13_Networks_2_EEG

July 10, 2025

1 Functional Networks

Structural networks are typically given in the form of a $N \times N$ connectivity matrix. We can also construct networks from functional data. For this purpose, any bivariate measure can be used. Here is an example with a bivariate measure obtained from sEEG data.

[2]:
```
from numpy import pi, linspace, sin, diff, arange, asarray, zeros, exp, array,␣
  ↪linspace, median, gradient, around
from numpy import zeros_like, triu_indices, triu_indices_from, tril_indices,␣
  ↪var, mean, std, sqrt, where, isnan, nan_to_num, delete, floor
from numpy import nan, flip, argwhere, ones, diag, correlate, corrcoef,␣
  ↪transpose, cov, flip, ceil, cos, sin, arctan
from numpy import angle, exp, amax, amin, absolute, meshgrid, fill_diagonal,␣
  ↪concatenate, c_, real, argsort, tile
from numpy import empty_like, log, logical_and, copy, greater, invert, nonzero,␣
  ↪count_nonzero, divide, repeat
from numpy import count_nonzero, triu_indices

from matplotlib.pyplot import xlabel, ylabel, hist, bar, yticks, legend, axis,␣
  ↪figure, xticks, gca, show

from scipy.signal import butter, sosfilt

from matplotlib.pyplot import subplots, figure

from pandas import read_csv

import networkx as nx
```

[3]:
```
def eeg_plot(data, offset, normalise=True):
    """
    Plot date columns in EEG style
    data:       two-dimensional array
    offset:     scaling factor
    normalise: normalisation of amplitudes to variance 1
    """
    from matplotlib.pyplot import subplots
    start = 0
    samples = data.shape[0]
    electrodes = data.shape[1]

    dataset = data[start:start+samples, :electrodes]
    means   = data[start:start+samples, :electrodes].mean(axis=0)
    devs    = data[start:start+samples, :electrodes].std(axis=0)

    fig, ax = subplots(figsize=(11, 10))

    if not normalise:
        ax.plot((dataset - means)      + offset*arange(electrodes-1,-1,-1),␣
  ↪linewidth=1);
    else:
        ax.plot((dataset - means)/devs + offset*arange(electrodes-1,-1,-1),␣
  ↪linewidth=1);

    ax.plot(zeros((samples, electrodes)) +␣
  ↪offset*arange(electrodes-1,-1,-1),'--',color='gray');
    ax.set(ylabel='Voltage')

    yticks([]);

    axis('tight');

    return fig, ax
```

[ ]:

```
```

1.1 Read EEG Data

[8]:

```
# read prefiltered 60 sec segment

folder      = '../Data/'
patient     = '1'          # '1'
seizure     = '02'         # '01' or '02' or '03'
series_type = 'Onset'      # 'Background' or 'Onset'

sr_chars = folder + 'sampling_rate.txt'

df1 = read_csv(sr_chars, header=None)

sr = df1.iloc[0, 0]

series_chars = folder + 'Pat' + patient + '_Sz' + seizure + '_' + series_type +␣
  ↪'_1_100Hz.csv'
```

```
df2 = read_csv(series_chars)
df2.head()

data_np = df2.to_numpy()
data_prefiltered = data_np[:, 1:]

all_labels = df2.columns[1:]

print('')
print(series_chars)
print('')
```

```
../Data/Pat1_Sz02_Onset_1_100Hz.csv
```

[10]:
```
letter_list = list()

for new in all_labels:

    if new[0] not in letter_list:

        letter_list.append(new[0])


label_dict = dict()

for ind, letter in enumerate(all_labels):

    if letter[0] in label_dict.keys():
            pass

    else:
        label_dict[letter[0]] = [ind]

        dict_ind = len(label_dict.keys())

        if letter[0] != all_labels[0][0]:
            previous_letter = letter_list[dict_ind - 2]
            label_dict[previous_letter].append(ind)

    if ind == len(all_labels)-1:
        label_dict[letter[0]].append(ind+1)

label_letters = list(label_dict.keys())
```

```
label_dict
```

