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Neuron Network

```
1  import networkx as nx
```

```
1  Error: ModuleNotFoundError: No module named 'networkx'
```

```
1  from pandas import read_csv
2
3  from matplotlib.pyplot import subplots, show
```

The C elegans Neuron Network

Data Import   Introduction to C elegans neurons

C elegans neurons in the worm atlas

Import the connectivity matrix.

```
1  data = read_csv('data/celegans131matrix_50.csv', header=None, dtype = "
      int")
2
3  neurons = data.to_numpy()
4
5  print(len(neurons))
```

```
1  50
```

```
1  fig, ax = subplots()
2
3  ax.imshow(neurons);
4
5  show()
```

Import the labels and convert the resulting dataframe into a dictionary. The function `to_dict` wraps the dictionary within a dictionary and therefore indexing is used to access the 'inner' dict.

```
1  neuron_Names = read_csv('data/celegans131labels_50.csv', header=None)
2
3  neuronNames = neuron_Names.to_dict()
4
5  neuronLabels = neuronNames[0]
6
7  print(neuronLabels)
```

```
1  {0: 'ADFL', 1: 'ADFR', 2: 'ADLL', 3: 'ADLR', 4: 'AFDL', 5: 'AFDR', 6: '
   AIAL', 7: 'AIAR', 8: 'AIBR', 9: 'AINL', 10: 'AINR', 11: 'AIZL', 12:
   'AIZR', 13: 'ALA', 14: 'ASEL', 15: 'ASER', 16: 'ASGL', 17: 'ASGR',
   18: 'ASHL', 19: 'ASHR', 20: 'ASIL', 21: 'ASIR', 22: 'ASJL', 23: '
   ASJR', 24: 'ASKL', 25: 'ASKR', 26: 'AUAL', 27: 'AUAR', 28: 'AVAL',
   29: 'AVAR', 30: 'AVBL', 31: 'AVBR', 32: 'AVDL', 33: 'AVDR', 34: '
   AVEL', 35: 'AVER', 36: 'AVHL', 37: 'AVHR', 38: 'AVJL', 39: 'AVJR',
   40: 'AVL', 41: 'AWAL', 42: 'AWAR', 43: 'AWBL', 44: 'AWBR', 45: 'AWCL
   ', 46: 'AWCR', 47: 'BAGL', 48: 'BAGR', 49: 'CEPDL'}
```

Graph Object and Network Display

The connectivity matrix can be converted to a Networkx graph.

```
1  neuronGraph  = nx.from_numpy_matrix(neurons,
2                                   create_using=nx.DiGraph)
```

```
1  Error: NameError: name 'nx' is not defined
```

```
1  neuronLayout = nx.random_layout(neuronGraph, seed=12)
```

```
1  Error: NameError: name 'nx' is not defined
```

```
1  nx.draw_networkx(neuronGraph, neuronLayout,
2        node_size=1000,
3        labels=neuronLabels)
```

```
1  Error: NameError: name 'nx' is not defined
```

View the degrees:

```
1  fig, ax = subplots()
2
3  ax.plot(dict(neuronGraph.degree).values(), '-o');
```

```
1  Error: NameError: name 'neuronGraph' is not defined
```

```
1  ax.set_xlabel('Index');
```

```
2  ax.set_ylabel('Degree');
3
4  show()
```

The network displayed in circular layout:

```
1  neuronGraph  = nx.from_numpy_matrix(neurons,
2                                      create_using=nx.DiGraph)
```

```
1  Error: NameError: name 'nx' is not defined
```

```
1  neuronLayout = nx.circular_layout(neuronGraph)
```

```
1  Error: NameError: name 'nx' is not defined
```

```
1  nx.draw_networkx(neuronGraph, neuronLayout,
2        node_size=1000,
3        labels=neuronLabels)
```

```
1  Error: NameError: name 'nx' is not defined
```

```
1  show()
```

Find node indices: The two BAG nodes 'BAGR' and 'BAGL' of the display (about 4 o'clock).

```
1  for index, name in enumerate(neuronLabels.values()):
2
3      if 'BAG' in name:
4
5          print(neuronLabels[index], index)
```

```
1  BAGL 47
2  BAGR 48
```

