Table of Contents

Summary

this script serves as a rudimentary 'methods' section. Note the iputs immediately below for the type of connectivity data and parcellation used. In short, the connectivity data is derived by taking age and gender matched structural data from the NKI rockland dataset via LEAD DBS. For each participant a 'normative' connectome is derived (PRE) and a lesioned normative connectome is estimated by taking into account their lesion map (POST). Basically any streamline that passes through the lesion location is deleted. A key parameter to test across is the number of connectomes to included in each normative connectome.

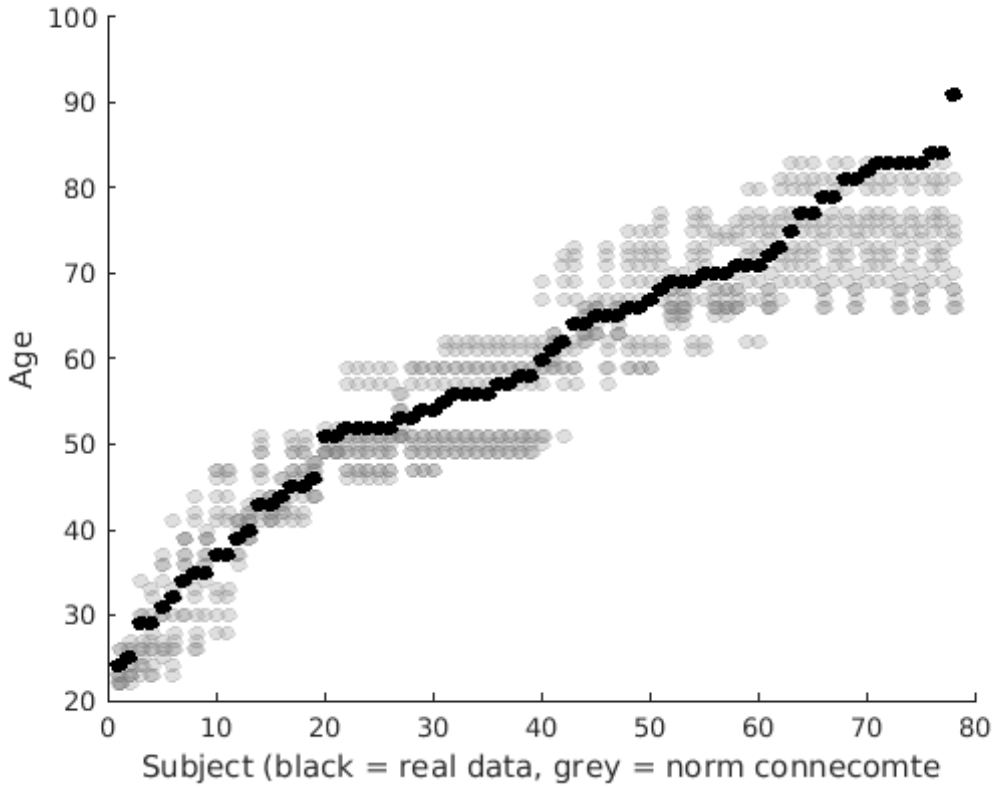
```
clearvars
close all

addpath('functions');
addpath(genpath('/projects/sw49/BCT'));
% inputs
basedir = '/scratch/sw49/1_LEADStrokeMapping/';
dataType = '_conbound10/'; %data type
parcLabel = '140/'; % label for parcellation
load('/projects/sw49/Atlas/140COG.mat');
behav.variables = [3,4,8,10,11,12,70,31]; %may be altered in future

% load connectomes
[Cpre,Cpost,nodata] =
 load_connectomes([basedir,'connectomes',dataType,parcLabel]);

% load behaviour and do exclusions
[data, key, P_ID] = load_stroke_behav;
behav.data = data(:,behav.variables);

exclude = sum(isnan(behav.data),2)>0;
exclude = exclude+nodata>0; %incorporate missing lesion data
behav.data(exclude,:) = [];
P_ID(exclude) = [];
Cpre(:,:,exclude) = [];
Cpost(:,:,exclude) = [];
behav.data(:,7) = behav.data(:,7)*-1; % reverse coded
```