[10]:
```
{'A': [0, 11],
 'B': [11, 22],
 'C': [22, 31],
 'E': [31, 40],
 'F': [40, 49],
 'Z': [49, 56],
 'O': [56, 67],
 'T': [67, 74],
 'U': [74, 81],
 'V': [81, 92],
 'W': [92, 107],
 'X': [107, 122]}
```

[12]:
```
data_prefiltered.shape
```

[12]:
```
(60000, 122)
```

[181]:
```
time_max = 60

init_cut  = 25

band_low  = 1
band_high = 20

order = 5

rows_max = int(time_max * sr)

sample_start = 0

sample_end = sample_start + rows_max

channel_start, channel_stop = 0, data_prefiltered.shape[1]

number_channels = channel_stop - channel_start


data_unfiltered = data_prefiltered[:, channel_start:channel_stop]


sos = butter(order, (band_low, band_high), btype='bandpass', fs=sr,␣
 ↪output='sos')

data_filtered = zeros((rows_max, number_channels))
```

```
for index, column in enumerate(data_unfiltered.transpose()):
    forward = sosfilt(sos, column)
    backwards = sosfilt(sos, forward[-1::-1])
    data_filtered[:, index] = backwards[-1::-1]

data_filtered.shape
```

```
[181]: (60000, 122)
```

