** (*W*)

The weighted clustering coefficient is the average “intensity” of triangles around a node.

**Parameters** **W** (NxN `numpy.ndarray`) – weighted directed connection matrix

**Returns** **C** – clustering coefficient vector

**Return type** Nx1 `numpy.ndarray`

### **Notes**

Methodological note (also see clustering\_coef\_bd) The weighted modification is as follows: - The numerator: adjacency matrix is replaced with weights matrix  $^1/3$  - The denominator: no changes from the binary version

The above reduces to symmetric and/or binary versions of the clustering coefficient for respective graphs.

### **brainconn.clustering.clustering\_coef\_wu**

#### **clustering\_coef\_wu** (*W*)

The weighted clustering coefficient is the average “intensity” of triangles around a node.

**Parameters** **W** (NxN `numpy.ndarray`) – weighted undirected connection matrix

**Returns** **C** – clustering coefficient vector

**Return type** Nx1 `numpy.ndarray`

### **brainconn.clustering.clustering\_coef\_wu\_sign**

#### **clustering\_coef\_wu\_sign** (*W*, *coef\_type*='default')

Returns the weighted clustering coefficient generalized or separated for positive and negative weights.

Three Algorithms are supported; herefore referred to as default, zhang, and constantini.

1. Default (Onnela et al.), as in the traditional clustering coefficient computation. Computed separately for positive and negative weights.



2. Zhang & Horvath. Similar to Onnela formula except weight information incorporated in denominator. Reduces sensitivity of the measure to weights directly connected to the node of interest. Computed separately for positive and negative weights.
3. Constantini & Perugini generalization of Zhang & Horvath formula. Takes both positive and negative weights into account simultaneously. Particularly sensitive to non-redundancy in path information based on sign. Returns only one value.

#### Parameters

- **W** (NxN `numpy.ndarray`) – weighted undirected connection matrix
- **corr\_type** (`{'default', 'zhang', 'constantini'}`) – Allowed values are 'default', 'zhang', 'constantini'

#### Returns

- **Cpos** (Nx1 `numpy.ndarray`) – Clustering coefficient vector for positive weights
- **Cneg** (Nx1 `numpy.ndarray`) – Clustering coefficient vector for negative weights, unless `coef_type == 'constantini'`.
- *References* – Onnela et al. (2005) Phys Rev E 71:065103 Zhang & Horvath (2005) Stat Appl Genet Mol Biol 41:1544-6115 Costantini & Perugini (2014) PLOS ONE 9:e88669

### brainconn.clustering.consensus\_und

#### consensus\_und(*D*, *tau*, *reps*=1000)

This algorithm seeks a consensus partition of the agreement matrix *D*. The algorithm used here is almost identical to the one introduced in Lancichinetti & Fortunato (2012): The agreement matrix *D* is thresholded at a level *TAU* to remove an weak elements. The resulting matrix is then partitions *REPS* number of times using the Louvain algorithm (in principle, any clustering algorithm that can handle weighted matrixes is a suitable alternative to the Louvain algorithm and can be substituted in its place). This clustering produces a set of partitions from which a new agreement is built. If the partitions have not converged to a single representative partition, the above process repeats itself, starting with the newly built agreement matrix.

NOTE: In this implementation, the elements of the agreement matrix must be converted into probabilities.

NOTE: This implementation is slightly different from the original algorithm proposed by Lanchichinetti & Fortunato. In its original version, if the thresholding produces singleton communities, those nodes are reconnected to the network. Here, we leave any singleton communities disconnected.

#### Parameters

- **D** (NxN `numpy.ndarray`) – agreement matrix with entries between 0 and 1 denoting the probability of finding node *i* in the same cluster as node *j*
- **tau** (`float`) – threshold which controls the resolution of the reclustering
- **reps** (`int`) – number of times the clustering algorithm is reapplied. default value is 1000.

**Returns** *ciu* – consensus partition

**Return type** Nx1 `numpy.ndarray`

### brainconn.clustering.get\_components

#### get\_components(*A*, *no\_depend*=False)

Returns the components of an undirected graph specified by the binary and undirected adjacency matrix *adj*.

Components and their constituent nodes are assigned the same index and stored in the vector, `comps`. The vector, `comp_sizes`, contains the number of nodes belonging to each component.

#### Parameters

- **A** (NxN `numpy.ndarray`) – binary undirected adjacency matrix
- **no\_depend** (*Any*) – Does nothing, included for backwards compatibility

#### Returns

- **comps** (Nx1 `numpy.ndarray`) – vector of component assignments for each node
- **comp\_sizes** (Mx1 `numpy.ndarray`) – vector of component sizes

#### Notes

Note: disconnected nodes will appear as components with a component size of 1

Note: The identity of each component (i.e. its numerical value in the result) is not guaranteed to be identical the value returned in BCT, matlab code, although the component topology is.

Many thanks to Nick Cullen for providing this implementation

### `brainconn.clustering.get_components_old`

`get_components_old` (*A*, *no\_depend=False*)

Returns the components of an undirected graph specified by the binary and undirected adjacency matrix `adj`. Components and their constituent nodes are assigned the same index and stored in the vector, `comps`. The vector, `comp_sizes`, contains the number of nodes belonging to each component.

#### Parameters

- **adj** (NxN `numpy.ndarray`) – binary undirected adjacency matrix
- **no\_depend** (*bool*) – If true, doesn't import networkx to do the calculation. Default value is false.

#### Returns

- **comps** (Nx1 `numpy.ndarray`) – vector of component assignments for each node
- **comp\_sizes** (Mx1 `numpy.ndarray`) – vector of component sizes

#### Notes

Note: disconnected nodes will appear as components with a component size of 1

Note: The identity of each component (i.e. its numerical value in the result) is not guaranteed to be identical the value returned in BCT, although the component topology is.

Note: networkx is used to do the computation efficiently. If networkx is not available a breadth-first search that does not depend on networkx is used instead, but this is less efficient. The corresponding BCT function does the computation by computing the Dulmage-Mendelsohn decomposition. I don't know what a Dulmage-Mendelsohn decomposition is and there doesn't appear to be a python equivalent. If you think of a way to implement this better, let me know.

**brainconn.clustering.number\_of\_components****number\_of\_components** (*A*)**brainconn.clustering.transitivity\_bd****transitivity\_bd** (*A*)

Transitivity is the ratio of ‘triangles to triplets’ in the network. (A classical version of the clustering coefficient).

**Parameters** **A** (NxN `numpy.ndarray`) – binary directed connection matrix

**Returns** **T** – transitivity scalar

**Return type** `float`

**Notes**

Methodological note: In directed graphs, 3 nodes generate up to 8 triangles (2\*2\*2 edges). The number of existing triangles is the main

diagonal of  $S^3/2$ . The number of all (in or out) neighbour pairs is  $K(K-1)/2$ . Each neighbour pair may generate two triangles. “False pairs” are  $i \leftrightarrow j$  edge pairs (these do not generate triangles). The number of false pairs is the main diagonal of  $A^2$ . Thus the maximum possible number of triangles = (2 edges)\*([ALL PAIRS] - [FALSE PAIRS])

$$= 2 * (K(K-1)/2 - \text{diag}(A^2)) = K(K-1) - 2(\text{diag}(A^2))$$

**brainconn.clustering.transitivity\_bu****transitivity\_bu** (*A*)

Transitivity is the ratio of ‘triangles to triplets’ in the network. (A classical version of the clustering coefficient).

**Parameters** **A** (NxN `numpy.ndarray`) – binary undirected connection matrix

**Returns** **T** – transitivity scalar

**Return type** `float`

**brainconn.clustering.transitivity\_wd****transitivity\_wd** (*W*)

Transitivity is the ratio of ‘triangles to triplets’ in the network. (A classical version of the clustering coefficient).

**Parameters** **W** (NxN `numpy.ndarray`) – weighted directed connection matrix

**Returns**

- **T** (*int*) – transitivity scalar
- *Methodological note (also see note for clustering\_coef\_bd)*
- *The weighted modification is as follows*
- - **The numerator** (*adjacency matrix is replaced with weights matrix ^ 1/3*)
- - **The denominator** (*no changes from the binary version*)
- *The above reduces to symmetric and/or binary versions of the clustering*

- coefficient for respective graphs.

## brainconn.clustering.transitivity\_wu

### transitivity\_wu(*W*)

Transitivity is the ratio of ‘triangles to triplets’ in the network. (A classical version of the clustering coefficient).

**Parameters** *W* (NxN `numpy.ndarray`) – weighted undirected connection matrix

**Returns** *T* – transitivity scalar

**Return type** `int`

## 1.3.3 brainconn.core: Core

Metrics which identify the most important nodes in graphs.

<code>brainconn.core</code>	Metrics which identify the most important nodes in graphs.
<code>brainconn.core.assortativity_bin(CIJ, flag)</code>	The assortativity coefficient is a correlation coefficient between the degrees of all nodes on two opposite ends of a link.
<code>brainconn.core.assortativity_wel(CIJ, flag)</code>	The assortativity coefficient is a correlation coefficient between the strengths (weighted degrees) of all nodes on two opposite ends of a link.
<code>brainconn.core.core_periphery_dir(W, gamma, C0)</code>	The optimal core/periphery subdivision is a partition of the network into two nonoverlapping groups of nodes, a core group and a periphery group.
<code>brainconn.core.kcore_bd(CIJ, k[, peel])</code>	The k-core is the largest subnetwork comprising nodes of degree at least k.
<code>brainconn.core.kcore_bu(CIJ, k[, peel])</code>	The k-core is the largest subnetwork comprising nodes of degree at least k.
<code>brainconn.core.local_assortativity_wu(CIJ, s)</code>	Local assortativity measures the extent to which nodes are connected to nodes of similar strength.
<code>brainconn.core.rich_club_bd(CIJ[, klevel])</code>	The rich club coefficient, <i>R</i> , at level <i>k</i> is the fraction of edges that connect nodes of degree <i>k</i> or higher out of the maximum number of edges that such nodes might share.
<code>brainconn.core.rich_club_bu(CIJ[, klevel])</code>	The rich club coefficient, <i>R</i> , at level <i>k</i> is the fraction of edges that connect nodes of degree <i>k</i> or higher out of the maximum number of edges that such nodes might share.
<code>brainconn.core.rich_club_wd(CIJ[, klevel])</code>	<b>param CIJ</b> weighted directed connection matrix
<code>brainconn.core.rich_club_wu(CIJ[, klevel])</code>	<b>param CIJ</b> weighted undirected connection matrix
<code>brainconn.core.score_wu(CIJ, s)</code>	The s-core is the largest subnetwork comprising nodes of strength at least <i>s</i> .

**brainconn.core.assortativity\_bin****assortativity\_bin** (*CIJ*, *flag=0*)

The assortativity coefficient is a correlation coefficient between the degrees of all nodes on two opposite ends of a link. A positive assortativity coefficient indicates that nodes tend to link to other nodes with the same or similar degree.

**Parameters**

- **CIJ** (*NxN numpy.ndarray*) – binary directed/undirected connection matrix
- **flag** (*int*) – 0 : undirected graph; degree/degree correlation 1 : directed graph; out-degree/in-degree correlation 2 : directed graph; in-degree/out-degree correlation 3 : directed graph; out-degree/out-degree correlation 4 : directed graph; in-degree/in-degree correlation

**Returns** *r* – assortativity coefficient**Return type** *float***Notes**

The function accepts weighted networks, but all connection weights are ignored. The main diagonal should be empty. For flag 1 the function computes the directed assortativity described in Rubinov and Sporns (2010) NeuroImage.

**brainconn.core.assortativity\_wei****assortativity\_wei** (*CIJ*, *flag=0*)

The assortativity coefficient is a correlation coefficient between the strengths (weighted degrees) of all nodes on two opposite ends of a link. A positive assortativity coefficient indicates that nodes tend to link to other nodes with the same or similar strength.

**Parameters**

- **CIJ** (*NxN numpy.ndarray*) – weighted directed/undirected connection matrix
- **flag** (*int*) – 0 : undirected graph; strength/strength correlation 1 : directed graph; out-strength/in-strength correlation 2 : directed graph; in-strength/out-strength correlation 3 : directed graph; out-strength/out-strength correlation 4 : directed graph; in-strength/in-strength correlation

**Returns** *r* – assortativity coefficient**Return type** *float***Notes**

**The main diagonal should be empty. For flag 1** the function computes the directed assortativity described in Rubinov and Sporns (2010) NeuroImage.

**brainconn.core.core\_periphery\_dir****core\_periphery\_dir** (*W*, *gamma=1*, *C0=None*)

The optimal core/periphery subdivision is a partition of the network into two nonoverlapping groups of nodes,

a core group and a periphery group. The number of core-group edges is maximized, and the number of within periphery edges is minimized.

The core-ness is a statistic which quantifies the goodness of the optimal core/periphery subdivision (with arbitrary relative value).

The algorithm uses a variation of the Kernighan-Lin graph partitioning algorithm to optimize a core-structure objective described in Borgatti & Everett (2000) Soc Networks 21:375-395

See Rubinov, Ypma et al. (2015) PNAS 112:10032-7

#### Parameters

- **W** (NxN `numpy.ndarray`) – directed connection matrix
- **gamma** (*core-ness resolution parameter*) – Default value = 1  $\gamma > 1$  detects small core, large periphery  $0 < \gamma < 1$  detects large core, small periphery
- **C0** (NxN `numpy.ndarray`) – Initial core structure

### `brainconn.core.kcore_bd`

**kcore\_bd** (*CIJ, k, peel=False*)

The k-core is the largest subnetwork comprising nodes of degree at least k. This function computes the k-core for a given binary directed connection matrix by recursively peeling off nodes with degree lower than k, until no such nodes remain.

#### Parameters

- **CIJ** (NxN `numpy.ndarray`) – binary directed adjacency matrix
- **k** (*int*) – level of k-core
- **peel** (*bool*) – If True, additionally calculates peelorder and peellevel. Defaults to False.

#### Returns

- **CIJkcore** (NxN `numpy.ndarray`) – connection matrix of the k-core. This matrix only contains nodes of degree at least k.
- **kn** (*int*) – size of k-core
- **peelorder** (Nx1 `numpy.ndarray`) – indices in the order in which they were peeled away during k-core decomposition. only returned if peel is specified.
- **peellevel** (Nx1 `numpy.ndarray`) – corresponding level - nodes in at the same level have been peeled away at the same time. only return if peel is specified

#### Notes

‘peelorder’ and ‘peellevel’ are similar the the k-core sub-shells described in Modha and Singh (2010).

### `brainconn.core.kcore_bu`

**kcore\_bu** (*CIJ, k, peel=False*)

The k-core is the largest subnetwork comprising nodes of degree at least k. This function computes the k-core for a given binary undirected connection matrix by recursively peeling off nodes with degree lower than k, until no such nodes remain.

#### Parameters

- **CIJ** (NxN `numpy.ndarray`) – binary undirected connection matrix
- **k** (`int`) – level of k-core
- **peel** (`bool`) – If True, additionally calculates peelorder and peellevel. Defaults to False.

#### Returns

- **CIJkcore** (NxN `numpy.ndarray`) – connection matrix of the k-core. This matrix only contains nodes of degree at least k.
- **kn** (`int`) – size of k-core
- **peelorder** (Nx1 `numpy.ndarray`) – indices in the order in which they were peeled away during k-core decomposition. only returned if peel is specified.
- **peellevel** (Nx1 `numpy.ndarray`) – corresponding level - nodes in at the same level have been peeled away at the same time. only return if peel is specified

#### Notes

‘peelorder’ and ‘peellevel’ are similar the the k-core sub-shells described in Modha and Singh (2010).

### brainconn.core.local\_assortativity\_wu\_sign

#### local\_assortativity\_wu\_sign (W)

Local assortativity measures the extent to which nodes are connected to nodes of similar strength. Adapted from Thechchanamoorthy et al. 2014 formula to allowed weighted/signed networks.

**Parameters** **W** (NxN `numpy.ndarray`) – undirected connection matrix with positive and negative weights

#### Returns

- **loc\_assort\_pos** (Nx1 `numpy.ndarray`) – local assortativity from positive weights
- **loc\_assort\_neg** (Nx1 `numpy.ndarray`) – local assortativity from negative weights

### brainconn.core.rich\_club\_bd

#### rich\_club\_bd (CIJ, klevel=None)

The rich club coefficient, R, at level k is the fraction of edges that connect nodes of degree k or higher out of the maximum number of edges that such nodes might share.

#### Parameters

- **CIJ** (NxN `numpy.ndarray`) – binary directed connection matrix
- **klevel** (`int` | `None`) – sets the maximum level at which the rich club coefficient will be calculated. If None (default), the maximum level is set to the maximum degree of the adjacency matrix

#### Returns

- **R** (Kx1 `numpy.ndarray`) – vector of rich-club coefficients for levels 1 to klevel
- **Nk** (`int`) – number of nodes with degree > k
- **Ek** (`int`) – number of edges remaining in subgraph with degree > k

**brainconn.core.rich\_club\_bu****rich\_club\_bu** (*CIJ*, *klevel=None*)

The rich club coefficient,  $R$ , at level  $k$  is the fraction of edges that connect nodes of degree  $k$  or higher out of the maximum number of edges that such nodes might share.

**Parameters**

- **CIJ** ( $N \times N$  `numpy.ndarray`) – binary undirected connection matrix
- **klevel** (`int` | `None`) – sets the maximum level at which the rich club coefficient will be calculated. If `None` (default), the maximum level is set to the maximum degree of the adjacency matrix

**Returns**

- **R** ( $K \times 1$  `numpy.ndarray`) – vector of rich-club coefficients for levels 1 to `klevel`
- **Nk** (`int`) – number of nodes with degree  $> k$
- **Ek** (`int`) – number of edges remaining in subgraph with degree  $> k$

**brainconn.core.rich\_club\_wd****rich\_club\_wd** (*CIJ*, *klevel=None*)**Parameters**

- **CIJ** ( $N \times N$  `numpy.ndarray`) – weighted directed connection matrix
- **klevel** (`int` | `None`) – sets the maximum level at which the rich club coefficient will be calculated. If `None` (default), the maximum level is set to the maximum degree of the adjacency matrix

**Returns** **Rw** – vector of rich-club coefficients for levels 1 to `klevel`**Return type**  $K \times 1$  `numpy.ndarray`**brainconn.core.rich\_club\_wu****rich\_club\_wu** (*CIJ*, *klevel=None*)**Parameters**

- **CIJ** ( $N \times N$  `numpy.ndarray`) – weighted undirected connection matrix
- **klevel** (`int` | `None`) – sets the maximum level at which the rich club coefficient will be calculated. If `None` (default), the maximum level is set to the maximum degree of the adjacency matrix

**Returns** **Rw** – vector of rich-club coefficients for levels 1 to `klevel`**Return type**  $K \times 1$  `numpy.ndarray`**brainconn.core.score\_wu****score\_wu** (*CIJ*, *s*)

The  $s$ -core is the largest subnetwork comprising nodes of strength at least  $s$ . This function computes the  $s$ -core for a given weighted undirected connection matrix. Computation is analogous to the more widely used  $k$ -core, but is based on node strengths instead of node degrees.



**Parameters**

- **CIJ** (NxN `numpy.ndarray`) – weighted undirected connection matrix
- **s** (`float`) – level of s-core. Note that can take on any fractional value.

**Returns**

- **CIJscore** (NxN `numpy.ndarray`) – connection matrix of the s-core. This matrix contains only nodes with a strength of at least s.
- **sn** (`int`) – size of s-core

**1.3.4 brainconn.degree: Degree**

Metrics which identify the most important nodes in graphs.