Anatomical Mapping

File 'celegans131positions_50.csv' contains information on how the nodes relate to each other in 2-D space. We can include this information to replace the layout.

```
1  neuronPos = read_csv('data/celegans131positions_50.csv', header=None)
2
3  neuronPos.items
```

```
1  <bound method DataFrame.items of          0        1
2  0   0.082393 -0.000984
3  1   0.083279 -0.003184
```

```
 4   2   0.082639 -0.013035
 5   3   0.083279 -0.011512
 6   4   0.086329 -0.002706
 7   5   0.086463 -0.000980
 8   6   0.065177  0.009346
 9   7   0.059030  0.011512
10   8   0.075441  0.006123
11   9   0.061980 -0.006149
12  10   0.061969 -0.003429
13  11   0.048698  0.002706
14  12   0.057560  0.003184
15  13   0.094056 -0.013227
16  14   0.069112  0.000492
17  15   0.071767 -0.000735
18  16   0.077966 -0.007625
19  17   0.080095 -0.010287
20  18   0.075507  0.000492
21  19   0.078380 -0.000980
22  20   0.076982 -0.012789
23  21   0.077156 -0.011757
24  22   0.063455  0.006641
25  23   0.062704  0.009063
26  24   0.088542 -0.010084
27  25   0.088668 -0.009553
28  26   0.068620  0.006149
29  27   0.067113  0.005389
30  28   0.089526  0.001722
31  29   0.090872 -0.000245
32  30   0.069112 -0.004427
33  31   0.071767 -0.006368
34  32   0.061734 -0.001476
35  33   0.066378 -0.001470
36  34   0.082885  0.002214
37  35   0.084014  0.003184
38  36   0.072063 -0.008608
39  37   0.076421 -0.012737
40  38   0.067636 -0.009346
41  39   0.072992 -0.009798
42  40   0.060990  0.009063
43  41   0.077966 -0.002951
44  42   0.078380 -0.005389
45  43   0.079196 -0.003935
46  44   0.082789 -0.006858
47  45   0.078458  0.004919
48  46   0.078625  0.004164
49  47   0.112890  0.000492
50  48   0.114630  0.003184
51  49   0.094199 -0.016233>
```

```python
1  nx.draw_networkx(neuronGraph, neuronPos.values,
2          node_size=1000,
```

```
3        labels=neuronLabels)
```

```
1  Error: NameError: name 'nx' is not defined
```

```
1  show()
```

```
1  new_pos = neuronPos.copy()
2  new_pos.values[:, 0] = -1*neuronPos.values[:, 0]
3
4  nx.draw_networkx(neuronGraph, new_pos.values,
5        node_size=1000,
6        labels=neuronLabels)
```

```
1  Error: NameError: name 'nx' is not defined
```

```
1  show()
```

The two BAG nodes to the right of the display are the sensory neurons used to monitor oxygen and carbon dioxide.

Here is some background: BAG genes, functions and connections

The graph display is in Matplotlib and can be handled as such. E.g. for possible Node shapes see: https://matplotlib.org/stable/api/markers_api.html#module-matplotlib.markers.

If you have a multi-panel figure, specify the axes for the network with keyword argument ax:

```
1  fig, ax = subplots(figsize=(14, 8), ncols=2)
2
3  nx.draw_networkx(neuronGraph, neuronLayout,
4        node_size=1000,
5        labels=neuronLabels,
6        ax=ax[0])
```

```
1  Error: NameError: name 'nx' is not defined
```

```
1  nx.draw_networkx(neuronGraph, neuronPos.values,
2        node_shape='H',
3        node_color='tomato',
4        node_size=1300,
5        labels=neuronLabels,
6        ax=ax[1])
```

```
1  Error: NameError: name 'nx' is not defined
```

```
1  ax[0].set_title('Circular view of C elegans network');
2  ax[1].set_title('Anatomical view of C elegans network');
3
4  show()
```

Keypoints

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