1.2 Pick electrode

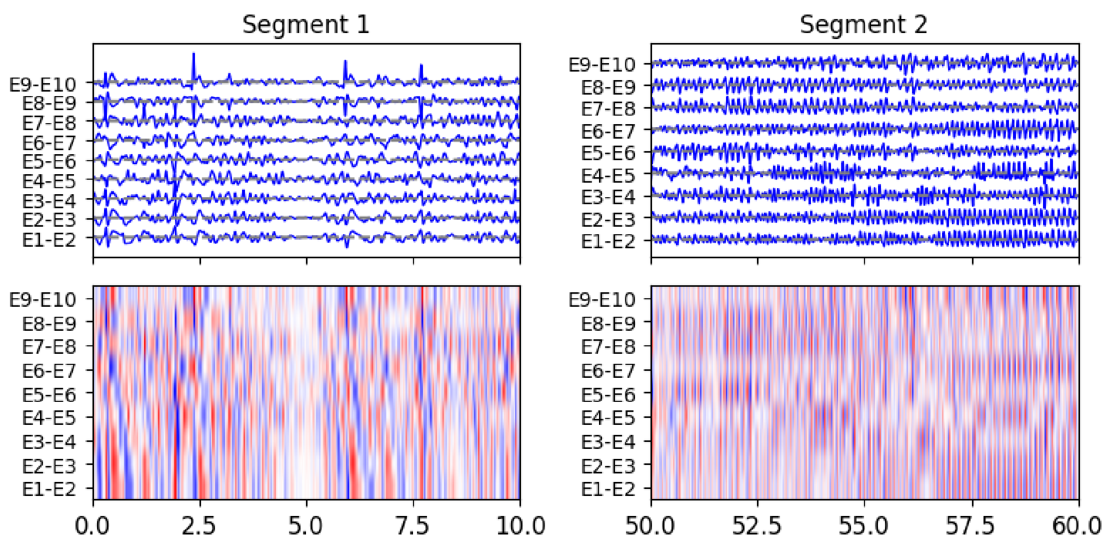
```
[184]: elec_name = 'E'

all_labels_np = asarray(all_labels)

elec_label_names = all_labels_np[label_dict[elec_name][0]:
 ↪label_dict[elec_name][1]]

data_chan      = data_filtered[:, label_dict[elec_name][0]:
 ↪label_dict[elec_name][1]]

chans = data_chan.shape[1]
```

```
[186]: seg_1_start = 0
rows_seg    = 10000
seg_1_stop  = seg_1_start + rows_seg

seg_2_start = 50000
seg_2_stop  = seg_2_start + rows_seg

data_chan_seg_1      = data_chan[seg_1_start:seg_1_stop, :]
data_chan_seg_2      = data_chan[seg_2_start:seg_2_stop, :]

means_1              = data_chan_seg_1.mean(axis=0)
devs_1               = data_chan_seg_1.std(axis=0)
data_chan_seg_1_norm = (data_chan_seg_1 - means_1)/devs_1

means_2              = data_chan_seg_2.mean(axis=0)
devs_2               = data_chan_seg_2.std(axis=0)
data_chan_seg_2_norm = (data_chan_seg_2 - means_2)/devs_2
```

```
[188]: offset = 6

#################################### Time Series
fig, ax = subplots(nrows=2, ncols=2, figsize=(8,4))

### Voltage Series
```

```
ax[0, 0].plot(data_chan_seg_1_norm + offset*arange(chans-1,-1,-1), linewidth=1,␣
  ↪color='b');
ax[0, 0].plot(zeros((rows_seg, chans)) +␣
  ↪offset*arange(chans-1,-1,-1),'--',color='gray');
ax[0, 0].set_yticks(offset*arange(chans))
ax[0, 0].set_yticklabels(elec_label_names)
ax[0, 0].margins(x=0)
ax[0, 0].set_xticks(linspace(0, rows_seg, 5))
labl =        linspace((sample_start+seg_1_start)//sr,␣
  ↪(sample_start+seg_1_stop)//sr, 5)
ax[0, 0].set_xticklabels([], fontsize=12)
ax[0, 0].set_title('Segment 1', fontsize=12)


### Voltage Heatmap
ax[1, 0].imshow(data_chan_seg_1_norm.T, aspect='auto', cmap='bwr', vmin=-3,␣
  ↪vmax=3);
ax[1, 0].set_yticks(arange(chans))
ax[1, 0].set_yticklabels(flip(elec_label_names));

ax[1, 0].set_xticks(linspace(0, rows_seg, 5))
labl =        linspace((sample_start+seg_1_start)//sr,␣
  ↪(sample_start+seg_1_stop)//sr, 5)
ax[1, 0].set_xticklabels(labl, fontsize=12)


### Voltage Series
ax[0, 1].plot(data_chan_seg_2_norm + offset*arange(chans-1,-1,-1), linewidth=1,␣
  ↪color='b');
ax[0, 1].plot(zeros((rows_seg, chans)) +␣
  ↪offset*arange(chans-1,-1,-1),'--',color='gray');
ax[0, 1].set_yticks(offset*arange(chans))
ax[0, 1].set_yticklabels(elec_label_names)
ax[0, 1].margins(x=0)
ax[0, 1].set_xticks(linspace(0, rows_seg, 5))
labl =        linspace((sample_start+seg_2_start)//sr,␣
  ↪(sample_start+seg_2_stop)//sr, 5)
ax[0, 1].set_xticklabels([], fontsize=12)
ax[0, 1].set_title('Segment 2', fontsize=12)


### Voltage Heatmap
ax[1, 1].imshow(data_chan_seg_2_norm.T, aspect='auto', cmap='bwr', vmin=-3,␣
  ↪vmax=3);
ax[1, 1].set_yticks(arange(chans))
ax[1, 1].set_yticklabels(flip(elec_label_names));
```

```
ax[1, 1].set_xticks(linspace(0, rows_seg, 5))
labl =        linspace((sample_start+seg_2_start)//sr,␣
 ↪(sample_start+seg_2_stop)//sr, 5)
ax[1, 1].set_xticklabels(labl, fontsize=12)


fig.tight_layout()

show()
```



1.3 Similarity Matrix

As one example, we can obtain a network matrix by calculating the correlations between each pair of subjects. The resulting matrix has dimensions 11 by 11. We can also use the Phase Lock Value matrix.