<code>brainconn.degree</code>	Metrics which identify the most important nodes in graphs.
<code>brainconn.degree.degrees_dir(CIJ)</code>	Node degree is the number of links connected to the node.
<code>brainconn.degree.degrees_und(CIJ)</code>	Node degree is the number of links connected to the node.
<code>brainconn.degree.jdegree(CIJ)</code>	This function returns a matrix in which the value of each element (u,v) corresponds to the number of nodes that have u outgoing connections and v incoming connections.
<code>brainconn.degree.strengths_dir(CIJ)</code>	Node strength is the sum of weights of links connected to the node.
<code>brainconn.degree.strengths_und(CIJ)</code>	Node strength is the sum of weights of links connected to the node.
<code>brainconn.degree.strengths_und_sign(W)</code>	Node strength is the sum of weights of links connected to the node.

**brainconn.degree.degrees\_dir****degrees\_dir (CIJ)**

Node degree is the number of links connected to the node. The indegree is the number of inward links and the outdegree is the number of outward links.

**Parameters** **CIJ** (NxN `numpy.ndarray`) – directed binary/weighted connection matrix

**Returns**

- **in\_degree** (Nx1 `numpy.ndarray`) – node in-degree
- **out\_degree** (Nx1 `numpy.ndarray`) – node out-degree
- **deg** (Nx1 `numpy.ndarray`) – node degree (in-degree + out-degree)

**Notes**

Inputs are assumed to be on the columns of the CIJ matrix. Weight information is discarded.

### Examples using `brainconn.degree.degrees_dir`

- *Calculate degree measures*

### `brainconn.degree.degrees_und`

#### `degrees_und (CIJ)`

Node degree is the number of links connected to the node.

**Parameters** `CIJ` (NxN `numpy.ndarray`) – undirected binary/weighted connection matrix

**Returns** `deg` – node degree

**Return type** Nx1 `numpy.ndarray`

#### Notes

Weight information is discarded.

### Examples using `brainconn.degree.degrees_und`

- *Calculate degree measures*

### `brainconn.degree.jdegree`

#### `jdegree (CIJ)`

This function returns a matrix in which the value of each element (u,v) corresponds to the number of nodes that have u outgoing connections and v incoming connections.

**Parameters** `CIJ` (NxN `numpy.ndarray`) – directed binary/weighted connection matrix

#### Returns

- `J` (ZxZ `numpy.ndarray`) – joint degree distribution matrix (shifted by one, replicates matlab one-based-indexing)
- `J_od (int)` – number of vertices with `out_degree>in_degree`
- `J_id (int)` – number of vertices with `in_degree>out_degree`
- `J_bl (int)` – number of vertices with `in_degree==out_degree`

#### Notes

Weights are discarded.

### Examples using `brainconn.degree.jdegree`

- *Calculate degree measures*

**brainconn.degree.strengths\_dir****strengths\_dir** (*CIJ*)

Node strength is the sum of weights of links connected to the node. The instrength is the sum of inward link weights and the outstrength is the sum of outward link weights.

**Parameters** **CIJ** (NxN `numpy.ndarray`) – directed weighted connection matrix

**Returns**

- **is** (Nx1 `numpy.ndarray`) – node in-strength
- **os** (Nx1 `numpy.ndarray`) – node out-strength
- **str** (Nx1 `numpy.ndarray`) – node strength (in-strength + out-strength)

**Notes**

Inputs are assumed to be on the columns of the CIJ matrix.

**Examples using brainconn.degree.strengths\_dir**

- *Calculate degree measures*

**brainconn.degree.strengths\_und****strengths\_und** (*CIJ*)

Node strength is the sum of weights of links connected to the node.

**Parameters** **CIJ** (NxN `numpy.ndarray`) – undirected weighted connection matrix

**Returns** **str** – node strengths

**Return type** Nx1 `numpy.ndarray`

**Examples using brainconn.degree.strengths\_und**

- *Calculate degree measures*

**brainconn.degree.strengths\_und\_sign****strengths\_und\_sign** (*W*)

Node strength is the sum of weights of links connected to the node.

**Parameters** **W** (NxN `numpy.ndarray`) – undirected connection matrix with positive and negative weights

**Returns**

- **Spos** (Nx1 `numpy.ndarray`) – nodal strength of positive weights
- **Sneg** (Nx1 `numpy.ndarray`) – nodal strength of positive weights
- **vpos** (*float*) – total positive weight
- **vneg** (*float*) – total negative weight

## Examples using `brainconn.degree.strengths_und_sign`

- *Calculate degree measures*

### 1.3.5 `brainconn.distance`: Distance

Metrics which identify the most important nodes in graphs.

<code>brainconn.distance</code>	Metrics which identify the most important nodes in graphs.
<code>brainconn.distance.breadthdist(CIJ)</code>	The binary reachability matrix describes reachability between all pairs of nodes.
<code>brainconn.distance.breadth(CIJ, source)</code>	Implementation of breadth-first search.
<code>brainconn.distance.charpath(D[, ...])</code>	The characteristic path length is the average shortest path length in the network.
<code>brainconn.distance.cycprob(Pq)</code>	Cycles are paths which begin and end at the same node.
<code>brainconn.distance.distance_bin(G)</code>	The distance matrix contains lengths of shortest paths between all pairs of nodes.
<code>brainconn.distance.distance_wei(G)</code>	The distance matrix contains lengths of shortest paths between all pairs of nodes.
<code>brainconn.distance.distance_wei_floyd(adjacency)</code>	Computes the topological length of the shortest possible path connecting every pair of nodes in the network.
<code>brainconn.distance.retrieve_shortest_path(s, ...)</code>	Returns nodes comprising shortest path between $s$ and $t$
<code>brainconn.distance.efficiency_bin(G[, local])</code>	The global efficiency is the average of inverse shortest path length, and is inversely related to the characteristic path length.
<code>brainconn.distance.efficiency_wei(Gw[, local])</code>	The global efficiency is the average of inverse shortest path length, and is inversely related to the characteristic path length.
<code>brainconn.distance.findpaths(CIJ, qmax, sources)</code>	Paths are sequences of linked nodes, that never visit a single node more than once.
<code>brainconn.distance.findwalks(CIJ)</code>	Walks are sequences of linked nodes, that may visit a single node more than once.
<code>brainconn.distance.mean_first_passage_time(...)</code>	Calculates mean first passage time of <i>adjacency</i>
<code>brainconn.distance.reachdist(CIJ[, ...])</code>	The binary reachability matrix describes reachability between all pairs of nodes.
<code>brainconn.distance.search_information(adjacency)</code>	Calculates search information of <i>adjacency</i> .

### `brainconn.distance.breadthdist`

#### **breadthdist** (*CIJ*)

The binary reachability matrix describes reachability between all pairs of nodes. An entry  $(u,v)=1$  means that there exists a path from node  $u$  to node  $v$ ; alternatively  $(u,v)=0$ .

The distance matrix contains lengths of shortest paths between all pairs of nodes. An entry  $(u,v)$  represents the length of shortest path from node  $u$  to node  $v$ . The average shortest path length is the characteristic path length of the network.

**Parameters** **CIJ** (NxN `numpy.ndarray`) – binary directed/undirected connection matrix

**Returns**

- **R** (NxN `numpy.ndarray`) – binary reachability matrix
- **D** (NxN `numpy.ndarray`) – distance matrix

**Notes**

slower but less memory intensive than “reachdist.m”.

**brainconn.distance.breadth**

**breadth** (*CIJ, source*)

Implementation of breadth-first search.

**Parameters**

- **CIJ** (NxN `numpy.ndarray`) – binary directed/undirected connection matrix
- **source** (*int*) – source vertex

**Returns**

- **distance** (Nx1 `numpy.ndarray`) – vector of distances between source and ith vertex (0 for source)
- **branch** (Nx1 `numpy.ndarray`) – vertex that precedes i in the breadth-first search (-1 for source)

**Notes**

Breadth-first search tree does not contain all paths (or all shortest paths), but allows the determination of at least one path with minimum distance. The entire graph is explored, starting from source vertex ‘source’.

**brainconn.distance.charpath**

**charpath** (*D, include\_diagonal=False, include\_infinite=True*)

The characteristic path length is the average shortest path length in the network. The global efficiency is the average inverse shortest path length in the network.

**Parameters**

- **D** (NxN `numpy.ndarray`) – distance matrix
- **include\_diagonal** (*bool*) – If True, include the weights on the diagonal. Default value is False.
- **include\_infinite** (*bool*) – If True, include infinite distances in calculation

**Returns**

- **lambda** (*float*) – characteristic path length
- **efficiency** (*float*) – global efficiency
- **ecc** (Nx1 `numpy.ndarray`) – eccentricity at each vertex
- **radius** (*float*) – radius of graph
- **diameter** (*float*) – diameter of graph

## Notes

The input distance matrix may be obtained with any of the distance functions, e.g. `distance_bin`, `distance_wei`. Characteristic path length is calculated as the global mean of the distance matrix `D`, excluding any 'Infs' but including distances on the main diagonal.

### `brainconn.distance.cycprob`

#### `cycprob` ( $Pq$ )

Cycles are paths which begin and end at the same node. Cycle probability for path length  $d$ , is the fraction of all paths of length  $d-1$  that may be extended to form cycles of length  $d$ .

**Parameters**  $Pq$  ( $N \times N \times Q$  `numpy.ndarray`) – Path matrix with  $Pq[i,j,q]$  = number of paths from  $i$  to  $j$  of length  $q$ . Produced by `findpaths()`

#### Returns

- **fcyc** ( $Q \times 1$  `numpy.ndarray`) – fraction of all paths that are cycles for each path length  $q$
- **pcyc** ( $Q \times 1$  `numpy.ndarray`) – probability that a non-cyclic path of length  $q-1$  can be extended to form a cycle of length  $q$  for each path length  $q$

### `brainconn.distance.distance_bin`

#### `distance_bin` ( $G$ )

The distance matrix contains lengths of shortest paths between all pairs of nodes. An entry  $(u,v)$  represents the length of shortest path from node  $u$  to node  $v$ . The average shortest path length is the characteristic path length of the network.

**Parameters**  $A$  ( $N \times N$  `numpy.ndarray`) – binary directed/undirected connection matrix

**Returns**  $D$  – distance matrix

**Return type**  $N \times N$

## Notes

Lengths between disconnected nodes are set to Inf. Lengths on the main diagonal are set to 0. Algorithm: Algebraic shortest paths.

### `brainconn.distance.distance_wei`

#### `distance_wei` ( $G$ )

The distance matrix contains lengths of shortest paths between all pairs of nodes. An entry  $(u,v)$  represents the length of shortest path from node  $u$  to node  $v$ . The average shortest path length is the characteristic path length of the network.

**Parameters**  $L$  ( $N \times N$  `numpy.ndarray`) – Directed/undirected connection-length matrix. NB  $L$  is not the adjacency matrix. See below.

#### Returns

- **D** ( $N \times N$  `numpy.ndarray`) – distance (shortest weighted path) matrix
- **B** ( $N \times N$  `numpy.ndarray`) – matrix of number of edges in shortest weighted path

## Notes

The input matrix must be a connection-length matrix, typically

obtained via a mapping from weight to length. For instance, in a weighted correlation network higher correlations are more naturally interpreted as shorter distances and the input matrix should consequently be some inverse of the connectivity matrix.

The number of edges in shortest weighted paths may in general

exceed the number of edges in shortest binary paths (i.e. shortest paths computed on the binarized connectivity matrix), because shortest weighted paths have the minimal weighted distance, but not necessarily the minimal number of edges.

Lengths between disconnected nodes are set to Inf. Lengths on the main diagonal are set to 0.

Algorithm: Dijkstra's algorithm.

## brainconn.distance.distance\_we\_i\_floyd

**distance\_we\_i\_floyd**(*adjacency*, *transform=None*)

Computes the topological length of the shortest possible path connecting every pair of nodes in the network.

### Parameters

- **D** (( $N \times N$ ) *array\_like*) – Weighted/unweighted, direct/undirected connection weight/length array
- **transform** (*str*, *optional*) – If *adjacency* is a connection weight array, specify a transform to map input connection weights to connection lengths. Options include ['log', 'inv'], where 'log' is  $-np.log(adjacency)$  and 'inv' is  $1/adjacency$ . Default: None

### Returns

- **SPL** (( $N \times N$ ) *ndarray*) – Weighted/unweighted shortest path-length array. If *D* is a directed graph, then *SPL* is not symmetric
- **hops** (( $N \times N$ ) *ndarray*) – Number of edges in the shortest path array. If *D* is unweighted, *SPL* and *hops* are identical.
- **Pmat** (( $N \times N$ ) *ndarray*) – Element [*i*,*j*] of this array indicates the next node in the shortest path between *i* and *j*. This array is used as an input argument for function *retrieve\_shortest\_path()*, which returns as output the sequence of nodes comprising the shortest path between a given pair of nodes.

## Notes

There may be more than one shortest path between any pair of nodes in the network. Non-unique shortest paths are termed shortest path degeneracies and are most likely to occur in unweighted networks. When the shortest-path is degenerate, the elements of *Pmat* correspond to the first shortest path discovered by the algorithm.

The input array may be either a connection weight or length array. The connection length array is typically obtained with a mapping from weight to length, such that higher weights are mapped to shorter lengths (see argument *transform*, above).

Originally written in Matlab by Andrea Avena-Koenigsberger (IU, 2012) [1] [2] [3] [4].

## References

### `brainconn.distance.retrieve_shortest_path`

**retrieve\_shortest\_path** (*s*, *t*, *hops*, *Pmat*)

Returns nodes comprising shortest path between *s* and *t*

This function finds the sequence of nodes that comprise the shortest path between a given source and target node.

#### Parameters

- **s** (*int*) – Source node, i.e. node where the shortest path begins
- **t** (*int*) – Target node, i.e. node where the shortest path ends
- **hops** (*(N x N) array\_like*) – Number of edges in the path. This array may be obtained as the second output argument of the function *distance\_wei\_floyd*.
- **Pmat** (*(N x N) array\_like*) – Array whose elements *Pmat[k,t]* indicate the next node in the shortest path between nodes *k* and *t*. This array may be obtained as the third output of the function *distance\_wei\_floyd*.

**Returns** **path** – Nodes (indices) comprising the shortest path between *s* and *t*

**Return type** ndarray

## Notes

Originally written in Matlab by Andrea Avena-Koenigsberger and Joaquin Goni (IU, 2012)

### `brainconn.distance.encyency_bin`

**encyency\_bin** (*G*, *local=False*)

The global efficiency is the average of inverse shortest path length, and is inversely related to the characteristic path length.

The local efficiency is the global efficiency computed on the neighborhood of the node, and is related to the clustering coefficient.

#### Parameters

- **A** (*NxN numpy.ndarray*) – binary undirected connection matrix
- **local** (*bool*) – If True, computes local efficiency instead of global efficiency. Default value = False.

#### Returns

- **Eglob** (*float*) – global efficiency, only if local=False
- **Eloc** (*Nx1 numpy.ndarray*) – local efficiency, only if local=True

### `brainconn.distance.encyency_wei`

**encyency\_wei** (*Gw*, *local=False*)

The global efficiency is the average of inverse shortest path length, and is inversely related to the characteristic path length.



The local efficiency is the global efficiency computed on the neighborhood of the node, and is related to the clustering coefficient.

#### Parameters

- **W** (NxN `numpy.ndarray`) – undirected weighted connection matrix (all weights in W must be between 0 and 1)
- **local** (`bool`) – If True, computes local efficiency instead of global efficiency. Default value = False.

#### Returns

- **Eglob** (`float`) – global efficiency, only if local=False
- **Eloc** (Nx1 `numpy.ndarray`) – local efficiency, only if local=True

#### Notes

The efficiency is computed using an auxiliary connection-length

matrix L, defined as  $L_{ij} = 1/W_{ij}$  for all nonzero  $L_{ij}$ ; This has an intuitive interpretation, as higher connection weights intuitively correspond to shorter lengths.

The weighted local efficiency broadly parallels the weighted

clustering coefficient of Onnela et al. (2005) and distinguishes the influence of different paths based on connection weights of the corresponding neighbors to the node in question. In other words, a path between two neighbors with strong connections to the node in question contributes more to the local efficiency than a path between two weakly connected neighbors. Note that this weighted variant of the local efficiency is hence not a strict generalization of the binary variant.

Algorithm: Dijkstra's algorithm

### brainconn.distance.findpaths

**findpaths** (*CIJ, qmax, sources, savepths=False*)

Paths are sequences of linked nodes, that never visit a single node more than once. This function finds all paths that start at a set of source nodes, up to a specified length. Warning: very memory-intensive.

#### Parameters

- **CIJ** (NxN `numpy.ndarray`) – binary directed/undirected connection matrix
- **qmax** (`int`) – maximal path length
- **sources** (Nx1 `numpy.ndarray`) – source units from which paths are grown
- **savepths** (`bool`) – True if all paths are to be collected and returned. This functionality is currently not enabled.

#### Returns

- **Pq** (NxNxQ `numpy.ndarray`) – Path matrix with  $P[i,j,q]$  = number of paths from i to j with length q
- **tpath** (`int`) – total number of paths found
- **plq** (Qx1 `numpy.ndarray`) – path length distribution as a function of q
- **qstop** (`int`) – path length at which findpaths is stopped

- **allpths** (*None*) – a matrix containing all paths up to *qmax*. This function is extremely complicated and reimplementing it in *bctpy* is not straightforward.
- **util** (*NxQ* `numpy.ndarray`) – node use index

## Notes

Note that  $P_q(:, :, N)$  can only carry entries on the diagonal, as all “legal” paths of length  $N-1$  must terminate. Cycles of length  $N$  are possible, with all vertices visited exactly once (except for source and target). ‘ $qmax = N$ ’ can wreak havoc (due to memory problems).

Note: Weights are discarded. Note: I am certain that this algorithm is rather inefficient - suggestions for improvements are welcome.

## `brainconn.distance.findwalks`

### `findwalks` (*CIJ*)

Walks are sequences of linked nodes, that may visit a single node more than once. This function finds the number of walks of a given length, between any two nodes.

**Parameters** **CIJ** (*NxN* `numpy.ndarray`) – binary directed/undirected connection matrix

#### Returns

- **Wq** (*NxNxQ* `numpy.ndarray`) –  $W_q[i, j, q]$  is the number of walks from *i* to *j* of length *q*
- **twalk** (*int*) – total number of walks found
- **wlq** (*Qx1* `numpy.ndarray`) – walk length distribution as a function of *q*

## Notes

$W_q$  grows very quickly for larger  $N, K, q$ . Weights are discarded.

## `brainconn.distance.mean_first_passage_time`

### `mean_first_passage_time` (*adjacency*)

Calculates mean first passage time of *adjacency*

The first passage time from *i* to *j* is the expected number of steps it takes a random walker starting at node *i* to arrive for the first time at node *j*. The mean first passage time is not a symmetric measure:  $mfpt(i, j)$  may be different from  $mfpt(j, i)$ .

**Parameters** **adjacency** (*(N x N) array\_like*) – Weighted/unweighted, direct/undirected connection weight/length array

**Returns** **MFPT** – Pairwise mean first passage time array

**Return type** (*N x N*) `ndarray`

## References

### brainconn.distance.reachdist

**reachdist** (*CIJ*, *ensure\_binary=True*)

The binary reachability matrix describes reachability between all pairs of nodes. An entry (u,v)=1 means that there exists a path from node u to node v; alternatively (u,v)=0.

The distance matrix contains lengths of shortest paths between all pairs of nodes. An entry (u,v) represents the length of shortest path from node u to node v. The average shortest path length is the characteristic path length of the network.

#### Parameters

- **CIJ** ( $N \times N$  `numpy.ndarray`) – binary directed/undirected connection matrix
- **ensure\_binary** (`bool`) – Binarizes input. Defaults to true. No user who is not testing something will ever want to not use this, use `distance_wei` instead for unweighted matrices.

