

**NITP Summer 2012**  
**Network Analysis Lab**  
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**NOTE: This lab requires Matlab and the functions in the Brain Connectivity Toolbox (BCT). If you don't have it yet, download it here: <https://sites.google.com/a/brain-connectivity-toolbox.net/bct/>**

In the lectures, we covered different methods for obtaining a connectional graph using diffusion weighted MRI and fMRI. Here we're going to start with the connectivity matrices and explore different properties of them using the BCT. **Make sure to check the reference functions at the end of this doc for help with the exercises!**

**Background:**

The data for these connectivity matrices were downloaded from the NKI/Rockland publicly available sample on INDI ([fcon\\_1000.projects.nitrc.org/indi/pro/nki.html](http://fcon_1000.projects.nitrc.org/indi/pro/nki.html)). The data were DTI and resting state fMRI for 196 subjects. After standard data preprocessing, regions of interest were defined from the fMRI data using a spatially constrained clustering method. For each ROI, the mean timeseries was calculated and correlated with all other regions to get the 188x188 fMRI connectivity matrix. These were then averaged across subjects to obtain the matrix used in this lab. These same ROIs were registered to the DTI data and used to count the number of fibers connecting any pair of ROIs to get the 188x188 DTI connectivity matrix. Again, these were averaged across subjects.

**Files:**

dti\_matrix.txt, fmri\_matrix.txt: the connectivity matrices (tab delimited text files)  
regions\_188.txt: list of the brain region names for each region in the network  
regions/mask\*.nii.gz: the nifti mask files for each region in the network  
regions/MNI152\_T1\_4mm\_brain.nii.gz: the standard space brain (use with the region mask files)

Open Matlab. First, load in the matrices and view them. Get a sense of the range and distribution of connectivity strengths in the two matrices.

```
>> cd ~/Desktop/NITP_network_lab_2012/  
>> load('dti_matrix.txt')  
>> load('fmri_matrix.txt')  
>> figure; imagesc(dti_matrix)  
>> figure; imagesc(fmri_matrix)
```

Binarize the matrices, thresholding to keep the strongest 20% of connections:

```
>> dti_matrix_bin=adjmatrix(dti_matrix,.2,false);  
>> fmri_matrix_bin=adjmatrix(fmri_matrix,.2,false);
```

How many components are in each graph after thresholding?  
Which nodes, if any, are disconnected?  
At what threshold do the networks fragments into multiple components?

Calculate the modules in the DTI graph using the Louvain algorithm:

```
>> [Comm_index_dti Q]=modularity_louvain_und(dti_matrix_bin)
>> [x i]=sort(Comm_index_dti');
>> dti_matrix_bin_sort=dti_matrix_bin(i,i);
What brain regions comprise the different modules?
```

Do the same for the fMRI graph. What brain regions comprise the different modules?  
Do these correspond to any known functional networks? How do the fMRI modules compare to the DTI modules? Which network has a higher Q value (more distinct modules)? Why might this be?

*Note: you can threshold the network at a higher level (e.g. only 5% of connections) to see how that might change the module membership.*

### Regional measures

Look at different measures of regional connectivity. Calculate the degree, clustering coefficient, betweenness centrality, and participation coefficient:

```
>> d=degrees_und(dti_matrix_bin);
>> cc=clustering_coef_bu(dti_matrix_bin);
>> bc=betweenness_bin(dti_matrix_bin);
>> P = participation_coef(dti_matrix_bin,Comm_index_dti);
```

Call the function *region\_sorted\_ranks* to create a 188x4 matrix called *sorted\_ranks* that has each region's rank for degree, clustering, betweenness, and participation.

```
>> sorted_ranks_dti=region_sorted_ranks(d,cc,bc,P)
```

Which regions are the highest for each measure? Take a look at these regions in fslview if you're interested. Look at the relationship between different measures in different brain regions.

*Advanced: which nodes are provincial hubs? Which regions are connector hubs?*

Do the same for the fMRI graph.

```
>> d=degrees_und(fmri_matrix_bin);
>> cc=clustering_coef_bu(fmri_matrix_bin);
>> bc=betweenness_bin(fmri_matrix_bin);
>> P = participation_coef(fmri_matrix_bin,Comm_index_fmri);
>> sorted_ranks_fmri=region_sorted_ranks(d,cc,bc,P)
```

How similar are the measures between DTI and fMRI?

### Global measures

Check out some of the global network measures. First, calculate the *distance matrix* for the graph:

```
>> dti_matrix_bin_distmat=distance_bin(dti_matrix_bin);
```

Calculate the characteristic path length and global efficiency:

```
>> [cpl_dti,eglob_dti]=charpath(dti_matrix_bin_distmat)
```

The mean clustering coefficient is just the mean of the regional clustering coefficients:

```
>> mcc_dti=mean(clustering_coef_bu(dti_matrix_bin))
```

Think about what the actual numerical values for cpl, eglob, and mcc mean.

Calculate a random network with the same number of connections as the true graph and calculate its distance matrix:

```
>> sim_dti_matrix=randmio_und(dti_matrix_bin,10);
```

```
>> sim_dti_distmat=distance_bin(sim_dti_matrix);
```

Determine the characteristic path length and mean clustering coefficient for the random network. How do they compare to the real network? If the values for real and random networks are different, why is that the case?

```
>> [sim_cpl_dti,sim_eglob_dti]=charpath(sim_dti_distmat)
```

```
>> sim_mcc_dti=mean(clustering_coef_bu(sim_dti_matrix))
```

Calculate the small worldness ( $\sigma$ ). The formula is:

$\Gamma = \text{real cc} / \text{random cc}$

$\Lambda = \text{real cpl} / \text{random cpl}$

$\sigma = \Gamma / \Lambda$

A network with  $\sigma > 1.2$  is roughly considered “small world”. Is this network a small world network?

*Note: the value of sigma will differ each time it is calculated because the network is randomly rewired in a different way each time. In practice, it's best to calculate a large number of sigma values (1000 or more) and average them.*

Do the same for the fMRI network. Is it more or less small world than the DTI network?

### Reference functions

To view a set of regions (based on region number) in fslview, go to terminal (or whatever your command line program is) and cd to the *regions* directory:

```
cd regions
```

Then call the bash script *fslview\_regions.sh* with the region numbers separated by spaces:

```
./fslview_regions.sh 4 10 14 5
```

To get the different components and component sizes of a graph:

```
[comps,comp_sizes]=get_components(adjmatrix(dti_matrix, .1, false))
```

**If you're interested in visualization:**

You can visualize these networks on our website,  
<http://umcd.humanconnectomeproject.org>. Select the study name 'NKI\_Rockland', the network name 'NKI\_dti\_avg' or 'NKI\_fc\_avg', set the other parameters, and click 'Analyze'. You can view the network in 3D and 2D and get other network statistics.