[191]:
```
# # Correlation
# data_chan_seg_1_corr = corrcoef(data_chan_seg_1, rowvar=False)

# fill_diagonal(data_chan_seg_1_corr, 0)

# data_chan_seg_1_corr_abs      = abs(data_chan_seg_1_corr)


# data_chan_seg_2_corr = corrcoef(data_chan_seg_2, rowvar=False)

# fill_diagonal(data_chan_seg_2_corr, 0)
# data_chan_seg_2_corr_abs      = abs(data_chan_seg_2_corr)
```

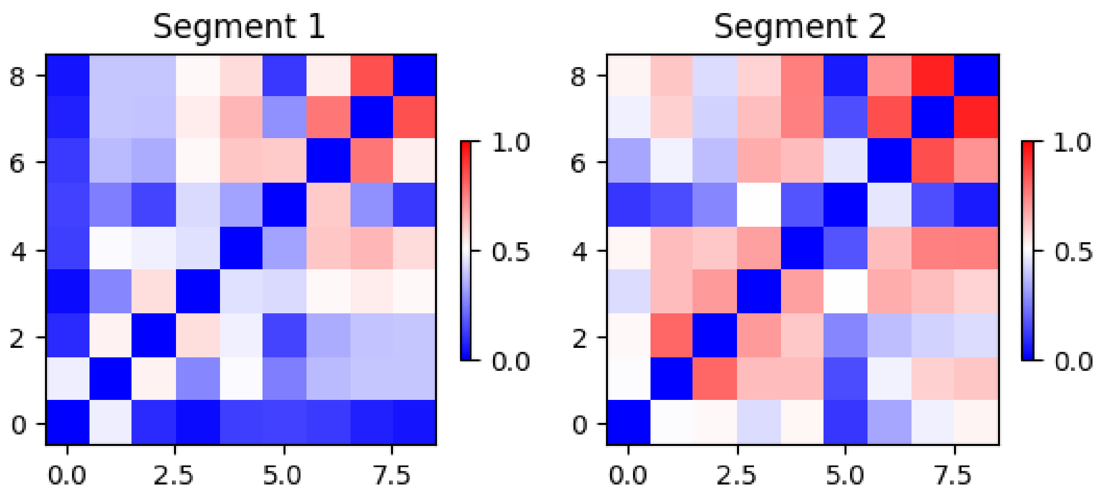
[193]:
```
def phase_lock(data):

    from scipy.signal import hilbert
    from numpy import unwrap, angle


    rows, chans   = data.shape
    signal_phases = zeros((rows, chans))

    for index, column in enumerate(data.transpose()):

        instantaneous_phase = angle(hilbert(column))
        inst_phase_unwrap = unwrap(instantaneous_phase)
        signal_phases[:, index] = inst_phase_unwrap

    phase_lock = zeros((chans, chans))

    for index1, column in enumerate(signal_phases.transpose()):
        for index2 in arange(index1+1, chans):

            phase_diff = column - signal_phases[:, index2]
            phase_lock[index1, index2] = abs(sum(exp(-1j*phase_diff)))/
 ↪phase_diff.size

    phase_lock = phase_lock + phase_lock.T

    return phase_lock
```

[195]:
```
# Phase Lock Matrix
data_chan_seg_1_phas = phase_lock(data_chan_seg_1)

fill_diagonal(data_chan_seg_1_phas, 0)

data_chan_seg_2_phas = phase_lock(data_chan_seg_2)

fill_diagonal(data_chan_seg_2_phas, 0)

data_chan_seg_2_phas.shape
```

[195]:
```
(9, 9)
```

[197]:
```
fig, ax = subplots(ncols=2, figsize=(6,6))

# Voltage matrices
im = ax[0].imshow(data_chan_seg_1_phas, cmap='bwr', origin='lower', vmax=1);
```

```
fig.colorbar(im, ax=ax[0], ticks=(0, 0.5, 1), shrink = 0.2);
ax[0].set_title('Segment 1')

# Voltage matrices
im = ax[1].imshow(data_chan_seg_2_phas, cmap='bwr', origin='lower', vmax=1);
fig.colorbar(im, ax=ax[1], ticks=(0, 0.5, 1), shrink = 0.2);
ax[1].set_title('Segment 2')

fig.tight_layout()

show()
```