#### Returns

- **R** ( $N \times N$  `numpy.ndarray`) – binary reachability matrix
- **D** ( $N \times N$  `numpy.ndarray`) – distance matrix

## Notes

faster but more memory intensive than “`breathdist.m`”.

### brainconn.distance.search\_information

**search\_information** (*adjacency*, *transform=None*, *has\_memory=False*)

Calculates search information of *adjacency*.

Computes the amount of information (measured in bits) that a random walker needs to follow the shortest path between a given pair of nodes [1] [2].

#### Parameters

- **adjacency** ( $(N \times N)$  `array_like`) – Weighted/unweighted, direct/undirected connection weight/length array
- **transform** (`str`, *optional*) – If *adjacency* is a connection weight array, specify a transform to map input connection weights to connection lengths. Options include ['log', 'inv'], where 'log' is  $-\log(\text{adjacency})$  and 'inv' is  $1/\text{adjacency}$ . Default: None
- **has\_memory** (`bool`, *optional*) – This flag defines whether or not the random walker “remembers” its previous step, which has the effect of reducing the amount of information needed to find the next state. Default: False

**Returns** **SI** – Pair-wise search information array. Note that  $SI[i,j]$  may be different from  $SI[j,i]$ ; hence, *SI* is not a symmetric matrix even when *adjacency* is symmetric.

**Return type** ( $N \times N$ ) `ndarray`

## References

### 1.3.6 brainconn.generative: Generative

Metrics which identify the most important nodes in graphs.

<code>brainconn.generative</code>	Metrics which identify the most important nodes in graphs.
<code>brainconn.generative.generative_model(A, D, ...)</code>	Generates synthetic networks using the models described in Betzel et al.
<code>brainconn.generative.evaluate_generative_model(A, ...)</code>	Generates synthetic networks with parameters provided and evaluates their energy function.

#### brainconn.generative.generative\_model

**generative\_model** (*A*, *D*, *m*, *eta*, *gamma*=None, *model\_type*='matching', *model\_var*='powerlaw', *epsilon*=1e-06, *copy*=True)

Generates synthetic networks using the models described in Betzel et al. (2016) Neuroimage. See this paper for more details.

Succinctly, the probability of forming a connection between nodes *u* and *v* is  $P(u,v) = E(u,v)^{\eta} * K(u,v)^{\gamma}$  where  $\eta$  and  $\gamma$  are hyperparameters,  $E(u,v)$  is the euclidean or similar distance measure, and  $K(u,v)$  is the algorithm that defines the model.

This describes the power law formulation, an alternative formulation uses the exponential function  $P(u,v) = \exp(E(u,v)^{\eta}) * \exp(K(u,v)^{\gamma})$

#### Parameters

- **A** (`numpy.ndarray`) – Binary network of seed connections
- **D** (`numpy.ndarray`) – Matrix of euclidean distances or other distances between nodes
- **m** (`int`) – Number of connections that should be present in the final synthetic network
- **eta** (`numpy.ndarray`) – A vector describing a range of values to estimate for  $\eta$ , the hyperparameter describing exponential weighting of the euclidean distance.
- **gamma** (`numpy.ndarray`) – A vector describing a range of values to estimate for  $\gamma$ , the hyperparameter describing exponential weighting of the basis algorithm. If *model\_type*='euclidean' or another distance metric, this can be None.
- **model\_type** (`Enum(str)`) –
  - euclidean** [Uses only euclidean distances to generate connection] probabilities
  - neighbors : count of common neighbors
  - matching : matching index, the normalized overlap in neighborhoods
  - clu-avg : Average clustering coefficient
  - clu-min : Minimum clustering coefficient
  - clu-max : Maximum clustering coefficient
  - clu-diff : Difference in clustering coefficient
  - clu-prod : Product of clustering coefficient
  - deg-avg : Average degree
  - deg-min : Minimum degree
  - deg-max : Maximum degree
  - deg-diff : Difference in degree
  - deg-prod : Product of degrees
- **model\_var** (`Enum(str)`) – Default value is powerlaw. If so, uses formulation of  $P(u,v)$  as described above. Alternate value is exponential. If so, uses  $P(u,v) = \exp(E(u,v)^{\eta}) * \exp(K(u,v)^{\gamma})$
- **epsilon** (`float`) – A small positive value added to all  $P(u,v)$ . The default value is 1e-6

- **copy** (*bool*) – Some algorithms add edges directly to the input matrix. Set this flag to make a copy of the input matrix instead. Defaults to True.

### brainconn.generative.evaluate\_generative\_model

**evaluate\_generative\_model** (*A*, *Atgt*, *D*, *eta*, *gamma=None*, *model\_type='matching'*,  
*model\_var='powerlaw'*, *epsilon=1e-06*)

Generates synthetic networks with parameters provided and evaluates their energy function. The energy function is defined as in Betzel et al. 2016. Basically it takes the Kolmogorov-Smirnov statistics of 4 network measures; comparing the degree distributions, clustering coefficients, betweenness centrality, and Euclidean distances between connected regions.

The energy is globally low if the synthetic network matches the target. Energy is defined as the maximum difference across the four statistics.

## 1.3.7 brainconn.modularity: Modularity

Metrics which identify the most important nodes in graphs.

<code>brainconn.modularity</code>	Metrics which identify the most important nodes in graphs.
<code>brainconn.modularity.ci2ls(ci)</code>	Convert from a community index vector to a 2D python list of modules The list is a pure python list, not requiring numpy.
<code>brainconn.modularity.ls2ci(ls[, zeroindexed])</code>	Convert from a 2D python list of modules to a community index vector.
<code>brainconn.modularity.community_louvain(W[,...])</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes which maximizes the number of within-group edges and minimizes the number of between-group edges.
<code>brainconn.modularity.link_communities(W[,...])</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes which maximizes the number of within-group edges and minimizes the number of between-group edges.
<code>brainconn.modularity.modularity_dir(A[,...])</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges.
<code>brainconn.modularity.modularity_finetune_dir(W)</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges.
<code>brainconn.modularity.modularity_finetune_und(W)</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges.
<code>brainconn.modularity.modularity_finetune_und_sign(W)</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges.

Continued on next page

Table 7 – continued from previous page

<code>brainconn.modularity.modularity_louvain_dir(W)</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges.
<code>brainconn.modularity.modularity_louvain_und(W)</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges.
<code>brainconn.modularity.modularity_louvain_und_sign(W)</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges.
<code>brainconn.modularity.modularity_probtune_und_sign(W)</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges.
<code>brainconn.modularity.modularity_und(A[, ...])</code>	The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges.
<code>brainconn.modularity.modularity_und_sign(W, ci)</code>	This function simply calculates the signed modularity for a given partition.
<code>brainconn.modularity.partition_distance(cx, cy)</code>	This function quantifies the distance between pairs of community partitions with information theoretic measures.

**brainconn.modularity.ci2ls****ci2ls** (*ci*)

Convert from a community index vector to a 2D python list of modules The list is a pure python list, not requiring numpy.

**Parameters**

- **ci** (`Nx1 numpy.ndarray`) – the community index vector
- **zeroindexed** (*bool*) – If True, ci uses zero-indexing (lowest value is 0). Defaults to False.

**Returns** *ls* – pure python list with lowest value zero-indexed (regardless of zero-indexing parameter)

**Return type** `listof(list)`

**brainconn.modularity.ls2ci****ls2ci** (*ls*, *zeroindexed=False*)

Convert from a 2D python list of modules to a community index vector. The list is a pure python list, not requiring numpy.

**Parameters**

- **ls** (`listof(list)`) – pure python list with lowest value zero-indexed (regardless of value of zeroindexed parameter)

- **zeroindexed** (*bool*) – If True, ci uses zero-indexing (lowest value is 0). Defaults to False.

**Returns** **ci** – community index vector

**Return type**  $N \times 1$  `numpy.ndarray`

### `brainconn.modularity.community_louvain`

**community\_louvain** (*W*, *gamma*=1, *ci*=None, *B*= 'modularity', *seed*=None)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes which maximizes the number of within-group edges and minimizes the number of between-group edges.

This function is a fast and accurate multi-iterative generalization of the louvain community detection algorithm. This function subsumes and improves upon `modularity_[louvain,finetune]_[und,dir]()` and additionally allows to optimize other objective functions (includes built-in Potts Model i Hamiltonian, allows for custom objective-function matrices).

#### Parameters

- **W** ( $N \times N$  `np.array`) – directed/undirected weighted/binary adjacency matrix
- **gamma** (`float`) – resolution parameter. default value=1. Values  $0 \leq \gamma < 1$  detect larger modules while  $\gamma > 1$  detects smaller modules. ignored if an objective function matrix is specified.
- **ci** ( $N \times 1$  `np.arraylike`) – initial community affiliation vector. default value=None
- **B** (`str` |  $N \times N$  `np.arraylike`) – string describing objective function type, or provides a custom  $N \times N$  objective-function matrix. builtin values  
 'modularity' uses Q-metric as objective function 'potts' uses Potts model Hamiltonian.  
 'negative\_sym' symmetric treatment of negative weights 'negative\_asym' asymmetric treatment of negative weights
- **seed** (`int` | None) – random seed. default value=None. if None, seeds from /dev/urandom.

#### Returns

- **ci** ( $N \times 1$  `np.array`) – final community structure
- **q** (`float`) – optimized q-statistic (modularity only)

### `brainconn.modularity.link_communities`

**link\_communities** (*W*, *type\_clustering*= 'single')

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes which maximizes the number of within-group edges and minimizes the number of between-group edges.

This algorithm uncovers overlapping community structure via hierarchical clustering of network links. This algorithm is generalized for weighted/directed/fully-connected networks

#### Parameters

- **W** ( $N \times N$  `np.array`) – directed weighted/binary adjacency matrix
- **type\_clustering** (`str`) – type of hierarchical clustering. 'single' for single-linkage, 'complete' for complete-linkage. Default value='single'

**Returns** **M** – nodal community affiliation matrix.

**Return type** CxN `numpy.ndarray`

### `brainconn.modularity.modularity_dir`

**modularity\_dir** (*A*, *gamma*=1, *kci*=None)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges. The modularity is a statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups.

#### Parameters

- **W** (NxN `numpy.ndarray`) – directed weighted/binary connection matrix
- **gamma** (`float`) – resolution parameter. default value=1. Values  $0 \leq \gamma < 1$  detect larger modules while  $\gamma > 1$  detects smaller modules.
- **kci** (Nx1 `numpy.ndarray` | None) – starting community structure. If specified, calculates the Q-metric on the community structure giving, without doing any optimization. Otherwise, if not specified, uses a spectral modularity maximization algorithm.

#### Returns

- **ci** (Nx1 `numpy.ndarray`) – optimized community structure
- **Q** (`float`) – maximized modularity metric

#### Notes

This algorithm is deterministic. The matlab function bearing this name incorrectly disclaims that the outcome depends on heuristics involving a random seed. The louvain method does depend on a random seed, but this function uses a deterministic modularity maximization algorithm.

### `brainconn.modularity.modularity_finetune_dir`

**modularity\_finetune\_dir** (*W*, *ci*=None, *gamma*=1, *seed*=None)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges. The modularity is a statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups.

This algorithm is inspired by the Kernighan-Lin fine-tuning algorithm and is designed to refine a previously detected community structure.

#### Parameters

- **W** (NxN `numpy.ndarray`) – directed weighted/binary connection matrix
- **ci** (Nx1 `numpy.ndarray` | None) – initial community affiliation vector
- **gamma** (`float`) – resolution parameter. default value=1. Values  $0 \leq \gamma < 1$  detect larger modules while  $\gamma > 1$  detects smaller modules.
- **seed** (`int` | None) – random seed. default value=None. if None, seeds from /dev/urandom.

#### Returns

- **ci** (Nx1 `numpy.ndarray`) – refined community affiliation vector



- **Q** (*float*) – optimized modularity metric

## Notes

Ci and Q may vary from run to run, due to heuristics in the algorithm. Consequently, it may be worth to compare multiple runs.

### brainconn.modularity.modularity\_finetime\_und

**modularity\_finetime\_und** (*W*, *ci=None*, *gamma=1*, *seed=None*)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges. The modularity is a statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups.

This algorithm is inspired by the Kernighan-Lin fine-tuning algorithm and is designed to refine a previously detected community structure.

#### Parameters

- **W** (*NxN numpy.ndarray*) – undirected weighted/binary connection matrix
- **ci** (*Nx1 numpy.ndarray | None*) – initial community affiliation vector
- **gamma** (*float*) – resolution parameter. default value=1. Values  $0 \leq \gamma < 1$  detect larger modules while  $\gamma > 1$  detects smaller modules.
- **seed** (*int | None*) – random seed. default value=None. if None, seeds from /dev/urandom.

#### Returns

- **ci** (*Nx1 numpy.ndarray*) – refined community affiliation vector
- **Q** (*float*) – optimized modularity metric

## Notes

Ci and Q may vary from run to run, due to heuristics in the algorithm. Consequently, it may be worth to compare multiple runs.

### brainconn.modularity.modularity\_finetime\_sign

**modularity\_finetime\_sign** (*W*, *qtype='sta'*, *gamma=1*, *ci=None*, *seed=None*)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges. The modularity is a statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups.

This algorithm is inspired by the Kernighan-Lin fine-tuning algorithm and is designed to refine a previously detected community structure.

#### Parameters

- **W** (*NxN numpy.ndarray*) – undirected weighted/binary connection matrix with positive and negative weights.

- **qtype** (*str*) – modularity type. Can be ‘sta’ (default), ‘pos’, ‘smp’, ‘gja’, ‘neg’. See Rubinov and Sporns (2011) for a description.
- **gamma** (*float*) – resolution parameter. default value=1. Values  $0 \leq \text{gamma} < 1$  detect larger modules while  $\text{gamma} > 1$  detects smaller modules.
- **ci** ( $\text{Nx1 numpy.ndarray} \mid \text{None}$ ) – initial community affiliation vector
- **seed** (*int* | *None*) – random seed. default value=None. if None, seeds from /dev/urandom.

#### Returns

- **ci** ( $\text{Nx1 numpy.ndarray}$ ) – refined community affiliation vector
- **Q** (*float*) – optimized modularity metric

#### Notes

Ci and Q may vary from run to run, due to heuristics in the algorithm. Consequently, it may be worth to compare multiple runs.

### brainconn.modularity.modularity\_louvain\_dir

**modularity\_louvain\_dir** (*W*, *gamma=1*, *hierarchy=False*, *seed=None*)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges. The modularity is a statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups.

The Louvain algorithm is a fast and accurate community detection algorithm (as of writing). The algorithm may also be used to detect hierarchical community structure.

#### Parameters

- **W** ( $\text{NxN numpy.ndarray}$ ) – directed weighted/binary connection matrix
- **gamma** (*float*) – resolution parameter. default value=1. Values  $0 \leq \text{gamma} < 1$  detect larger modules while  $\text{gamma} > 1$  detects smaller modules.
- **hierarchy** (*bool*) – Enables hierarchical output. Defalut value=False
- **seed** (*int* | *None*) – random seed. default value=None. if None, seeds from /dev/urandom.

#### Returns

- **ci** ( $\text{Nx1 numpy.ndarray}$ ) – refined community affiliation vector. If hierarchical output enabled, it is an  $\text{NxH numpy.ndarray}$  instead with multiple iterations
- **Q** (*float*) – optimized modularity metric. If hierarchical output enabled, becomes an  $\text{Hx1}$  array of floats instead.

#### Notes

Ci and Q may vary from run to run, due to heuristics in the algorithm. Consequently, it may be worth to compare multiple runs.

**brainconn.modularity.modularity\_louvain\_und****modularity\_louvain\_und** (*W*, *gamma*=1, *hierarchy*=False, *seed*=None)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges. The modularity is a statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups.

The Louvain algorithm is a fast and accurate community detection algorithm (as of writing). The algorithm may also be used to detect hierarchical community structure.

**Parameters**

- **W** (NxN `numpy.ndarray`) – undirected weighted/binary connection matrix
- **gamma** (`float`) – resolution parameter. default value=1. Values  $0 \leq \text{gamma} < 1$  detect larger modules while  $\text{gamma} > 1$  detects smaller modules.
- **hierarchy** (`bool`) – Enables hierarchical output. Default value=False
- **seed** (`int` | `None`) – random seed. default value=None. if None, seeds from /dev/urandom.

**Returns**

- **ci** (Nx1 `numpy.ndarray`) – refined community affiliation vector. If hierarchical output enabled, it is an NxH `numpy.ndarray` instead with multiple iterations
- **Q** (`float`) – optimized modularity metric. If hierarchical output enabled, becomes an Hx1 array of floats instead.

**Notes**

Ci and Q may vary from run to run, due to heuristics in the algorithm. Consequently, it may be worth to compare multiple runs.

**brainconn.modularity.modularity\_louvain\_und\_sign****modularity\_louvain\_und\_sign** (*W*, *gamma*=1, *qtype*='sta', *seed*=None)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges. The modularity is a statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups.

The Louvain algorithm is a fast and accurate community detection algorithm (at the time of writing).

Use this function as opposed to `modularity_louvain_und()` only if the network contains a mix of positive and negative weights. If the network contains all positive weights, the output will be equivalent to that of `modularity_louvain_und()`.

**Parameters**

- **W** (NxN `numpy.ndarray`) – undirected weighted/binary connection matrix with positive and negative weights
- **qtype** (`str`) – modularity type. Can be 'sta' (default), 'pos', 'smp', 'gja', 'neg'. See Rubinov and Sporns (2011) for a description.
- **gamma** (`float`) – resolution parameter. default value=1. Values  $0 \leq \text{gamma} < 1$  detect larger modules while  $\text{gamma} > 1$  detects smaller modules.

- **seed** (*int* / *None*) – random seed. default value=*None*. if *None*, seeds from */dev/urandom*.

**Returns**

- **ci** (*Nx1 numpy.ndarray*) – refined community affiliation vector
- **Q** (*float*) – optimized modularity metric

**Notes**

Ci and Q may vary from run to run, due to heuristics in the algorithm. Consequently, it may be worth to compare multiple runs.

**brainconn.modularity.modularity\_probtune\_und\_sign**

**modularity\_probtune\_und\_sign** (*W*, *qtype*='sta', *gamma*=1, *ci*=*None*, *p*=0.45, *seed*=*None*)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges. The modularity is a statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups. High-modularity degeneracy is the presence of many topologically distinct high-modularity partitions of the network.

This algorithm is inspired by the Kernighan-Lin fine-tuning algorithm and is designed to probabilistically refine a previously detected community by incorporating random node moves into a finetuning algorithm.

**Parameters**

- **W** (*NxN numpy.ndarray*) – undirected weighted/binary connection matrix with positive and negative weights
- **qtype** (*str*) – modularity type. Can be 'sta' (default), 'pos', 'smp', 'gja', 'neg'. See Rubinov and Sporns (2011) for a description.
- **gamma** (*float*) – resolution parameter. default value=1. Values  $0 \leq \gamma < 1$  detect larger modules while  $\gamma > 1$  detects smaller modules.
- **ci** (*Nx1 numpy.ndarray* | *None*) – initial community affiliation vector
- **p** (*float*) – probability of random node moves. Default value = 0.45
- **seed** (*int* / *None*) – random seed. default value=*None*. if *None*, seeds from */dev/urandom*.

**Returns**

- **ci** (*Nx1 numpy.ndarray*) – refined community affiliation vector
- **Q** (*float*) – optimized modularity metric

**Notes**

Ci and Q may vary from run to run, due to heuristics in the algorithm. Consequently, it may be worth to compare multiple runs.

**brainconn.modularity.modularity\_und****modularity\_und** (*A*, *gamma=1*, *kci=None*)

The optimal community structure is a subdivision of the network into nonoverlapping groups of nodes in a way that maximizes the number of within-group edges, and minimizes the number of between-group edges. The modularity is a statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups.