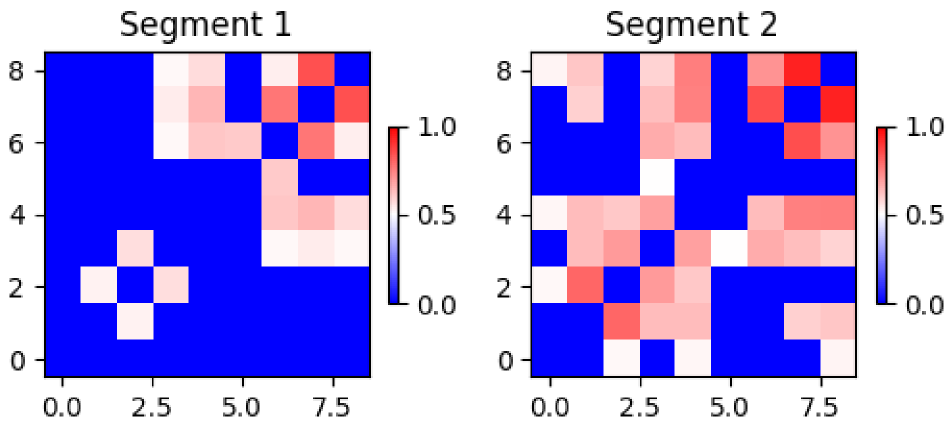


1.4 Thresholded Similarity Matrix

To find a pattern in the correlations we can threshold the interactions and thus obtain either a binary network matrix (entries are either 0 or 1), or a quantitative edge strength for values above the threshold.

[200]:
```
threshold = 0.5

data_chan_seg_1_phas[data_chan_seg_1_phas <= threshold] = 0
data_chan_seg_2_phas[data_chan_seg_2_phas <= threshold] = 0

fig, ax = subplots(ncols=2, figsize = (6, 6))

im1 = ax[0].imshow(data_chan_seg_1_phas, cmap='bwr', origin='lower', vmin=0,␣
  ↪vmax=1);
ax[0].set_title('Segment 1')

fig.colorbar(im1, ax=ax[0], orientation='vertical', shrink=0.2);
```

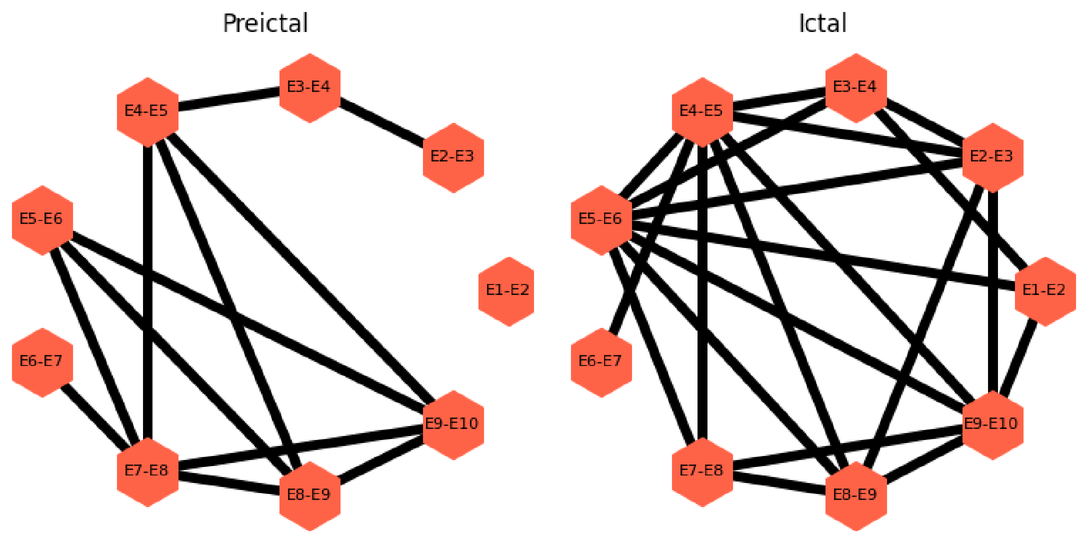
```
im2 = ax[1].imshow(data_chan_seg_2_phas, cmap='bwr', origin='lower', vmin=0,␣
  ↪vmax=1);
ax[1].set_title('Segment 2')

fig.colorbar(im2, ax=ax[1], orientation='vertical', shrink=0.2);

show()
```



1.5 Construct Network from Matrix

We construct the network obtained from the above thresholded matrix, i.e. ignoring subthreshold correlations.