**Parameters**

- **W** ( $N \times N$  `numpy.ndarray`) – undirected weighted/binary connection matrix
- **gamma** (`float`) – resolution parameter. default value=1. Values  $0 \leq \gamma < 1$  detect larger modules while  $\gamma > 1$  detects smaller modules.
- **kci** ( $N \times 1$  `numpy.ndarray` | `None`) – starting community structure. If specified, calculates the Q-metric on the community structure giving, without doing any optimization. Otherwise, if not specified, uses a spectral modularity maximization algorithm.

**Returns**

- **ci** ( $N \times 1$  `numpy.ndarray`) – optimized community structure
- **Q** (`float`) – maximized modularity metric

**Notes**

This algorithm is deterministic. The matlab function bearing this name incorrectly disclaims that the outcome depends on heuristics involving a random seed. The louvain method does depend on a random seed, but this function uses a deterministic modularity maximization algorithm.

**brainconn.modularity.modularity\_und\_sign****modularity\_und\_sign** (*W*, *ci*, *qtype='sta'*)

This function simply calculates the signed modularity for a given partition. It does not do automatic partition generation right now.

**Parameters**

- **W** ( $N \times N$  `numpy.ndarray`) – undirected weighted/binary connection matrix with positive and negative weights
- **ci** ( $N \times 1$  `numpy.ndarray`) – community partition
- **qtype** (`str`) – modularity type. Can be 'sta' (default), 'pos', 'smp', 'gja', 'neg'. See Rubinov and Sporns (2011) for a description.

**Returns**

- **ci** ( $N \times 1$  `numpy.ndarray`) – the partition which was input (for consistency of the API)
- **Q** (`float`) – maximized modularity metric

**Notes**

uses a deterministic algorithm

**brainconn.modularity.partition\_distance****partition\_distance** (*cx*, *cy*)

This function quantifies the distance between pairs of community partitions with information theoretic measures.

**Parameters**

- **cx** (Nx1 `numpy.ndarray`) – community affiliation vector X
- **cy** (Nx1 `numpy.ndarray`) – community affiliation vector Y

**Returns**

- **VIn** (Nx1 `numpy.ndarray`) – normalized variation of information
- **MIIn** (Nx1 `numpy.ndarray`) – normalized mutual information

**Notes**

(Definitions:  $VIn = [H(X) + H(Y) - 2MI(X,Y)]/\log(n)$   $MIIn = 2MI(X,Y)/[H(X)+H(Y)]$ )

where H is entropy, MI is mutual information and n is number of nodes)

**1.3.8 brainconn.motifs: Motifs**

Metrics which identify the most important nodes in graphs.

<code>brainconn.motifs</code>	Metrics which identify the most important nodes in graphs.
<code>brainconn.motifs.find_motif34(m[, n])</code>	This function returns all motif isomorphs for a given motif id and class (3 or 4).
<code>brainconn.motifs.make_motif34lib()</code>	This function generates the motif34lib.mat library required for all other motif computations.
<code>brainconn.motifs.motif3funct_bin(A)</code>	Functional motifs are subsets of connection patterns embedded within anatomical motifs.
<code>brainconn.motifs.motif3funct_wei(W)</code>	Functional motifs are subsets of connection patterns embedded within anatomical motifs.
<code>brainconn.motifs.motif3struct_bin(A)</code>	Structural motifs are patterns of local connectivity.
<code>brainconn.motifs.motif3struct_wei(W)</code>	Structural motifs are patterns of local connectivity.
<code>brainconn.motifs.motif4funct_bin(A)</code>	Functional motifs are subsets of connection patterns embedded within anatomical motifs.
<code>brainconn.motifs.motif4funct_wei(W)</code>	Functional motifs are subsets of connection patterns embedded within anatomical motifs.
<code>brainconn.motifs.motif4struct_bin(A)</code>	Structural motifs are patterns of local connectivity.
<code>brainconn.motifs.motif4struct_wei(W)</code>	Structural motifs are patterns of local connectivity.

**brainconn.motifs.find\_motif34****find\_motif34** (*m*, *n=None*)

This function returns all motif isomorphs for a given motif id and class (3 or 4). The function also returns the motif id for a given motif matrix

1. **Input: Motif\_id, e.g. 1 to 13, if class is 3** Motif\_class, number of nodes, 3 or 4.

Output: Motif\_matrices, all isomorphs for the given motif

2. Input: Motif\_matrix e.g. [0 1 0; 0 0 1; 1 0 0] Output Motif\_id e.g. 1 to 13, if class is 3

#### Parameters

- **m** (*int* | *matrix*) – In use case 1, a motif\_id which is an integer. In use case 2, the entire matrix of the motif (e.g. [0 1 0; 0 0 1; 1 0 0])
- **n** (*int* | *None*) – In use case 1, the motif class, which is the number of nodes. This is either 3 or 4. In use case 2, None.

**Returns** **M** – In use case 1, returns all isomorphs for the given motif In use case 2, returns the motif\_id for the specified motif matrix

**Return type** `numpy.ndarray` | `int`

### brainconn.motifs.make\_motif34lib

#### make\_motif34lib()

This function generates the motif34lib.mat library required for all other motif computations. Not to be called externally.

### brainconn.motifs.motif3funct\_bin

#### motif3funct\_bin(A)

Functional motifs are subsets of connection patterns embedded within anatomical motifs. Motif frequency is the frequency of occurrence of motifs around a node.

**Parameters** **A** (NxN `numpy.ndarray`) – binary directed connection matrix

#### Returns

- **F** (13xN `numpy.ndarray`) – motif frequency matrix
- **f** (13x1 `numpy.ndarray`) – motif frequency vector (averaged over all nodes)

### brainconn.motifs.motif3funct\_wei

#### motif3funct\_wei(W)

Functional motifs are subsets of connection patterns embedded within anatomical motifs. Motif frequency is the frequency of occurrence of motifs around a node. Motif intensity and coherence are weighted generalizations of motif frequency.

**Parameters** **W** (NxN `numpy.ndarray`) – weighted directed connection matrix (all weights between 0 and 1)

#### Returns

- **I** (13xN `numpy.ndarray`) – motif intensity matrix
- **Q** (13xN `numpy.ndarray`) – motif coherence matrix
- **F** (13xN `numpy.ndarray`) – motif frequency matrix

#### Notes

Average intensity and coherence are given by  $I/F$  and  $Q/F$ .

**brainconn.motifs.motif3struct\_bin****motif3struct\_bin** (*A*)

Structural motifs are patterns of local connectivity. Motif frequency is the frequency of occurrence of motifs around a node.

**Parameters** **A** (NxN `numpy.ndarray`) – binary directed connection matrix

**Returns**

- **F** (13xN `numpy.ndarray`) – motif frequency matrix
- **f** (13x1 `numpy.ndarray`) – motif frequency vector (averaged over all nodes)

**brainconn.motifs.motif3struct\_wei****motif3struct\_wei** (*W*)

Structural motifs are patterns of local connectivity. Motif frequency is the frequency of occurrence of motifs around a node. Motif intensity and coherence are weighted generalizations of motif frequency.

**Parameters** **W** (NxN `numpy.ndarray`) – weighted directed connection matrix (all weights between 0 and 1)

**Returns**

- **I** (13xN `numpy.ndarray`) – motif intensity matrix
- **Q** (13xN `numpy.ndarray`) – motif coherence matrix
- **F** (13xN `numpy.ndarray`) – motif frequency matrix

**Notes**

Average intensity and coherence are given by  $I/F$  and  $Q/F$ .

**brainconn.motifs.motif4func\_bin****motif4func\_bin** (*A*)

Functional motifs are subsets of connection patterns embedded within anatomical motifs. Motif frequency is the frequency of occurrence of motifs around a node.

**Parameters** **A** (NxN `numpy.ndarray`) – binary directed connection matrix

**Returns**

- **F** (199xN `numpy.ndarray`) – motif frequency matrix
- **f** (199x1 `numpy.ndarray`) – motif frequency vector (averaged over all nodes)

**brainconn.motifs.motif4func\_wei****motif4func\_wei** (*W*)

Functional motifs are subsets of connection patterns embedded within anatomical motifs. Motif frequency is the frequency of occurrence of motifs around a node. Motif intensity and coherence are weighted generalizations of motif frequency.

**Parameters** **W** (NxN `numpy.ndarray`) – weighted directed connection matrix (all weights between 0 and 1)



**Returns**

- **I** (199xN `numpy.ndarray`) – motif intensity matrix
- **Q** (199xN `numpy.ndarray`) – motif coherence matrix
- **F** (199xN `numpy.ndarray`) – motif frequency matrix

**Notes**

Average intensity and coherence are given by  $I/F$  and  $Q/F$ .

**brainconn.motifs.motif4struct\_bin****motif4struct\_bin** (*A*)

Structural motifs are patterns of local connectivity. Motif frequency is the frequency of occurrence of motifs around a node.

**Parameters** **A** (NxN `numpy.ndarray`) – binary directed connection matrix

**Returns**

- **F** (199xN `numpy.ndarray`) – motif frequency matrix
- **f** (199x1 `numpy.ndarray`) – motif frequency vector (averaged over all nodes)

**brainconn.motifs.motif4struct\_wei****motif4struct\_wei** (*W*)

Structural motifs are patterns of local connectivity. Motif frequency is the frequency of occurrence of motifs around a node. Motif intensity and coherence are weighted generalizations of motif frequency.

**Parameters** **W** (NxN `numpy.ndarray`) – weighted directed connection matrix (all weights between 0 and 1)

**Returns**

- **I** (199xN `numpy.ndarray`) – motif intensity matrix
- **Q** (199xN `numpy.ndarray`) – motif coherence matrix
- **F** (199xN `numpy.ndarray`) – motif frequency matrix

**Notes**

Average intensity and coherence are given by  $I/F$  and  $Q/F$ .

**1.3.9 brainconn.physical\_connectivity: Physical connectivity**

Metrics which identify the most important nodes in graphs.

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*brainconn.physical\_connectivity*

Metrics which identify the most important nodes in graphs.

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Table 9 – continued from previous page

<code>brainconn.physical_connectivity.density_dir(CIJ)</code>	Density is the fraction of present connections to possible connections.
<code>brainconn.physical_connectivity.density_und(CIJ)</code>	Density is the fraction of present connections to possible connections.
<code>brainconn.physical_connectivity.rentian_scaling(A, ...)</code>	Physical Rentian scaling (or more simply Rentian scaling) is a property of systems that are cost-efficiently embedded into physical space.

### `brainconn.physical_connectivity.density_dir`

#### `density_dir(CIJ)`

Density is the fraction of present connections to possible connections.

**Parameters** `CIJ` (NxN `numpy.ndarray`) – directed weighted/binary connection matrix

#### **Returns**

- `kden` (*float*) – density
- `N` (*int*) – number of vertices
- `k` (*int*) – number of edges

#### **Notes**

Assumes `CIJ` is directed and has no self-connections. Weight information is discarded.

### `brainconn.physical_connectivity.density_und`

#### `density_und(CIJ)`

Density is the fraction of present connections to possible connections.

**Parameters** `CIJ` (NxN `numpy.ndarray`) – undirected (weighted/binary) connection matrix

#### **Returns**

- `kden` (*float*) – density
- `N` (*int*) – number of vertices
- `k` (*int*) – number of edges

#### **Notes**

Assumes `CIJ` is undirected and has no self-connections. Weight information is discarded.

### `brainconn.physical_connectivity.rentian_scaling`

#### `rentian_scaling(A, xyz, n)`

Physical Rentian scaling (or more simply Rentian scaling) is a property of systems that are cost-efficiently embedded into physical space. It is what is called a “topo-physical” property because it combines information regarding the topological organization of the graph with information about the physical placement of connections. Rentian scaling is present in very large scale integrated circuits, the *C. elegans* neuronal network, and

morphometric and diffusion-based graphs of human anatomical networks. Rentian scaling is determined by partitioning the system into cubes, counting the number of nodes inside of each cube (N), and the number of edges traversing the boundary of each cube (E). If the system displays Rentian scaling, these two variables N and E will scale with one another in loglog space. The Rent's exponent is given by the slope of  $\log_{10}(E)$  vs.  $\log_{10}(N)$ , and can be reported alone or can be compared to the theoretical minimum Rent's exponent to determine how cost efficiently the network has been embedded into physical space. Note: if a system displays Rentian scaling, it does not automatically mean that the system is cost-efficiently embedded (although it does suggest that). Validation occurs when comparing to the theoretical minimum Rent's exponent for that system.

#### Parameters

- **A** ( $N \times N$  `numpy.ndarray`) – unweighted, binary, symmetric adjacency matrix
- **xyz** ( $N \times 3$  `numpy.ndarray`) – vector of node placement coordinates
- **n** (`int`) – Number of partitions to compute. Each partition is a data point; you want a large enough number to adequately compute Rent's exponent.

#### Returns

- **N** ( $M \times 1$  `numpy.ndarray`) – Number of nodes in each of the M partitions
- **E** ( $M \times 1$  `numpy.ndarray`)

#### Notes

Subsequent Analysis: Rentian scaling plots are then created by: `figure; loglog(E,N,'*')`; To determine the Rent's exponent,  $p$ , it is important not to use partitions which may be affected by boundary conditions. In Bassett et al. 2010 PLoS CB, only partitions with  $N < M/2$  were used in the estimation of the Rent's exponent. Thus, we can define  $N_{\text{prime}} = N(\text{find}(N < M/2))$  and  $E_{\text{prime}} = E(\text{find}(N < M/2))$ . Next we need to determine the slope of  $E_{\text{prime}}$  vs.  $N_{\text{prime}}$  in loglog space, which is the Rent's exponent. There are many ways of doing this with more or less statistical rigor. Robustfit in MATLAB is one such option:

```
[b,stats] = robustfit(log10(N_prime),log10(E_prime))
```

Then the Rent's exponent is  $b(1,2)$  and the standard error of the estimation is given by  $\text{stats.se}(1,2)$ .

Note:  $n=5000$  was used in Bassett et al. 2010 in PLoS CB.

### 1.3.10 brainconn.reference: Reference

Metrics which identify the most important nodes in graphs.

<code>brainconn.reference</code>	Metrics which identify the most important nodes in graphs.
<code>brainconn.reference.latmio_dir_connected(R, itr)</code>	This function "latticizes" a directed network, while preserving the in- and out-degree distributions.
<code>brainconn.reference.latmio_dir(R, itr[, D])</code>	This function "latticizes" a directed network, while preserving the in- and out-degree distributions.
<code>brainconn.reference.latmio_und_connected(R, itr)</code>	This function "latticizes" an undirected network, while preserving the degree distribution.
<code>brainconn.reference.latmio_und(R, itr[, D])</code>	This function "latticizes" an undirected network, while preserving the degree distribution.

Continued on next page

Table 10 – continued from previous page

<code>brainconn.reference.makeevenCIJ(n, sz_cl)</code>	<code>k</code>	This function generates a random, directed network with a specified number of fully connected modules linked together by evenly distributed remaining random connections.
<code>brainconn.reference.makefractalCIJ(mx_lvl, ...)</code>		This function generates a directed network with a hierarchical modular organization.
<code>brainconn.reference.makerandCIJdegreesfixed(...)</code>		This function generates a directed random network with a specified in-degree and out-degree sequence.
<code>brainconn.reference.makerandCIJ_dir(n, k)</code>		This function generates a directed random network
<code>brainconn.reference.makerandCIJ_und(n, k)</code>		This function generates an undirected random network
<code>brainconn.reference.makinglatticeCIJ(n, k)</code>		This function generates a directed lattice network with toroidal boundary conditions (i.e.
<code>brainconn.reference.maketoeplitzCIJ(n, k, s)</code>		This function generates a directed network with a Gaussian drop-off in edge density with increasing distance from the main diagonal.
<code>brainconn.reference.null_model_dir_sign(W, ...)</code>		This function randomizes an directed network with positive and negative weights, while preserving the degree and strength distributions.
<code>brainconn.reference.null_model_und_sign(W, ...)</code>		This function randomizes an undirected network with positive and negative weights, while preserving the degree and strength distributions.
<code>brainconn.reference.randmio_dir(R, itr)</code>		This function randomizes a directed network, while preserving the in- and out-degree distributions.
<code>brainconn.reference.randmio_dir_connected(R, itr)</code>		This function randomizes a directed network, while preserving the in- and out-degree distributions.
<code>brainconn.reference.randmio_dir_signed(R, itr)</code>		This function randomizes a directed weighted network with positively and negatively signed connections, while preserving the positive and negative degree distributions.
<code>brainconn.reference.randmio_und(R, itr)</code>		This function randomizes an undirected network, while preserving the degree distribution.
<code>brainconn.reference.randmio_und_connected(R, itr)</code>		This function randomizes an undirected network, while preserving the degree distribution.
<code>brainconn.reference.randmio_und_signed(R, itr)</code>		This function randomizes an undirected weighted network with positive and negative weights, while simultaneously preserving the degree distribution of positive and negative weights.
<code>brainconn.reference.randomize_graph_partial_und(A, ...)</code>		<code>A = RANDOMIZE_GRAPH_PARTIAL_UND(A,B,MAXSWAP)</code> takes adjacency matrices A and B and attempts to randomize matrix A by performing MAXSWAP rewirings.
<code>brainconn.reference.randomizer_bin_und(R, alpha)</code>		This function randomizes a binary undirected network, while preserving the degree distribution.

**brainconn.reference.latmio\_dir\_connected****latmio\_dir\_connected** (*R*, *itr*, *D=None*)

This function “latticizes” a directed network, while preserving the in- and out-degree distributions. In weighted networks, the function preserves the out-strength but not the in-strength distributions. The function also ensures that the randomized network maintains connectedness, the ability for every node to reach every other node in

the network. The input network for this function must be connected.

#### Parameters

- **R** ( $N \times N$  `numpy.ndarray`) – directed binary/weighted connection matrix
- **itr** (`int`) – rewiring parameter. Each edge is rewired approximately itr times.
- **D** (`numpy.ndarray` | `None`) – distance-to-diagonal matrix. Defaults to the actual distance matrix if not specified.

#### Returns

- **Rlatt** ( $N \times N$  `numpy.ndarray`) – latticized network in original node ordering
- **Rrp** ( $N \times N$  `numpy.ndarray`) – latticized network in node ordering used for latticization
- **ind\_rp** ( $N \times 1$  `numpy.ndarray`) – node ordering used for latticization
- **eff** (`int`) – number of actual rewirings carried out

### brainconn.reference.latmio\_dir

**latmio\_dir** (*R*, *itr*, *D=None*)

This function “latticizes” a directed network, while preserving the in- and out-degree distributions. In weighted networks, the function preserves the out-strength but not the in-strength distributions.

#### Parameters

- **R** ( $N \times N$  `numpy.ndarray`) – directed binary/weighted connection matrix
- **itr** (`int`) – rewiring parameter. Each edge is rewired approximately itr times.
- **D** (`numpy.ndarray` | `None`) – distance-to-diagonal matrix. Defaults to the actual distance matrix if not specified.

#### Returns

- **Rlatt** ( $N \times N$  `numpy.ndarray`) – latticized network in original node ordering
- **Rrp** ( $N \times N$  `numpy.ndarray`) – latticized network in node ordering used for latticization
- **ind\_rp** ( $N \times 1$  `numpy.ndarray`) – node ordering used for latticization
- **eff** (`int`) – number of actual rewirings carried out

### brainconn.reference.latmio\_und\_connected

**latmio\_und\_connected** (*R*, *itr*, *D=None*)

This function “latticizes” an undirected network, while preserving the degree distribution. The function does not preserve the strength distribution in weighted networks. The function also ensures that the randomized network maintains connectedness, the ability for every node to reach every other node in the network. The input network for this function must be connected.

#### Parameters

- **R** ( $N \times N$  `numpy.ndarray`) – undirected binary/weighted connection matrix
- **itr** (`int`) – rewiring parameter. Each edge is rewired approximately itr times.
- **D** (`numpy.ndarray` | `None`) – distance-to-diagonal matrix. Defaults to the actual distance matrix if not specified.

#### Returns

- **Rlatt** (NxN `numpy.ndarray`) – latticized network in original node ordering
- **Rrp** (NxN `numpy.ndarray`) – latticized network in node ordering used for latticization
- **ind\_rp** (Nx1 `numpy.ndarray`) – node ordering used for latticization
- **eff** (*int*) – number of actual rewirings carried out

### `brainconn.reference.latmio_und`

**latmio\_und** (*R*, *itr*, *D=None*)

This function “latticizes” an undirected network, while preserving the degree distribution. The function does not preserve the strength distribution in weighted networks.

#### Parameters

- **R** (NxN `numpy.ndarray`) – undirected binary/weighted connection matrix
- **itr** (*int*) – rewiring parameter. Each edge is rewired approximately itr times.
- **D** (`numpy.ndarray` | None) – distance-to-diagonal matrix. Defaults to the actual distance matrix if not specified.

#### Returns

- **Rlatt** (NxN `numpy.ndarray`) – latticized network in original node ordering
- **Rrp** (NxN `numpy.ndarray`) – latticized network in node ordering used for latticization
- **ind\_rp** (Nx1 `numpy.ndarray`) – node ordering used for latticization
- **eff** (*int*) – number of actual rewirings carried out

### `brainconn.reference.makeevenCIJ`

**makeevenCIJ** (*n*, *k*, *sz\_cl*)

This function generates a random, directed network with a specified number of fully connected modules linked together by evenly distributed remaining random connections.

#### Parameters

- **N** (*int*) – number of vertices (must be power of 2)
- **K** (*int*) – number of edges
- **sz\_cl** (*int*) – size of clusters (must be power of 2)

**Returns** **CIJ** – connection matrix

**Return type** NxN `numpy.ndarray`

#### Notes

**N must be a power of 2.** A warning is generated if all modules contain more edges than K. Cluster size is  $2^{sz\_cl}$ ;

**brainconn.reference.makefractalCIJ****makefractalCIJ** (*mx\_lvl*, *E*, *sz\_cl*)

This function generates a directed network with a hierarchical modular organization. All modules are fully connected and connection density decays as  $1/(E^n)$ , with  $n$  = index of hierarchical level.

**Parameters**

- **mx\_lvl** (*int*) – number of hierarchical levels,  $N = 2^{\text{mx\_lvl}}$
- **E** (*int*) – connection density fall off per level
- **sz\_cl** (*int*) – size of clusters (must be power of 2)

**Returns**

- **CIJ** ( $N \times N$  `numpy.ndarray`) – connection matrix
- **K** (*int*) – number of connections present in output CIJ

**brainconn.reference.makerandCIJdegreesfixed****makerandCIJdegreesfixed** (*inv*, *outv*)

This function generates a directed random network with a specified in-degree and out-degree sequence.

**Parameters**

- **inv** ( $N \times 1$  `numpy.ndarray`) – in-degree vector
- **outv** ( $N \times 1$  `numpy.ndarray`) – out-degree vector

**Returns** **CIJ****Return type**  $N \times N$  `numpy.ndarray`**Notes****Necessary conditions include:**

$$\begin{aligned} \text{length}(\text{in}) &= \text{length}(\text{out}) = n \\ \text{sum}(\text{in}) &= \text{sum}(\text{out}) = k \\ \text{in}(i), \text{out}(i) &< n-1 \\ \text{in}(i) + \text{out}(j) &< n+2 \\ \text{in}(i) + \text{out}(i) &< n \end{aligned}$$

No connections are placed on the main diagonal

The algorithm used in this function is not, technically, guaranteed to terminate. If a valid distribution of in and out degrees is provided, this function will find it in bounded time with probability  $1-(1/(2*(k^2)))$ . This turns out to be a serious problem when computing infinite degree matrices, but offers good performance otherwise.

**brainconn.reference.makerandCIJ\_dir****makerandCIJ\_dir** (*n*, *k*)

This function generates a directed random network

**Parameters**

- **N** (*int*) – number of vertices
- **K** (*int*) – number of edges

**Returns** **CIJ** – directed random connection matrix

**Return type** NxN `numpy.ndarray`

### Notes

no connections are placed on the main diagonal.

## `brainconn.reference.makerandCIJ_und`

**makerandCIJ\_und** ( $n, k$ )

This function generates an undirected random network

### Parameters

- **N** (`int`) – number of vertices
- **K** (`int`) – number of edges

**Returns** **CIJ** – undirected random connection matrix

**Return type** NxN `numpy.ndarray`

### Notes

no connections are placed on the main diagonal.

## `brainconn.reference.makinglatticeCIJ`

**makinglatticeCIJ** ( $n, k$ )

This function generates a directed lattice network with toroidal boundary conditions (i.e. with ring-like “wrapping around”).

### Parameters

- **N** (`int`) – number of vertices
- **K** (`int`) – number of edges

**Returns** **CIJ** – connection matrix

**Return type** NxN `numpy.ndarray`

### Notes

The lattice is made by placing connections as close as possible to the main diagonal, with wrapping around. No connections are made on the main diagonal. In/Outdegree is kept approx. constant at  $K/N$ .

## `brainconn.reference.maketoeplitzCIJ`

**maketoeplitzCIJ** ( $n, k, s$ )

This function generates a directed network with a Gaussian drop-off in edge density with increasing distance from the main diagonal. There are toroidal boundary conditions (i.e. no ring-like “wrapping around”).

### Parameters

- **N** (`int`) – number of vertices



- $K$  (*int*) – number of edges
- $s$  (*float*) – standard deviation of toeplitz

**Returns**  $CIJ$  – connection matrix

**Return type**  $N \times N$  `numpy.ndarray`

### Notes

no connections are placed on the main diagonal.

### `brainconn.reference.null_model_dir_sign`

`null_model_dir_sign` ( $W$ , *bin\_swaps*=5, *wei\_freq*=0.1)

This function randomizes an directed network with positive and negative weights, while preserving the degree and strength distributions. This function calls `randmio_dir.m`

#### Parameters

- $W$  ( $N \times N$  `numpy.ndarray`) – directed weighted connection matrix
- **bin\_swaps** (*int*) – average number of swaps in each edge binary randomization. Default value is 5. 0 swaps implies no binary randomization.
- **wei\_freq** (*float*) – frequency of weight sorting in weighted randomization.  $0 \leq \text{wei\_freq} < 1$ .  $\text{wei\_freq} == 1$  implies that weights are sorted at each step.  $\text{wei\_freq} == 0.1$  implies that weights sorted each 10th step (faster, default value)  
 $\text{wei\_freq} == 0$  implies no sorting of weights (not recommended)

#### Returns

- $W0$  ( $N \times N$  `numpy.ndarray`) – randomized weighted connection matrix
- $R$  (*4-tuple of floats*) – Correlation coefficients between strength sequences of input and output connection matrices, `rpos_in`, `rpos_out`, `rneg_in`, `rneg_out`

### Notes

The value of **bin\_swaps** is ignored when binary topology is fully connected (e.g. when the network has no negative weights).

**Randomization may be better (and execution time will be slower) for** higher values of **bin\_swaps** and **wei\_freq**. Higher values of **bin\_swaps** may enable a more random binary organization, and higher values of **wei\_freq** may enable a more accurate conservation of strength sequences.

**R** are the correlation coefficients between positive and negative in-strength and out-strength sequences of input and output connection matrices and are used to evaluate the accuracy with which strengths were preserved. Note that correlation coefficients may be a rough measure of strength-sequence accuracy and one could implement more formal tests (such as the Kolmogorov-Smirnov test) if desired.

**brainconn.reference.null\_model\_und\_sign****null\_model\_und\_sign** (*W*, *bin\_swaps*=5, *wei\_freq*=0.1)

This function randomizes an undirected network with positive and negative weights, while preserving the degree and strength distributions. This function calls `randmio_und.m`

**Parameters**

- **W** (NxN `numpy.ndarray`) – undirected weighted connection matrix
- **bin\_swaps** (*int*) – average number of swaps in each edge binary randomization. Default value is 5. 0 swaps implies no binary randomization.
- **wei\_freq** (*float*) – frequency of weight sorting in weighted randomization.  $0 \leq \text{wei\_freq} < 1$ . `wei_freq == 1` implies that weights are sorted at each step. `wei_freq == 0.1` implies that weights sorted each 10th step (faster, default value)  
`wei_freq == 0` implies no sorting of weights (not recommended)

**Returns**

- **W0** (NxN `numpy.ndarray`) – randomized weighted connection matrix
- **R** (4-tuple of floats) – Correlation coefficients between strength sequences of input and output connection matrices, `rpos_in`, `rpos_out`, `rneg_in`, `rneg_out`

**Notes**

**The value of `bin_swaps` is ignored when binary topology is fully** connected (e.g. when the network has no negative weights).

**Randomization may be better (and execution time will be slower) for** higher values of `bin_swaps` and `wei_freq`. Higher values of `bin_swaps` may enable a more random binary organization, and higher values of `wei_freq` may enable a more accurate conservation of strength sequences.

**R are the correlation coefficients between positive and negative** strength sequences of input and output connection matrices and are used to evaluate the accuracy with which strengths were preserved. Note that correlation coefficients may be a rough measure of strength-sequence accuracy and one could implement more formal tests (such as the Kolmogorov-Smirnov test) if desired.

**brainconn.reference.randmio\_dir****randmio\_dir** (*R*, *itr*)

This function randomizes a directed network, while preserving the in- and out-degree distributions. In weighted networks, the function preserves the out-strength but not the in-strength distributions.

**Parameters**

- **W** (NxN `numpy.ndarray`) – directed binary/weighted connection matrix
- **itr** (*int*) – rewiring parameter. Each edge is rewired approximately `itr` times.

**Returns**

- **R** (NxN `numpy.ndarray`) – randomized network
- **eff** (*int*) – number of actual rewirings carried out

**brainconn.reference.randmio\_dir\_connected****randmio\_dir\_connected** (*R*, *itr*)

This function randomizes a directed network, while preserving the in- and out-degree distributions. In weighted networks, the function preserves the out-strength but not the in-strength distributions. The function also ensures that the randomized network maintains connectedness, the ability for every node to reach every other node in the network. The input network for this function must be connected.

**Parameters**

- **W** (NxN `numpy.ndarray`) – directed binary/weighted connection matrix
- **itr** (*int*) – rewiring parameter. Each edge is rewired approximately itr times.

**Returns**

- **R** (NxN `numpy.ndarray`) – randomized network
- **eff** (*int*) – number of actual rewirings carried out

**brainconn.reference.randmio\_dir\_signed****randmio\_dir\_signed** (*R*, *itr*)

This function randomizes a directed weighted network with positively and negatively signed connections, while preserving the positive and negative degree distributions. In weighted networks by default the function preserves the out-degree strength but not the in-strength distributions

**Parameters**

- **W** (NxN `numpy.ndarray`) – directed binary/weighted connection matrix
- **itr** (*int*) – rewiring parameter. Each edge is rewired approximately itr times.

**Returns**

- **R** (NxN `numpy.ndarray`) – randomized network
- **eff** (*int*) – number of actual rewirings carried out

**brainconn.reference.randmio\_und****randmio\_und** (*R*, *itr*)

This function randomizes an undirected network, while preserving the degree distribution. The function does not preserve the strength distribution in weighted networks.

**Parameters**

- **W** (NxN `numpy.ndarray`) – undirected binary/weighted connection matrix
- **itr** (*int*) – rewiring parameter. Each edge is rewired approximately itr times.

**Returns**

- **R** (NxN `numpy.ndarray`) – randomized network
- **eff** (*int*) – number of actual rewirings carried out

**brainconn.reference.randmio\_und\_connected****randmio\_und\_connected** (*R*, *itr*)

This function randomizes an undirected network, while preserving the degree distribution. The function does not preserve the strength distribution in weighted networks. The function also ensures that the randomized network maintains connectedness, the ability for every node to reach every other node in the network. The input network for this function must be connected.

NOTE the changes to the BCT matlab function of the same name made in the Jan 2016 release have not been propagated to this function because of substantially decreased time efficiency in the implementation. Expect these changes to be merged eventually.

**Parameters**

- **W** (NxN `numpy.ndarray`) – undirected binary/weighted connection matrix
- **itr** (*int*) – rewiring parameter. Each edge is rewired approximately itr times.

**Returns**

- **R** (NxN `numpy.ndarray`) – randomized network
- **eff** (*int*) – number of actual rewirings carried out

**brainconn.reference.randmio\_und\_signed****randmio\_und\_signed** (*R*, *itr*)

This function randomizes an undirected weighted network with positive and negative weights, while simultaneously preserving the degree distribution of positive and negative weights. The function does not preserve the strength distribution in weighted networks.

**Parameters**

- **W** (NxN `numpy.ndarray`) – undirected binary/weighted connection matrix
- **itr** (*int*) – rewiring parameter. Each edge is rewired approximately itr times.

**Returns** **R** – randomized network

**Return type** NxN `numpy.ndarray`

**brainconn.reference.randomize\_graph\_partial\_und****randomize\_graph\_partial\_und** (*A*, *B*, *maxswap*)

**A = RANDOMIZE\_GRAPH\_PARTIAL\_UND(A,B,MAXSWAP)** takes adjacency matrices **A** and **B** and attempts to randomize matrix **A** by performing MAXSWAP rewirings. The rewirings will avoid any spots where matrix **B** is nonzero.

**Parameters**

- **A** (NxN `numpy.ndarray`) – undirected adjacency matrix to randomize
- **B** (NxN `numpy.ndarray`) – mask; edges to avoid
- **maxswap** (*int*) – number of rewirings

**Returns** **A** – randomized matrix

**Return type** NxN `numpy.ndarray`

## Notes

1. Graph may become disconnected as a result of rewiring. Always important to check.
2. A can be weighted, though the weighted degree sequence will not be preserved.
3. A must be undirected.

### brainconn.reference.randomizer\_bin\_und

#### randomizer\_bin\_und(*R*, *alpha*)

This function randomizes a binary undirected network, while preserving the degree distribution. The function directly searches for rewirable edge pairs (rather than trying to rewired edge pairs at random), and hence avoids long loops and works especially well in dense matrices.

#### Parameters

- **A** (*NxN numpy.ndarray*) – binary undirected connection matrix
- **alpha** (*float*) – fraction of edges to rewire

**Returns** **R** – randomized network

**Return type** *NxN numpy.ndarray*

## 1.3.11 brainconn.similarity: Similarity

Metrics which identify the most important nodes in graphs.

<i>brainconn.similarity</i>	Metrics which identify the most important nodes in graphs.
<i>brainconn.similarity.corr_flat_dir</i> (a1, a2)	Returns the correlation coefficient between two flattened adjacency matrices.
<i>brainconn.similarity.corr_flat_und</i> (a1, a2)	Returns the correlation coefficient between two flattened adjacency matrices.
<i>brainconn.similarity.dice_pairwise_und</i> (a1, a2)	Calculates pairwise dice similarity for each vertex between two matrices.
<i>brainconn.similarity.edge_nei_overlap_bd</i> (CIJ)	This function determines the neighbors of two nodes that are linked by an edge, and then computes their overlap.
<i>brainconn.similarity.edge_nei_overlap_bu</i> (CIJ)	This function determines the neighbors of two nodes that are linked by an edge, and then computes their overlap.
<i>brainconn.similarity.gtom</i> (adj, nr_steps)	The m-th step generalized topological overlap measure (GTOM) quantifies the extent to which a pair of nodes have similar m-th step neighbors.
<i>brainconn.similarity.matching_ind</i> (CIJ)	For any two nodes u and v, the matching index computes the amount of overlap in the connection patterns of u and v.

Continued on next page

Table 11 – continued from previous page

<code>brainconn.similarity.matching_ind_und(CIJ0)</code>	M0 = MATCHING_IND_UND(CIJ) computes matching index for undirected graph specified by adjacency matrix CIJ.
--	--

**brainconn.similarity.corr\_flat\_dir****corr\_flat\_dir** (*a1*, *a2*)

Returns the correlation coefficient between two flattened adjacency matrices. Similarity metric for weighted matrices.

**Parameters**

- **A1** (NxN `numpy.ndarray`) – directed matrix 1
- **A2** (NxN `numpy.ndarray`) – directed matrix 2

**Returns** **r** – Correlation coefficient describing edgewise similarity of *a1* and *a2*

**Return type** `float`

**brainconn.similarity.corr\_flat\_und****corr\_flat\_und** (*a1*, *a2*)

Returns the correlation coefficient between two flattened adjacency matrices. Only the upper triangular part is used to avoid double counting undirected matrices. Similarity metric for weighted matrices.

**Parameters**

- **A1** (NxN `numpy.ndarray`) – undirected matrix 1
- **A2** (NxN `numpy.ndarray`) – undirected matrix 2

**Returns** **r** – Correlation coefficient describing edgewise similarity of *a1* and *a2*

**Return type** `float`

**brainconn.similarity.dice\_pairwise\_und****dice\_pairwise\_und** (*a1*, *a2*)

Calculates pairwise dice similarity for each vertex between two matrices. Treats the matrices as binary and undirected.

**Parameters**

- **A1** (NxN `numpy.ndarray`) – Matrix 1
- **A2** (NxN `numpy.ndarray`) – Matrix 2

**Returns** **D** – dice similarity vector

**Return type** Nx1 `numpy.ndarray`

**brainconn.similarity.edge\_nei\_overlap\_bd****edge\_nei\_overlap\_bd** (*CIJ*)

This function determines the neighbors of two nodes that are linked by an edge, and then computes their overlap. Connection matrix must be binary and directed. Entries of 'EC' that are 'inf' indicate that no edge is present.

Entries of ‘EC’ that are 0 denote “local bridges”, i.e. edges that link completely non-overlapping neighborhoods. Low values of EC indicate edges that are “weak ties”.

If CIJ is weighted, the weights are ignored. Neighbors of a node can be linked by incoming, outgoing, or reciprocal connections.

**Parameters** **CIJ** (NxN `numpy.ndarray`) – directed binary/weighted connection matrix

**Returns**

- **EC** (NxN `numpy.ndarray`) – edge neighborhood overlap matrix
- **ec** (Kx1 `numpy.ndarray`) – edge neighborhood overlap per edge vector
- **degij** (NxN `numpy.ndarray`) – degrees of node pairs connected by each edge

### **brainconn.similarity.edge\_nei\_overlap\_bu**

**edge\_nei\_overlap\_bu** (CIJ)

This function determines the neighbors of two nodes that are linked by an edge, and then computes their overlap. Connection matrix must be binary and directed. Entries of ‘EC’ that are ‘inf’ indicate that no edge is present. Entries of ‘EC’ that are 0 denote “local bridges”, i.e. edges that link completely non-overlapping neighborhoods. Low values of EC indicate edges that are “weak ties”.

If CIJ is weighted, the weights are ignored.

**Parameters** **CIJ** (NxN `numpy.ndarray`) – undirected binary/weighted connection matrix

**Returns**

- **EC** (NxN `numpy.ndarray`) – edge neighborhood overlap matrix
- **ec** (Kx1 `numpy.ndarray`) – edge neighborhood overlap per edge vector
- **degij** (NxN `numpy.ndarray`) – degrees of node pairs connected by each edge

### **brainconn.similarity.gtom**

**gtom** (adj, nr\_steps)

The m-th step generalized topological overlap measure (GTOM) quantifies the extent to which a pair of nodes have similar m-th step neighbors. Mth-step neighbors are nodes that are reachable by a path of at most length m.

This function computes the the M x M generalized topological overlap measure (GTOM) matrix for number of steps, numSteps.