[203]:
```
graph_1 = nx.Graph(data_chan_seg_1_phas)
graph_2 = nx.Graph(data_chan_seg_2_phas)

if elec_name == 'B':

    node_dict = {
        0: 'B1-B2',
        1: 'B2-B3',
        2: 'B3-B4',
        3: 'B4-B5',
        4: 'B5-B6',
        5: 'B6-B7',
        6: 'B7-B8',
        7: 'B8-B9',
        8: 'B9-B10',
        9: 'B10-B11',
        10: 'B11-B12'
    }

elif elec_name == 'E':

    node_dict = {
        0: 'E1-E2',
        1: 'E2-E3',
        2: 'E3-E4',
        3: 'E4-E5',
        4: 'E5-E6',
        5: 'E6-E7',
        6: 'E7-E8',
        7: 'E8-E9',
        8: 'E9-E10'
    }

nx.relabel_nodes(graph_1, node_dict, copy=False)
nx.relabel_nodes(graph_2, node_dict, copy=False)

layout = nx.circular_layout(graph_1)

fig, ax = subplots(ncols=2, figsize=(8,4))

nx.draw(graph_1, layout, ax=ax[0],
        with_labels=True,
        node_color='tomato',
        node_size=1200, width=5,
        node_shape='h', font_size=8)

nx.draw(graph_2, layout, ax=ax[1],
        with_labels=True,
        node_color='tomato',
        node_size=1200, width=5,
        node_shape='h', font_size=8)


ax[0].set_title('Preictal')
ax[1].set_title('Ictal');

fig.tight_layout()

show()
```



```
[205]: phas_mean_1 = mean(data_chan_seg_1_phas, axis=0)
       phas_mean_2 = mean(data_chan_seg_2_phas, axis=0)

       phas_mean_1
```

```
[205]: array([0.        , 0.05835136, 0.12114296, 0.23693205, 0.20252542,
              0.06700431, 0.33697102, 0.31010449, 0.27293087])
```

```
[207]: from numpy import triu_indices

       # Get the indices of the correlation coefficients for 15 data columns
       phas_1_coeff_indices = triu_indices(data_chan_seg_1_phas.shape[0], k=1)

       # Get the correlation coefficients
       phas_1_coeffs = abs(data_chan_seg_1_phas[phas_1_coeff_indices])
       phas_2_coeffs = abs(data_chan_seg_2_phas[phas_1_coeff_indices])

       phas_1_coeffs.size
```