**Parameters**

- **adj** (NxN `numpy.ndarray`) – connection matrix
- **nr\_steps** (*int*) – number of steps

**Returns** **gt** – GTOM matrix

**Return type** NxN `numpy.ndarray`

### **Notes**

When numSteps is equal to 1, GTOM is identical to the topological overlap measure (TOM) from reference [2]. In that case the ‘gt’ matrix records, for each pair of nodes, the fraction of neighbors the two nodes share in common, where “neighbors” are one step removed. As ‘numSteps’ is increased, neighbors that are further out are

considered. Elements of 'gt' are bounded between 0 and 1. The 'gt' matrix can be converted from a similarity to a distance matrix by taking 1-gt.

### **brainconn.similarity.matching\_ind**

#### **matching\_ind**(CIJ)

For any two nodes u and v, the matching index computes the amount of overlap in the connection patterns of u and v. Self-connections and u-v connections are ignored. The matching index is a symmetric quantity, similar to a correlation or a dot product.

**Parameters** **CIJ** (NxN `numpy.ndarray`) – adjacency matrix

**Returns**

- **Min** (NxN `numpy.ndarray`) – matching index for incoming connections
- **Mout** (NxN `numpy.ndarray`) – matching index for outgoing connections
- **Mall** (NxN `numpy.ndarray`) – matching index for all connections

#### **Notes**

Does not use self- or cross connections for comparison. Does not use connections that are not present in BOTH u and v. All output matrices are calculated for upper triangular only.

### **brainconn.similarity.matching\_ind\_und**

#### **matching\_ind\_und**(CIJ0)

M0 = MATCHING\_IND\_UND(CIJ) computes matching index for undirected graph specified by adjacency matrix CIJ. Matching index is a measure of similarity between two nodes' connectivity profiles (excluding their mutual connection, should it exist).

**Parameters** **CIJ** (NxN `numpy.ndarray`) – undirected adjacency matrix

**Returns** **M0** – matching index matrix

**Return type** NxN `numpy.ndarray`

## **1.3.12 brainconn.nbs: Network-based statistic**

Network-based statistic calculation.

---

<code>brainconn.nbs</code>	Network-based statistic calculation.
<code>brainconn.nbs.nbs_bct</code> (x, y, thresh[, k, ...])	Performs the NBS for populations X and Y for a t-statistic threshold of alpha.

---

### **brainconn.nbs.nbs\_bct**

**nbs\_bct** (x, y, thresh, k=1000, tail='both', paired=False, verbose=False)

Performs the NBS for populations X and Y for a t-statistic threshold of alpha.

**Parameters**

- **x** (NxNxP `numpy.ndarray`) – matrix representing the first population with P subjects.



must be symmetric.

- **y** ( $N \times N \times Q$  `numpy.ndarray`) – matrix representing the second population with  $Q$  subjects.  $Q$  need not equal  $P$ . must be symmetric.
- **thresh** (`float`) – minimum t-value used as threshold
- **k** (`int`, optional) – number of permutations used to estimate the empirical null distribution
- **tail** (`{'both', 'left', 'right'}`, *optional*) – enables specification of particular alternative hypothesis ‘left’ : mean population of  $X <$  mean population of  $Y$  ‘right’ : mean population of  $Y <$  mean population of  $X$  ‘both’ : means are unequal (default)
- **paired** (`bool`, optional) – use paired sample t-test instead of population t-test. requires both subject populations to have equal  $N$ . default value = `False`
- **verbose** (`bool`, optional) – print some extra information each iteration. defaults value = `False`

### Returns

- **pval** ( $C \times 1$  `numpy.ndarray`) – A vector of corrected p-values for each component of the networks identified. If at least one p-value is less than alpha, the omnibus null hypothesis can be rejected at alpha significance. The null hypothesis is that the value of the connectivity from each edge has equal mean across the two populations.
- **adj** ( $I \times I \times C$  `numpy.ndarray`) – an adjacency matrix identifying the edges comprising each component. edges are assigned indexed values.
- **null** ( $K \times 1$  `numpy.ndarray`) – A vector of  $K$  sampled from the null distribution of maximal component size.

### Notes

The NBS[R5426218f292b-1]\_ is a nonparametric statistical test used to isolate the components of an  $N \times N$  undirected connectivity matrix that differ significantly between two distinct populations. Each element of the connectivity matrix stores a connectivity value and each member of the two populations possesses a distinct connectivity matrix. A component of a connectivity matrix is defined as a set of interconnected edges.

The NBS is essentially a procedure to control the family-wise error rate, in the weak sense, when the null hypothesis is tested independently at each of the  $N(N-1)/2$  edges comprising the undirected connectivity matrix. The NBS can provide greater statistical power than conventional procedures for controlling the family-wise error rate, such as the false discovery rate, if the set of edges at which the null hypothesis is rejected constitutes a large component or components.

The NBS comprises four steps:

1. Perform a two-sample T-test at each edge independently to test the hypothesis that the value of connectivity between the two populations come from distributions with equal means.
2. Threshold the T-statistic available at each edge to form a set of suprathreshold edges.
3. Identify any components in the adjacency matrix defined by the set of suprathreshold edges. These are referred to as observed components. Compute the size of each observed component identified; that is, the number of edges it comprises.
4. Repeat  $K$  times steps 1-3, each time randomly permuting members of the two populations and storing the size of the largest component identified for each permutation. This yields an empirical estimate of the null distribution of maximal component size. A corrected p-value for each observed component is then calculated using this null distribution.

## References

### 1.3.13 brainconn.utils: Utility functions

Utility functions.

<code>brainconn.utils</code>	Utility functions.
<code>brainconn.utils.matrix</code>	Other utility functions.
<code>brainconn.utils.visualization</code>	Tools for visualizing graphs.
<code>brainconn.utils.misc</code>	Miscellaneous utility functions.

#### brainconn.utils.matrix

Other utility functions.

#### Functions

<code>autofix(W[, copy])</code>	Fix a bunch of common problems.
<code>binarize(W[, copy])</code>	Binarizes an input weighted connection matrix.
<code>invert(W[, copy])</code>	Inverts elementwise the weights in an input connection matrix.
<code>normalize(W[, copy])</code>	Normalizes an input weighted connection matrix.
<code>threshold_absolute(W, thr[, copy])</code>	This function thresholds the connectivity matrix by absolute weight magnitude.
<code>threshold_proportional(W, p[, copy])</code>	This function “thresholds” the connectivity matrix by preserving a proportion $p$ ( $0 < p < 1$ ) of the strongest weights.
<code>weight_conversion(W, wcm[, copy])</code>	$W_{bin} = \text{weight\_conversion}(W, \text{'binarize'})$ ; $W_{nrm} = \text{weight\_conversion}(W, \text{'normalize'})$ ; $L = \text{weight\_conversion}(W, \text{'lengths'})$ ;

#### brainconn.utils.matrix.autofix

**autofix** ( $W$ ,  $copy=True$ )

Fix a bunch of common problems. More specifically, remove Inf and NaN, ensure exact binariness and symmetry (i.e. remove floating point instability), and zero diagonal.

##### Parameters

- **W** (`numpy.ndarray`) – weighted connectivity matrix
- **copy** (`bool`) – if True, returns a copy of the matrix. Otherwise, modifies the matrix in place. Default value=True.

**Returns** **W** – connectivity matrix with fixes applied

**Return type** `numpy.ndarray`

**brainconn.utils.matrix.binarize****binarize** (*W*, *copy=True*)

Binarizes an input weighted connection matrix. If *copy* is not set, this function will *modify W in place*.

**Parameters**

- **W** (`NxN numpy.ndarray`) – weighted connectivity matrix
- **copy** (`bool`) – if True, returns a copy of the matrix. Otherwise, modifies the matrix in place. Default value=True.

**Returns** **W** – binary connectivity matrix

**Return type** `NxN numpy.ndarray`

**brainconn.utils.matrix.invert****invert** (*W*, *copy=True*)

Inverts elementwise the weights in an input connection matrix. In other words, change the from the matrix of internode strengths to the matrix of internode distances.

If *copy* is not set, this function will *modify W in place*.

**Parameters**

- **W** (`numpy.ndarray`) – weighted connectivity matrix
- **copy** (`bool`) – if True, returns a copy of the matrix. Otherwise, modifies the matrix in place. Default value=True.

**Returns** **W** – inverted connectivity matrix

**Return type** `numpy.ndarray`

**brainconn.utils.matrix.normalize****normalize** (*W*, *copy=True*)

Normalizes an input weighted connection matrix. If *copy* is not set, this function will *modify W in place*.

**Parameters**

- **W** (`numpy.ndarray`) – weighted connectivity matrix
- **copy** (`bool`) – if True, returns a copy of the matrix. Otherwise, modifies the matrix in place. Default value=True.

**Returns** **W** – normalized connectivity matrix

**Return type** `numpy.ndarray`

**brainconn.utils.matrix.threshold\_absolute****threshold\_absolute** (*W*, *thr*, *copy=True*)

This function thresholds the connectivity matrix by absolute weight magnitude. All weights below the given threshold, and all weights on the main diagonal (self-self connections) are set to 0.

If *copy* is not set, this function will *modify W in place*.

**Parameters**

- **W** (`numpy.ndarray`) – weighted connectivity matrix
- **thr** (`float`) – absolute weight threshold
- **copy** (`bool`) – if True, returns a copy of the matrix. Otherwise, modifies the matrix in place. Default value=True.

**Returns** **W** – thresholded connectivity matrix

**Return type** `numpy.ndarray`

### brainconn.utils.matrix.threshold\_proportional

**threshold\_proportional** (*W, p, copy=True*)

This function “thresholds” the connectivity matrix by preserving a proportion  $p$  ( $0 < p < 1$ ) of the strongest weights. All other weights, and all weights on the main diagonal (self-self connections) are set to 0.

If copy is not set, this function will *modify W in place*.

#### Parameters

- **W** (`numpy.ndarray`) – weighted connectivity matrix
- **p** (`float`) – proportional weight threshold ( $0 < p < 1$ )
- **copy** (`bool`) – if True, returns a copy of the matrix. Otherwise, modifies the matrix in place. Default value=True.

**Returns** **W** – thresholded connectivity matrix

**Return type** `numpy.ndarray`

### Notes

The proportion of elements set to 0 is a fraction of all elements in the matrix, whether or not they are already 0. That is, this function has the following behavior:

```
>> x = np.random.random((10,10)) >> x_25 = threshold_proportional(x, .25) >> np.size(np.where(x_25))
#note this double counts each nonzero element 46 >> x_125 = threshold_proportional(x, .125) >>
np.size(np.where(x_125)) 22 >> x_test = threshold_proportional(x_25, .5) >> np.size(np.where(x_test)) 46
```

That is, the 50% thresholding of `x_25` does nothing because  $\geq 50\%$  of the elements in `x_25` are already  $\leq 0$ . This behavior is the same as in BCT. Be careful with matrices that are both signed and sparse.

### brainconn.utils.matrix.weight\_conversion

**weight\_conversion** (*W, wcm, copy=True*)

```
W_bin = weight_conversion(W, 'binarize'); W_nrm = weight_conversion(W, 'normalize'); L =
weight_conversion(W, 'lengths');
```

This function may either binarize an input weighted connection matrix, normalize an input weighted connection matrix or convert an input weighted connection matrix to a weighted connection-length matrix.

Binarization converts all present connection weights to 1.

Normalization scales all weight magnitudes to the range  $[0,1]$  and should be done prior to computing some weighted measures, such as the weighted clustering coefficient.

Conversion of connection weights to connection lengths is needed prior to computation of weighted distance-based measures, such as distance and betweenness centrality. In a weighted connection network, higher weights are naturally interpreted as shorter lengths. The connection-lengths matrix here is defined as the inverse of the connection-weights matrix.

If copy is not set, this function will *modify W in place*.

#### Parameters

- **W** (NxN `numpy.ndarray`) – weighted connectivity matrix
- **wcm** (`str`) – weight conversion command. ‘binarize’ : binarize weights ‘normalize’ : normalize weights ‘lengths’ : convert weights to lengths (invert matrix)
- **copy** (`bool`) – if True, returns a copy of the matrix. Otherwise, modifies the matrix in place. Default value=True.

**Returns** **W** – connectivity matrix with specified changes

**Return type** NxN `numpy.ndarray`

#### Notes

This function is included for compatibility with BCT. But there are other functions `binarize()`, `normalize()` and `invert()` which are simpler to call directly.

### brainconn.utils.visualization

Tools for visualizing graphs.

#### Functions

<code>adjacency_plot_und(A, coord[, tube])</code>	This function in matlab is a visualization helper which translates an adjacency matrix and an Nx3 matrix of spatial coordinates, and plots a 3D isometric network connecting the undirected unweighted nodes using a specific plotting format.
<code>align_matrices(m1, m2[, dfun, verbose, H, ...])</code>	This function aligns two matrices relative to one another by reordering the nodes in M2.
<code>backbone_wu(CIJ, avgdeg)</code>	The network backbone contains the dominant connections in the network and may be used to aid network visualization.
<code>grid_communities(c)</code>	(X,Y,INDSORT) = GRID_COMMUNITIES(C) takes a vector of community assignments C and returns three output arguments for visualizing the communities.
<code>reorderMAT(m[, H, cost])</code>	This function reorders the connectivity matrix in order to place more edges closer to the diagonal.
<code>reorder_matrix(m1[, cost, verbose, H, Texp, ...])</code>	This function rearranges the nodes in matrix M1 such that the matrix elements are squeezed along the main diagonal.
<code>reorder_mod(A, ci)</code>	This function reorders the connectivity matrix by modular structure and may hence be useful in visualization of modular structure.

Continued on next page

Table 15 – continued from previous page

<code>writetoPAJ(CIJ, fname, directed)</code>	This function writes a Pajek .net file from a numpy matrix
---	--

## brainconn.utils.visualization.adjacency\_plot\_und

### `adjacency_plot_und` (*A*, *coord*, *tube=False*)

This function in matlab is a visualization helper which translates an adjacency matrix and an Nx3 matrix of spatial coordinates, and plots a 3D isometric network connecting the undirected unweighted nodes using a specific plotting format. Including the formatted output is not useful at all for bctpy since matplotlib will not be able to plot it in quite the same way.

Instead of doing this, I have included code that will plot the adjacency matrix onto nodes at the given spatial coordinates in mayavi

This routine is basically a less featureful version of the 3D brain in cvu, the connectome visualization utility which I also maintain. cvu uses freesurfer surfaces and annotations to get the node coordinates (rather than leaving them up to the user) and has many other interactive visualization features not included here for the sake of brevity.

There are other similar visualizations in the ConnectomeViewer and the UCLA multimodal connectivity database.

Note that unlike other bctpy functions, this function depends on mayavi.

## brainconn.utils.visualization.align\_matrices

### `align_matrices` (*m1*, *m2*, *dfun='sqrdiff'*, *verbose=False*, *H=1000000.0*, *Texp=1*, *T0=0.001*, *Hbrk=10*)

This function aligns two matrices relative to one another by reordering the nodes in M2. The function uses a version of simulated annealing.

#### Parameters

- **M1** (NxN `numpy.ndarray`) – first connection matrix
- **M2** (NxN `numpy.ndarray`) – second connection matrix
- **dfun** (*str*) –  
**distance metric to use for matching** 'absdiff' : absolute difference 'sqrdiff' : squared difference (default) 'cosang' : cosine of vector angle
- **verbose** (*bool*) – print out cost at each iteration. Default False.
- **H** (*int*) – annealing parameter, default value 1e6
- **Texp** (*int*) – annealing parameter, default value 1. Coefficient of H s.t.  $Texp0=1-Texp/H$
- **T0** (*float*) – annealing parameter, default value 1e-3
- **Hbrk** (*int*) – annealing parameter, default value = 10. Coefficient of H s.t.  $Hbrk0 = H/Hkbr$

#### Returns

- **Mreordered** (NxN `numpy.ndarray`) – reordered connection matrix M2
- **Mindices** (Nx1 `numpy.ndarray`) – reordered indices
- **cost** (*float*) – objective function distance between M1 and Mreordered

## Notes

Connection matrices can be weighted or binary, directed or undirected. They must have the same number of nodes. M1 can be entered in any node ordering.

Note that in general, the outcome will depend on the initial condition (the setting of the random number seed). Also, there is no good way to determine optimal annealing parameters in advance - these parameters will need to be adjusted “by hand” (particularly H, Texp, T0, and Hbrk). For large and/or dense matrices, it is highly recommended to perform exploratory runs varying the settings of ‘H’ and ‘Texp’ and then select the best values.

Based on extensive testing, it appears that T0 and Hbrk can remain unchanged in most cases. Texp may be varied from 1-1/H to 1-10/H, for example. H is the most important parameter - set to larger values as the problem size increases. Good solutions can be obtained for matrices up to about 100 nodes. It is advisable to run this function multiple times and select the solution(s) with the lowest ‘cost’.

If the two matrices are related it may be very helpful to pre-align them by reordering along their largest eigenvectors:

```
[v,~] = eig(M1); v1 = abs(v(:,end)); [a1,b1] = sort(v1); [v,~] = eig(M2); v2 = abs(v(:,end)); [a2,b2] = sort(v2); [a,b,c] = overlapMAT2(M1(b1,b1),M2(b2,b2),'dfun',1);
```

Setting ‘Texp’ to zero cancels annealing and uses a greedy algorithm instead.

## brainconn.utils.visualization.backbone\_wu

### backbone\_wu (CIJ, avgdeg)

The network backbone contains the dominant connections in the network and may be used to aid network visualization. This function computes the backbone of a given weighted and undirected connection matrix CIJ, using a minimum-spanning-tree based algorithm.

#### Parameters

- **CIJ** (NxN `numpy.ndarray`) – weighted undirected connection matrix
- **avgdeg** (`int`) – desired average degree of backbone

#### Returns

- **CIJtree** (NxN `numpy.ndarray`) – connection matrix of the minimum spanning tree of CIJ
- **CIJclus** (NxN `numpy.ndarray`) – connection matrix of the minimum spanning tree plus strongest connections up to some average degree ‘avgdeg’. Identical to CIJtree if the degree requirement is already met.

## Notes

NOTE: nodes with zero strength are discarded. NOTE: CIJclus will have a total average degree exactly equal to (or very close to) ‘avgdeg’.

NOTE: ‘avgdeg’ backfill is handled slightly differently than in Hagmann et al 2008.

## brainconn.utils.visualization.grid\_communities

### grid\_communities (c)

(X,Y,INDSORT) = GRID\_COMMUNITIES(C) takes a vector of community assignments C and returns three

output arguments for visualizing the communities. The third is INDSORT, which is an ordering of the vertices so that nodes with the same community assignment are next to one another. The first two arguments are vectors that, when overlaid on the adjacency matrix using the PLOT function, highlight the communities.

**Parameters** **c** (Nx1 `numpy.ndarray`) – community assignments

**Returns**

- **bounds** (*list*) – list containing the communities
- **indsort** (`numpy.ndarray`) – indices

## Notes

Note: This function returns considerably different values than in matlab due to differences between matplotlib and matlab. This function has been designed to work with matplotlib, as in the following example:

```
ci,_=modularity_und(adj) bounds,ixes=grid_communities(ci) pylab.imshow(adj[np.ix_(ixes,ixes)],interpolation='none',cmap='B')
for b in bounds:
```

```
    pylab.axvline(x=b,color='red') pylab.axhline(y=b,color='red')
```

Note that I adapted the idea from the matlab function of the same name, and have not tested the functionality extensively.

## brainconn.utils.visualization.reorderMAT

**reorderMAT** (*m*, *H=5000*, *cost='line'*)

This function reorders the connectivity matrix in order to place more edges closer to the diagonal. This often helps in displaying community structure, clusters, etc.

**Parameters**

- **MAT** (NxN `numpy.ndarray`) – connection matrix
- **H** (*int*) – number of reordering attempts
- **cost** (*str*) – 'line' or 'circ' for shape of lattice (linear or ring lattice). Default is linear lattice.

**Returns**

- **MATreordered** (NxN `numpy.ndarray`) – reordered connection matrix
- **MATindices** (Nx1 `numpy.ndarray`) – reordered indices
- **MATcost** (*float*) – objective function cost of reordered matrix

## Notes

I'm not 100% sure how the algorithms between this and `reorder_matrix` differ, but this code looks a ton sketchier and might have had some minor bugs in it. Considering `reorder_matrix()` does the same thing using a well vetted simulated annealing algorithm, just use that. ~rlaplant



**brainconn.utils.visualization.reorder\_matrix**

**reorder\_matrix** (*m1*, *cost*='line', *verbose*=False, *H*=10000.0, *Texp*=10, *T0*=0.001, *Hbrk*=10)

This function rearranges the nodes in matrix M1 such that the matrix elements are squeezed along the main diagonal. The function uses a version of simulated annealing.

**Parameters**

- **M1** (NxN `numpy.ndarray`) – connection matrix weighted/binary directed/undirected
- **cost** (*str*) – ‘line’ or ‘circ’ for shape of lattice (linear or ring lattice). Default is linear lattice.
- **verbose** (*bool*) – print out cost at each iteration. Default False.
- **H** (*int*) – annealing parameter, default value 1e6
- **Texp** (*int*) – annealing parameter, default value 1. Coefficient of H s.t.  $Texp0=1-Texp/H$
- **T0** (*float*) – annealing parameter, default value 1e-3
- **Hbrk** (*int*) – annealing parameter, default value = 10. Coefficient of H s.t.  $Hbrk0 = H/Hkbr$

**Returns**

- **Mreordered** (NxN `numpy.ndarray`) – reordered connection matrix
- **Mindices** (Nx1 `numpy.ndarray`) – reordered indices
- **Mcost** (*float*) – objective function cost of reordered matrix

**Notes**

Note that in general, the outcome will depend on the initial condition (the setting of the random number seed). Also, there is no good way to determine optimal annealing parameters in advance - these paramters will need to be adjusted “by hand” (particularly H, Texp, and T0). For large and/or dense matrices, it is highly recommended to perform exploratory runs varying the settings of ‘H’ and ‘Texp’ and then select the best values.

Based on extensive testing, it appears that T0 and Hbrk can remain unchanged in most cases. Texp may be varied from 1-1/H to 1-10/H, for example. H is the most important parameter - set to larger values as the problem size increases. It is advisable to run this function multiple times and select the solution(s) with the lowest ‘cost’.

Setting ‘Texp’ to zero cancels annealing and uses a greedy algorithm instead.

**brainconn.utils.visualization.reorder\_mod**

**reorder\_mod** (*A*, *ci*)

This function reorders the connectivity matrix by modular structure and may hence be useful in visualization of modular structure.

**Parameters**

- **A** (NxN `numpy.ndarray`) – binary/weighted connectivity matrix
- **ci** (Nx1 `numpy.ndarray`) – module affiliation vector

**Returns**

- **On** (Nx1 `numpy.ndarray`) – new node order
- **Ar** (NxN `numpy.ndarray`) – reordered connectivity matrix

## brainconn.utils.visualization.writetoPAJ

**writetoPAJ** (*CIJ, fname, directed*)

This function writes a Pajek .net file from a numpy matrix

### Parameters

- **CIJ** ( $N \times N$  `numpy.ndarray`) – adjacency matrix
- **fname** (`str`) – filename
- **directed** (`bool`) – True if the network is directed and False otherwise. The data format may be required to know this for some reason so I am afraid to just use directed as the default value.

## brainconn.utils.misc

Miscellaneous utility functions.

### Functions

<code>cuberoot(x)</code>	Correctly handle the cube root for negative weights, instead of uselessly crashing as in python or returning the wrong root as in matlab
<code>dummyvar(cis[, return_sparse])</code>	This is an efficient implementation of matlab's "dummyvar" command using sparse matrices.
<code>get_resource_path()</code>	Returns the path to general resources, terminated with separator.
<code>pick_four_unique_nodes_quickly(n)</code>	This is equivalent to <code>np.random.choice(n, 4, replace=False)</code>
<code>teachers_round(x)</code>	Do rounding such that .5 always rounds to 1, and not bankers rounding.

## brainconn.utils.misc.cuberoot

**cuberoot** (*x*)

Correctly handle the cube root for negative weights, instead of uselessly crashing as in python or returning the wrong root as in matlab

## brainconn.utils.misc.dummyvar

**dummyvar** (*cis, return\_sparse=False*)

This is an efficient implementation of matlab's "dummyvar" command using sparse matrices.

**input:** **partitions**,  $N \times M$  array-like containing **M** partitions of **N** nodes into  $\leq N$  distinct communities

**output:** **dummyvar**, an  $N \times R$  matrix containing **R** column variables (**indicator** variables) with **N** entries, where **R** is the total number of communities summed across each of the **M** partitions.

i.e.  $r = \sum((\max(\text{len}(\text{unique}(\text{partitions}[i]))) \text{ for } i \text{ in range}(m)))$

### brainconn.utils.misc.get\_resource\_path

#### `get_resource_path()`

Returns the path to general resources, terminated with separator. Resources are kept outside package folder in “datasets”. Based on function by Yaroslav Halchenko used in Neurosynth Python package.

### brainconn.utils.misc.pick\_four\_unique\_nodes\_quickly

#### `pick_four_unique_nodes_quickly(n)`

This is equivalent to `np.random.choice(n, 4, replace=False)`

Another fellow suggested `np.random.random(n).argpartition(4)` which is clever but still substantially slower.

### brainconn.utils.misc.teachers\_round

#### `teachers_round(x)`

Do rounding such that .5 always rounds to 1, and not bankers rounding. This is for compatibility with matlab functions, and ease of testing.

### Exceptions

---

`BCTParamError`

---

## 1.4 Example gallery

### 1.4.1 Degree

#### Calculate centrality measures

Centrality is a thing with stuff and things.

```
# sphinx_gallery_thumbnail_number = 3
```

#### Start with the necessary imports

```
import os.path as op

import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt

import brainconn
```

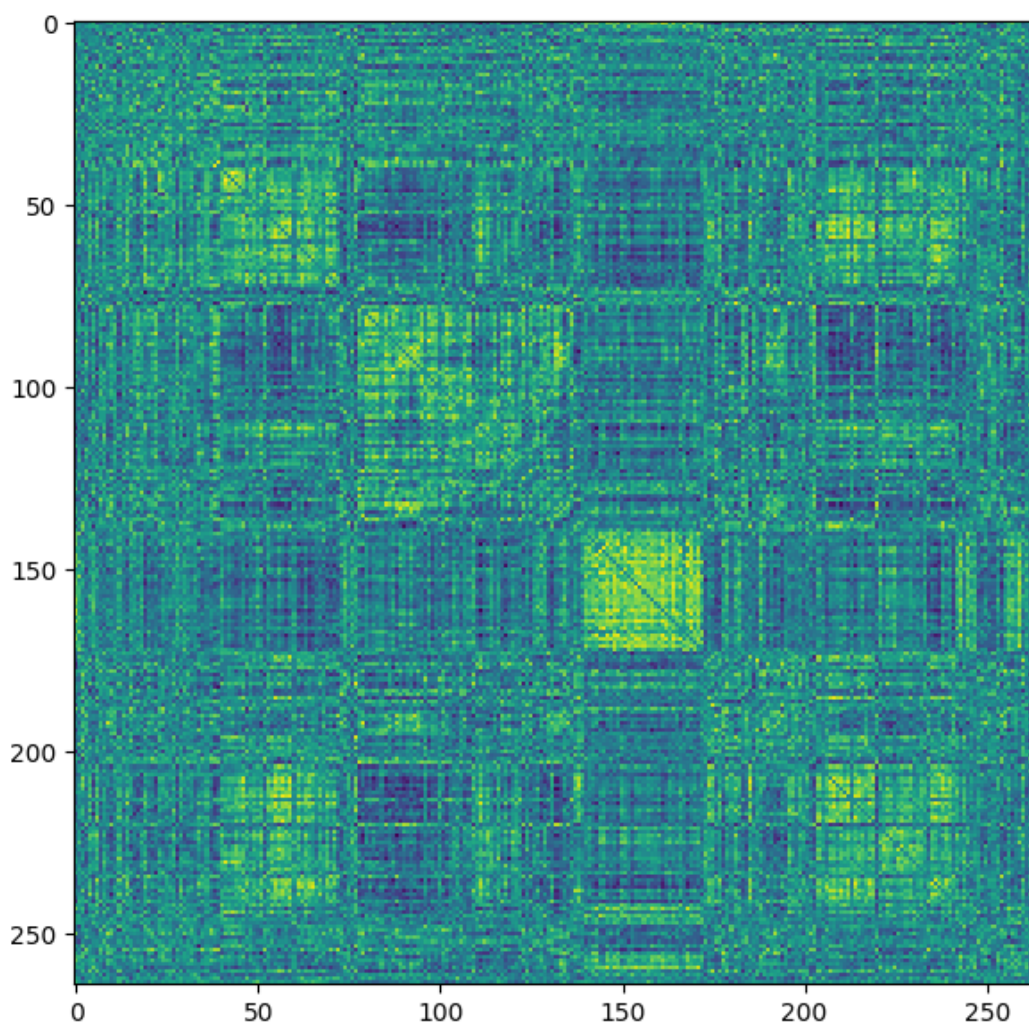
## Get some data

```
corr = np.loadtxt(op.join(brainconn.utils.get_resource_path(), 'example_corr.txt'))

# Zero diagonal
adj_wei = corr - np.eye(corr.shape[0])
adj_bin = brainconn.utils.binarize(brainconn.utils.threshold_proportional(adj_wei, 0.
↪2))
```

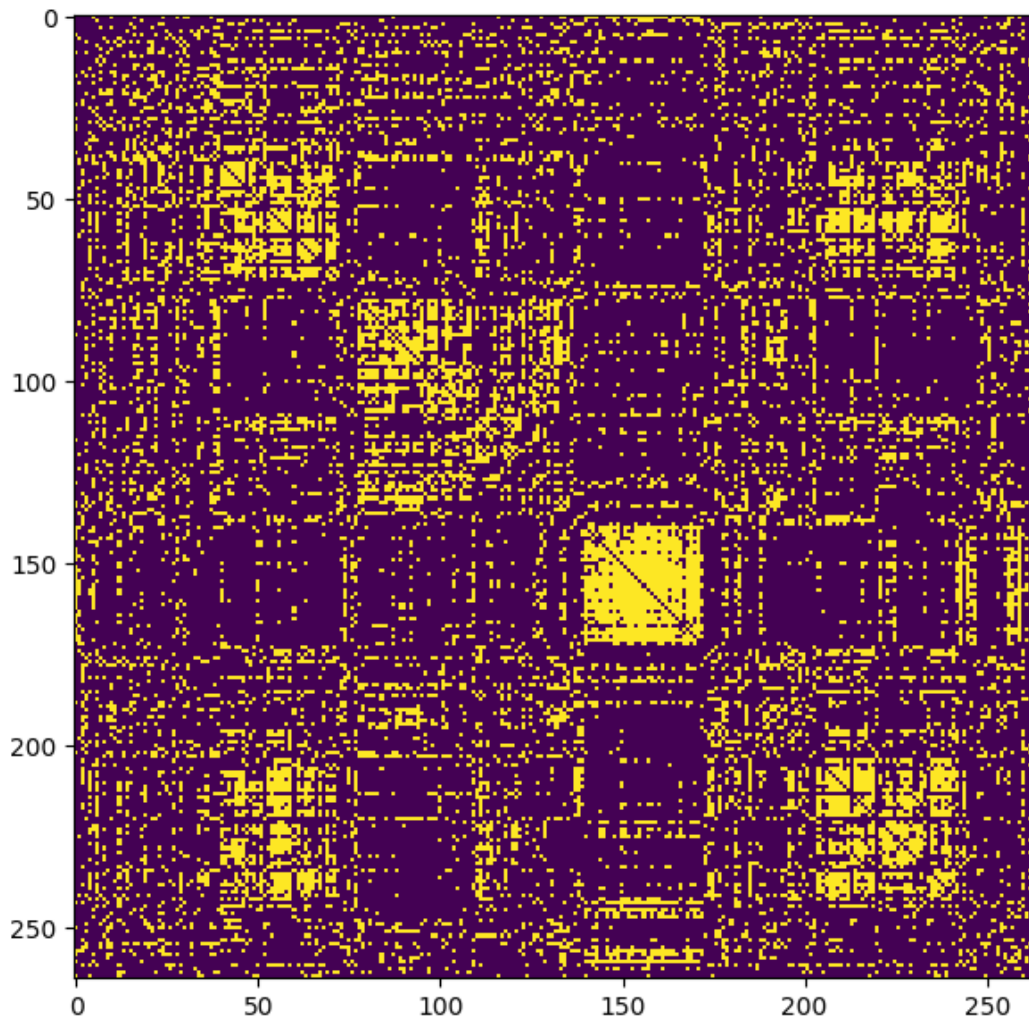
## Look at weighted adjacency matrix

```
fig, ax = plt.subplots(figsize=(7, 7))
ax.imshow(adj_wei)
fig.show()
```



### Look at binary adjacency matrix

```
fig, ax = plt.subplots(figsize=(7, 7))  
ax.imshow(adj_bin)  
fig.show()
```



### Compute stuff

```
betw_wei = brainconn.centralities.betweenness_wei(adj_wei)
betw_bin = brainconn.centralities.betweenness_bin(adj_bin)
edg_betw_wei = brainconn.centralities.edge_betweenness_wei(adj_wei)[0]
idx = np.triu_indices(edg_betw_wei.shape[0], k=1)
edg_betw_wei = edg_betw_wei[idx]
edg_betw_wei = edg_betw_wei[edg_betw_wei > 0]
edg_betw_bin = brainconn.centralities.edge_betweenness_bin(adj_bin)[0]
idx = np.triu_indices(edg_betw_bin.shape[0], k=1)
edg_betw_bin = edg_betw_bin[idx]
edg_betw_bin = edg_betw_bin[edg_betw_bin > 0]
```

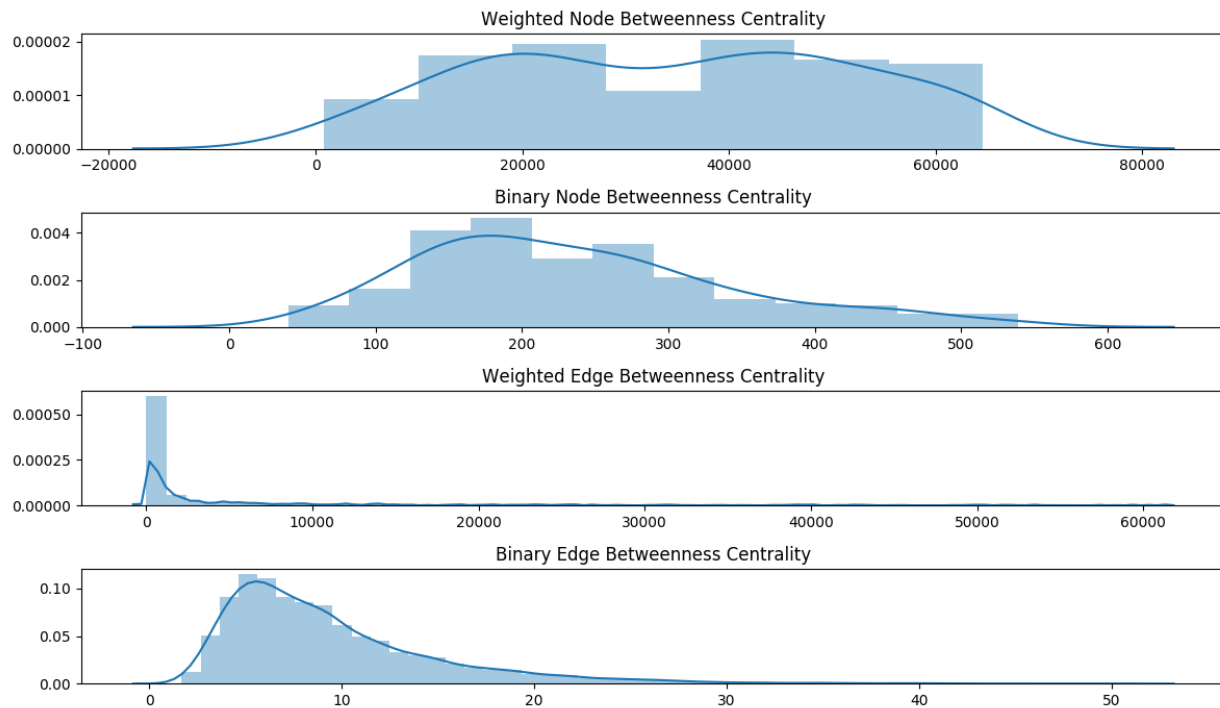
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```

vals = [betw_wei, betw_bin, edg_betw_wei, edg_betw_bin]
names = ['Weighted Node Betweenness Centrality',
         'Binary Node Betweenness Centrality',
         'Weighted Edge Betweenness Centrality',
         'Binary Edge Betweenness Centrality']
fig, axes = plt.subplots(nrows=4, figsize=(12, 7))
for i in range(4):
    sns.distplot(vals[i], ax=axes[i])
    axes[i].set_title(names[i])
fig.tight_layout()
fig.show()

```



Total running time of the script: ( 1 minutes 1.232 seconds)

## 1.4.2 Centrality

### Calculate degree measures

Degree is another thing with stuff and things.