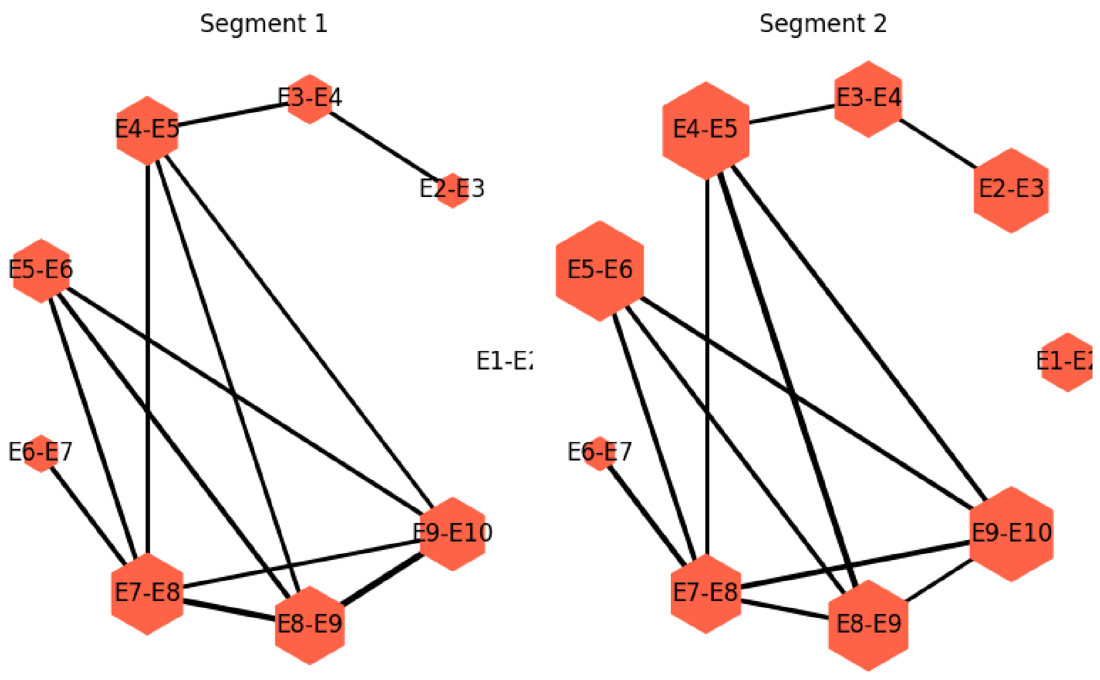
```
[207]: 36
```

1.6 Advanced Display

The size of the nodes can be scaled with their mean correlation.

The size of the edges can be scaled with the correlation coefficient.

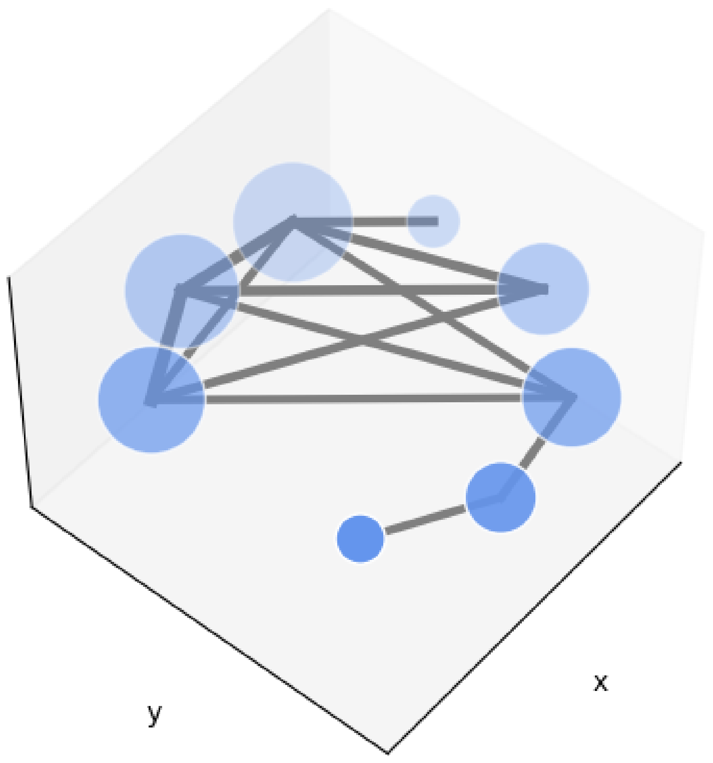
```
[210]: fig, ax = subplots(ncols=2, figsize=(8,5))

       nx.draw(graph_1, layout, ax=ax[0],
               with_labels=True,
               node_color='tomato',
               node_size=5000*phas_mean_1, width=4*phas_1_coeffs[phas_1_coeffs > 0],
               node_shape='h')

       nx.draw(graph_1, layout, ax=ax[1],
               with_labels=True,
               node_color='tomato',
               node_size=5000*phas_mean_2, width=4*phas_2_coeffs[phas_2_coeffs > 0],
               node_shape='h')

       ax[0].set_title('Segment 1')
       ax[1].set_title('Segment 2');

       fig.tight_layout()

       show()
```



Here is a 3D view of the seizure network:

[213]:
```
from mpl_toolkits.mplot3d import Axes3D

# 3D layout
pos = nx.circular_layout(graph_1, dim=3)
```