```
# sphinx_gallery_thumbnail_number = 5
```

### Start with the necessary imports

```
import os.path as op
```

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```
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt

from brainconn import degree, utils
```

## Get some data

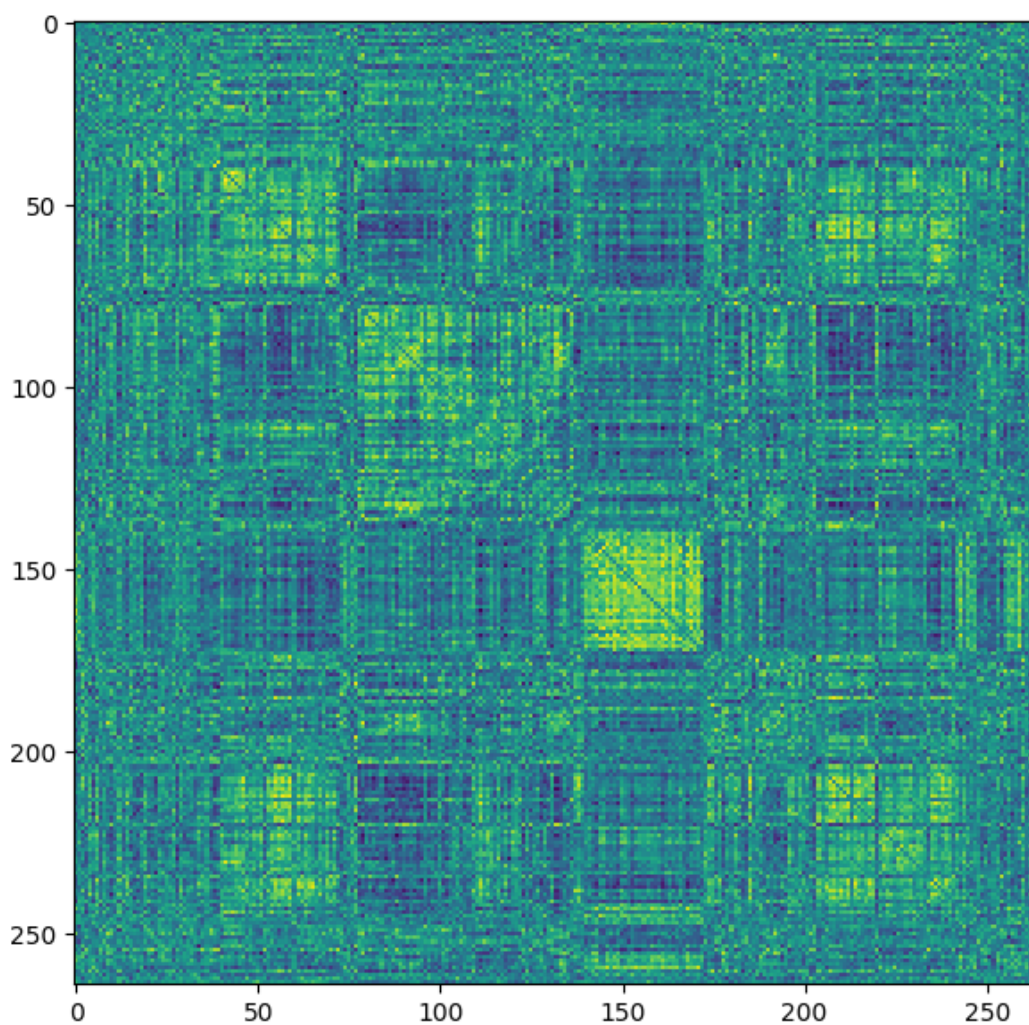
```
corr = np.loadtxt(op.join(utils.get_resource_path(), 'example_corr.txt'))

# Zero diagonal
adj_wei = corr - np.eye(corr.shape[0])
adj_wei_dir = adj_wei + (np.triu(adj_wei) / 2)
adj_bin = utils.binarize(utils.threshold_proportional(adj_wei, 0.2))
adj_bin_dir = utils.binarize(utils.threshold_proportional(adj_wei_dir, 0.2))
```

## Look at weighted undirected adjacency matrix

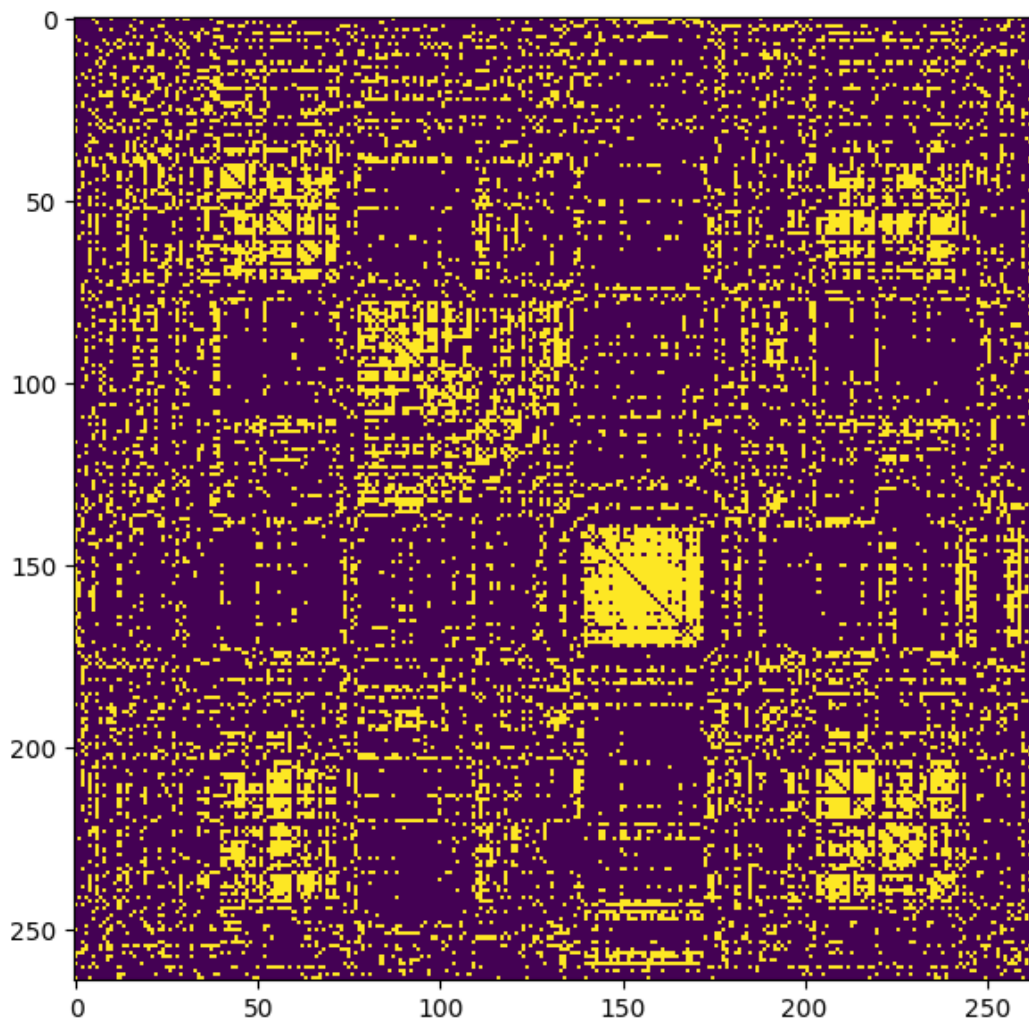
```
fig, ax = plt.subplots(figsize=(7, 7))
ax.imshow(adj_wei)
fig.show()
```





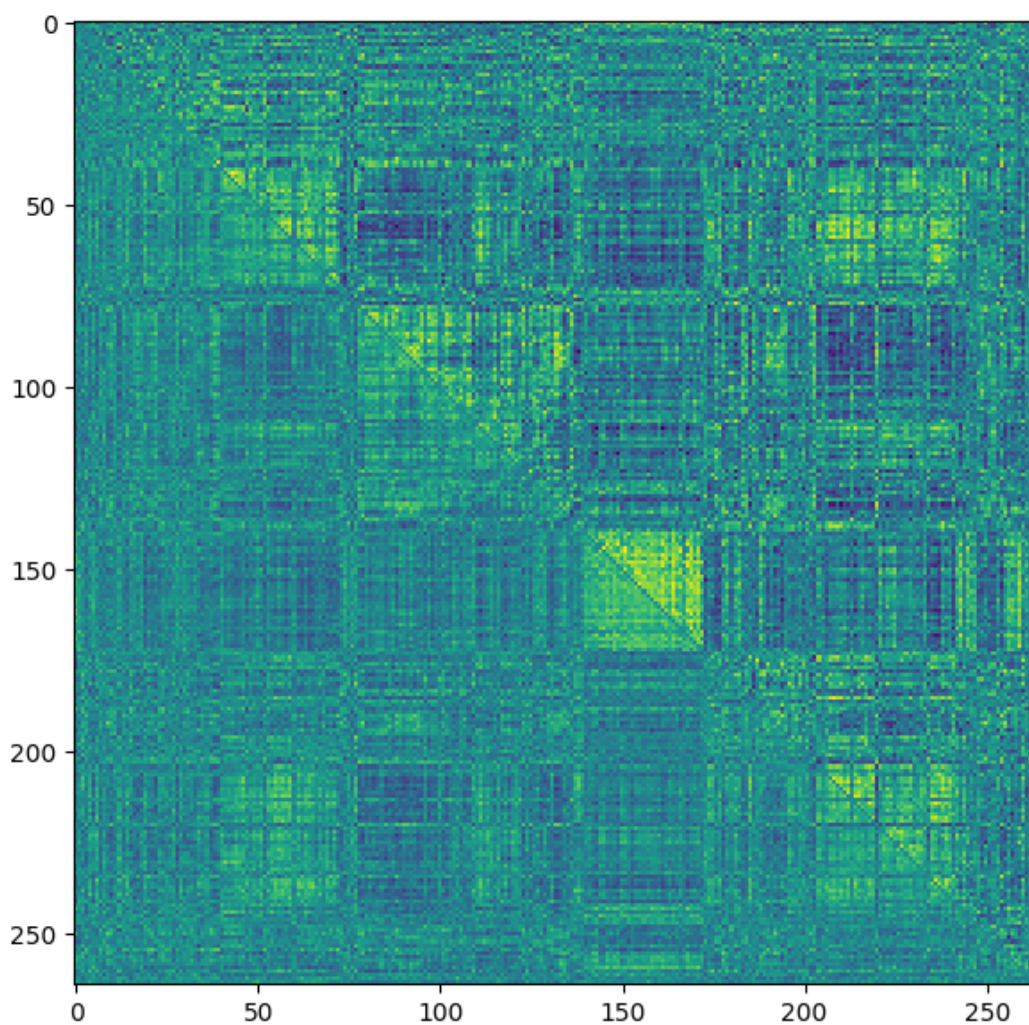
#### Look at binary undirected adjacency matrix

```
fig, ax = plt.subplots(figsize=(7, 7))  
ax.imshow(adj_bin)  
fig.show()
```



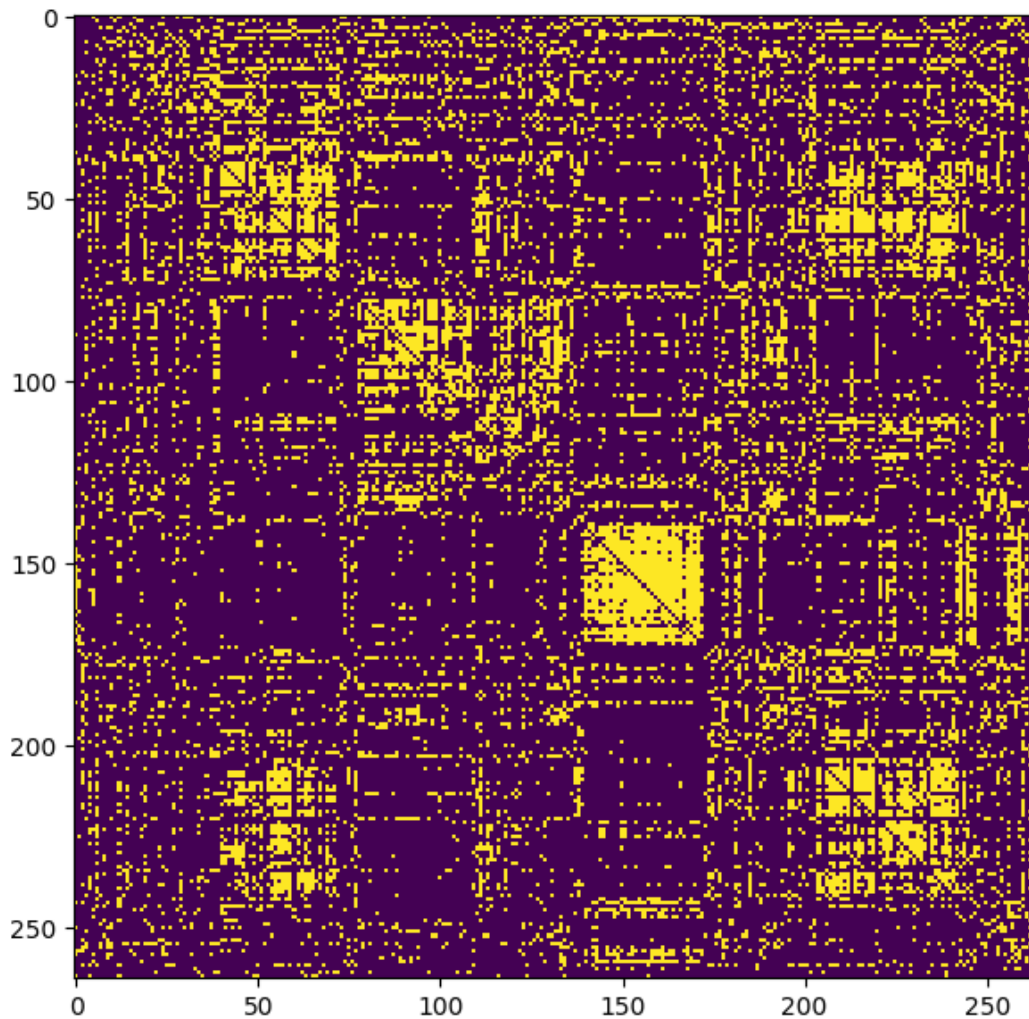
### Look at weighted directed adjacency matrix

```
fig, ax = plt.subplots(figsize=(7, 7))
ax.imshow(adj_wei_dir)
fig.show()
```



### Look at binary directed adjacency matrix

```
fig, ax = plt.subplots(figsize=(7, 7))  
ax.imshow(adj_bin_dir)  
fig.show()
```



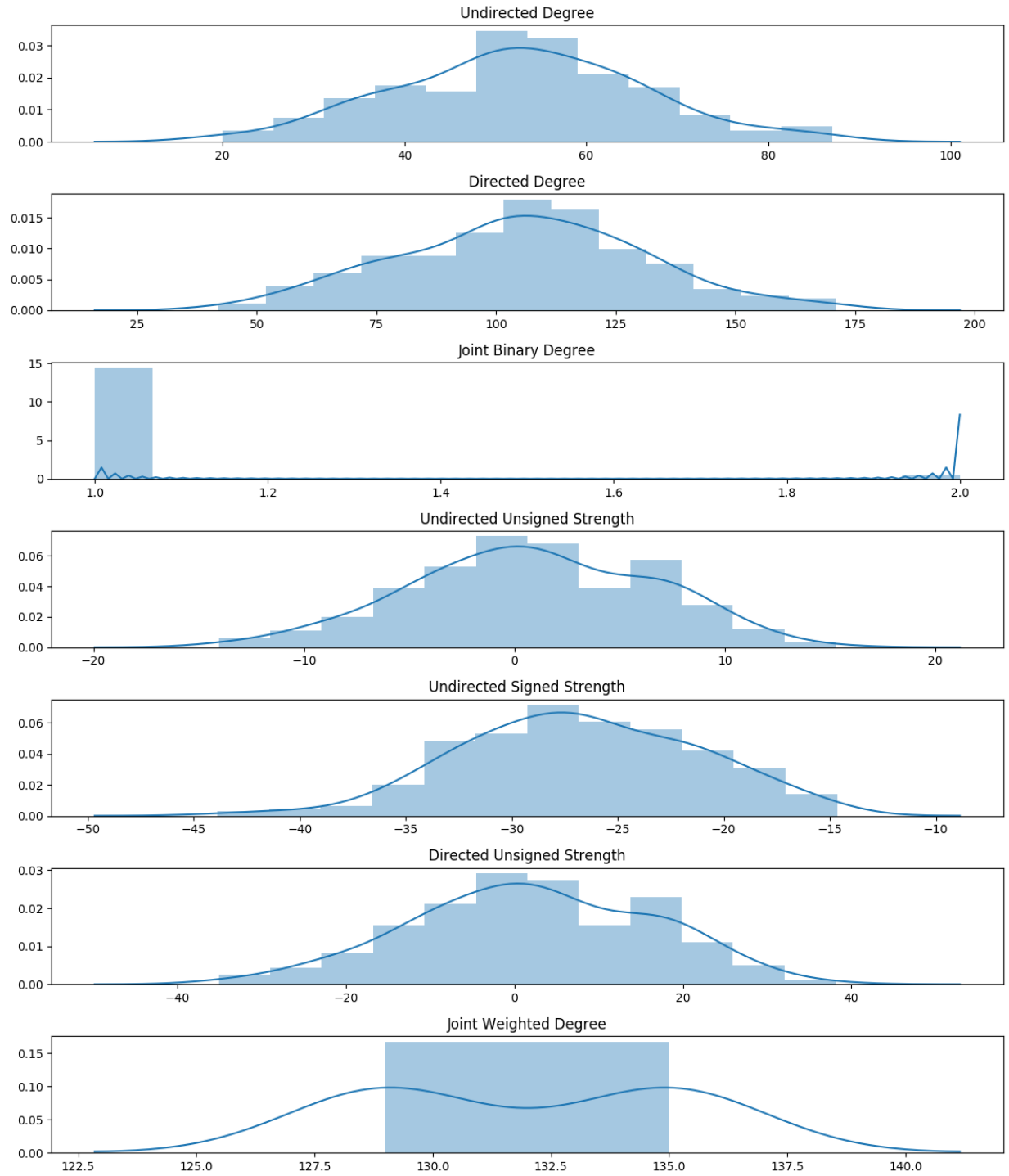
### Compute stuff

```
degr_und = degree.degrees_und(adj_bin)
_, _, degr_dir = degree.degrees_dir(adj_bin_dir)
jdeg_bin, _, _, _ = degree.jdegree(adj_bin_dir)
stre_und = degree.strengths_und(adj_wei)
_, stre_und_neg, _, _ = degree.strengths_und_sign(adj_wei)
stre_dir = degree.strengths_dir(adj_wei_dir)
jdeg_wei, _, _, _ = degree.jdegree(adj_wei_dir)
jdeg_bin = jdeg_bin[jdeg_bin > 0]
jdeg_wei = jdeg_wei[jdeg_wei > 0]
```

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```
vals = [degr_und, degr_dir, jdeg_bin, stre_und, stre_und_neg, stre_dir,
        jdeg_weil]
names = ['Undirected Degree',
         'Directed Degree',
         'Joint Binary Degree',
         'Undirected Unsigned Strength',
         'Undirected Signed Strength',
         'Directed Unsigned Strength',
         'Joint Weighted Degree']
fig, axes = plt.subplots(nrows=len(names), figsize=(12, 2*len(names)))
for i in range(len(names)):
    sns.distplot(vals[i], ax=axes[i])
    axes[i].set_title(names[i])
fig.tight_layout()
fig.show()
```



Total running time of the script: ( 0 minutes 0.602 seconds)

## 1.5 History of changes

### 1.5.1 brainconn 0.0.2 (current)

- Change structure from single algorithms submodule to separated submodules: centrality, clustering, core, degree, distance, generative, modularity, motifs, physical\_connectivity, reference, and similarity.

### 1.5.2 brainconn 0.0.1

- Rename fork of BCT to brainconn for further independent development

### 1.5.3 BCT 0.4.1

- Refactor code into multiple files
- Fix bug in efficiency\_bin
- Fix bugs in modularity\_louvain\_und
- Fix bugs in participation\_coef\_b\*
- Add some test cases

### 1.5.4 BCT 0.4.0

- Add various new functions from Jan 2015 release of BCT
- Fix various bugs documented in github issues

### 1.5.5 BCT 0.3.3

- Fix small bug in latmio\_und\_connected causing failure for sparse matrices
- Add non-networkx dependent algorithm to get\_components (but less efficient)
- Add an implementation of consensus clustering and fix bug in agreement
- Fix bug causing clustering\_coef\_bu to always return 0
- Remembered to update changelog
- Fix some bugs in modularity\_louvain\_dir and related
- Fix bug in NBS and add optional paired-sample test statistic (sviter)

### 1.5.6 BCT 0.3.2

- Change several functions including threshold\_proportional and binarize have copy=True as default argument
- Fix bug in threshold\_proportional where copying behavior did not work symmetric matrices.
- Fix minor quirk in threshold\_proportional where np.round rounds to nearest even number (optimizes floating point) which is discrepant with BCT
- Add a test suite with some functions

- Fix typo in `rich_club_bu`
- Refactor `x[range(n), range(n)]` to `np.fill_diagonal`
- Fix off-by-one bug in `modularity_[prob/fine]tune_und_sign`

### **1.5.7 BCT 0.3.1**

- Fix bug in NBS
- Fix series of bugs in `null_models`

### **1.5.8 BCT 0.3**

- Added NBS
- Added in all of the new functions from the Dec 2013 release of BCT
- Fixed numerous bugs having to do with indexing errors in modularity
- Fixed several odd bugs with `clustering_coef`, `efficiency`, `distance`
- For the next release, I clearly need a real test suite.



## CHAPTER 2

---

### Indices and tables

---

- `genindex`
- `modindex`
- `search`



---

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