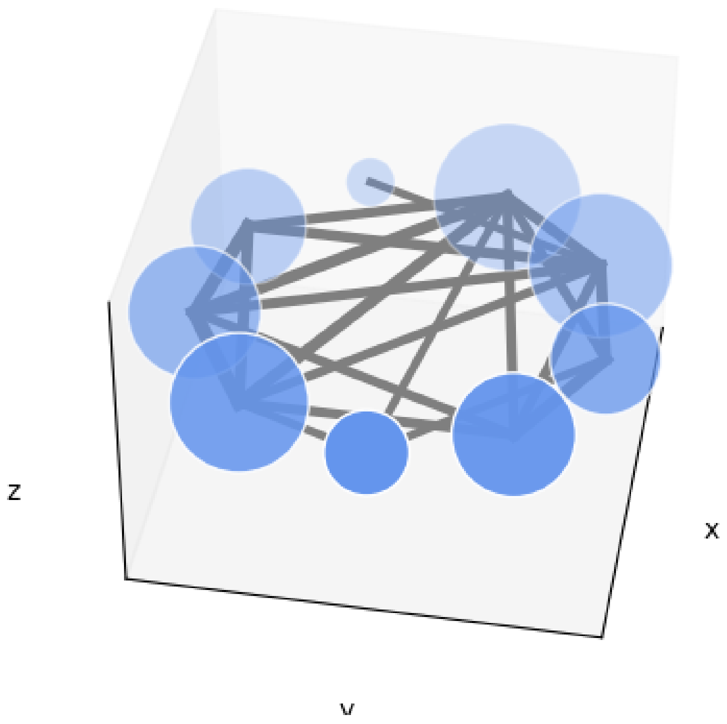
```
# Extract node and edge positions from the layout
node_xyz = array([pos[v] for v in sorted(graph_1)])
edge_xyz = array([(pos[u], pos[v]) for u, v in graph_1.edges()])

# Create the 3D figure
fig = figure(figsize=(6, 5))
ax  = fig.add_subplot(111, projection="3d")

# Plot the nodes - alpha is scaled by "depth" automatically
ax.scatter(*node_xyz.T, s=6000*phas_mean_1, c='cornflowerblue', ec="w")

# Plot the edges
for index, vizedge in enumerate(edge_xyz):
    ax.plot(*vizedge.T, color="tab:gray",␣
 ↪linewidth=(6*phas_1_coeffs[phas_1_coeffs > 0])[index])



def _format_axes(ax):
    """Visualization options for the 3D axes."""
    # Gridlines on/off
    ax.grid(False)

    # Suppress tick labels
    for dim in (ax.xaxis, ax.yaxis, ax.zaxis):
        dim.set_ticks([])

    # Set axes labels
    ax.set_xlabel("x")
    ax.set_ylabel("y")
    ax.set_zlabel("z")


_format_axes(ax)

ax.view_init(50, 40);

show()
```



```
[ ]:
```

```
[216]: from mpl_toolkits.mplot3d import Axes3D

# 3D layout
pos = nx.circular_layout(graph_2, dim=3)

# Extract node and edge positions from the layout
node_xyz = array([pos[v] for v in sorted(graph_2)])
edge_xyz = array([(pos[u], pos[v]) for u, v in graph_2.edges()])

# Create the 3D figure
fig = figure(figsize=(6, 5))
ax  = fig.add_subplot(111, projection="3d")

# Plot the nodes - alpha is scaled by "depth" automatically
ax.scatter(*node_xyz.T, s=6000*phas_mean_2, c='cornflowerblue', ec="w")

# Plot the edges
for index, vizedge in enumerate(edge_xyz):
    ax.plot(*vizedge.T, color="tab:gray",␣
 ↪linewidth=(6*phas_2_coeffs[phas_2_coeffs > 0])[index])
```

```python
def _format_axes(ax):
    """Visualization options for the 3D axes."""
    # Gridlines on/off
    ax.grid(False)

    # Suppress tick labels
    for dim in (ax.xaxis, ax.yaxis, ax.zaxis):
        dim.set_ticks([])

    # Set axes labels
    ax.set_xlabel("x")
    ax.set_ylabel("y")
    ax.set_zlabel("z")


_format_axes(ax)

ax.view_init(40, 10);

show()
```



```
[ ]:
```

2 Try it yourself

Now try segments of different lengths of the data to compare the changes in matrix properties. You can check the graph, the degrees and the clustering coefficients.