Participant demographics

```
disp([num2str(length(P_ID)),' participants']);
disp([num2str(sum(behav.data(:,1))),' males'])
disp(['Mean age = ',num2str(mean(behav.data(:,2))),...
```

```
    ', std = ',num2str(std(behav.data(:,2))),...
    ', range = ',num2str(min(behav.data(:,2))),...
    ' - ',num2str(max(behav.data(:,2)))]);
disp(['Mean education = ',num2str(mean(behav.data(:,3))),...
    ', std = ',num2str(std(behav.data(:,3))),...
    ', range = ',num2str(min(behav.data(:,3))),...
    ' - ',num2str(max(behav.data(:,3)))]);

% connectome density
Node = size(Cpre,1);
NodeTotal = (Node*(Node-1))/2;
for i = 1:length(P_ID)
    density.pre(i) = sum(sum(Cpre(:,:,i)>0))/NodeTotal;
    density.post(i) = sum(sum(Cpost(:,:,i)>0))/NodeTotal;
    disconnected(i) = sum(sum(Cpre(:,:,i),1)+sum(Cpre(:,:,i),2)'==0);
end

disp(['Average density pre = ',num2str(mean(density.pre)),' & post =
 ',...
    num2str(mean(density.post))]);
disp([num2str(sum(disconnected)), ' empty nodes']);

% connectomic age
AI = load([[basedir,'tracts',dataType],P_ID{1},'_Lesion.mat']);
Cdata = load(AI.Analysis.path2connectome,'age','sub');
for i = 1:length(P_ID)

    % load analysis information
    AI = load([[basedir,'tracts',dataType],P_ID{i},'_Lesion.mat']);

    for j = 1:length(AI.Analysis.subIDX);
        idx = AI.Analysis.subIDX(j)== Cdata.sub;
        tmp(j) = max(Cdata.age(idx));
    end

    ConnectomeAge.raw{i} = tmp;
    ConnectomeAge.range(i,1) = min(ConnectomeAge.raw{i});
    ConnectomeAge.range(i,2) = max(ConnectomeAge.raw{i});
    ConnectomeAge.range(i,3) = ConnectomeAge.range(i,2)-
ConnectomeAge.range(i,1);
    ConnectomeAge.mean(i) = mean(ConnectomeAge.raw{i});
    ConnectomeAge.diff(i) = abs(ConnectomeAge.mean(i)-
behav.data(i,2));
end

disp(['Average range of connectomes =
 ',num2str(mean(ConnectomeAge.range(:,3))),...
    ', std = ',num2str(std(ConnectomeAge.range(:,3))),...
    ' and distance to actual age =
 ',num2str(mean(ConnectomeAge.diff))]);

figure
lw = 1;
alpha = 0.25;
```

```
col = [0.5 0.5 0.5];
s = 30;
a = 0;
b = 0.2;
%--------------------------
[y,idx] = sort(behav.data(:,2),'ascend');

for i =1:length(y)
    % draw scatter
    data = ConnectomeAge.raw{idx(i)};
    r = a + (b-a).*rand(length(data),1);
    scatter(r+i,data,...
        'MarkerEdgeColor',col,...
        'LineWidth',lw,...
        'MarkerFaceAlpha',alpha,...
        'MarkerEdgeAlpha',alpha,...
        'MarkerFaceColor', col,...
        'SizeData',s); hold on
end

scatter(1:length(y),y,...
        'MarkerEdgeColor','k',...
        'LineWidth',lw,...
        'MarkerFaceColor', 'k',...
        'SizeData',s); hold on
ylabel('Age')
xlabel('Subject (black = real data, grey = norm connecomte');

78 participants
28 males
Mean age = 59.3718, std = 16.6219, range = 24 - 91
Mean education = 11.7821, std = 2.7852, range = 7 - 19
Average density pre = 0.35307 & post = 0.34247
0 empty nodes
Average range of connectomes = 11.9231, std = 4.5748 and distance to
 actual age = 2.5564
```

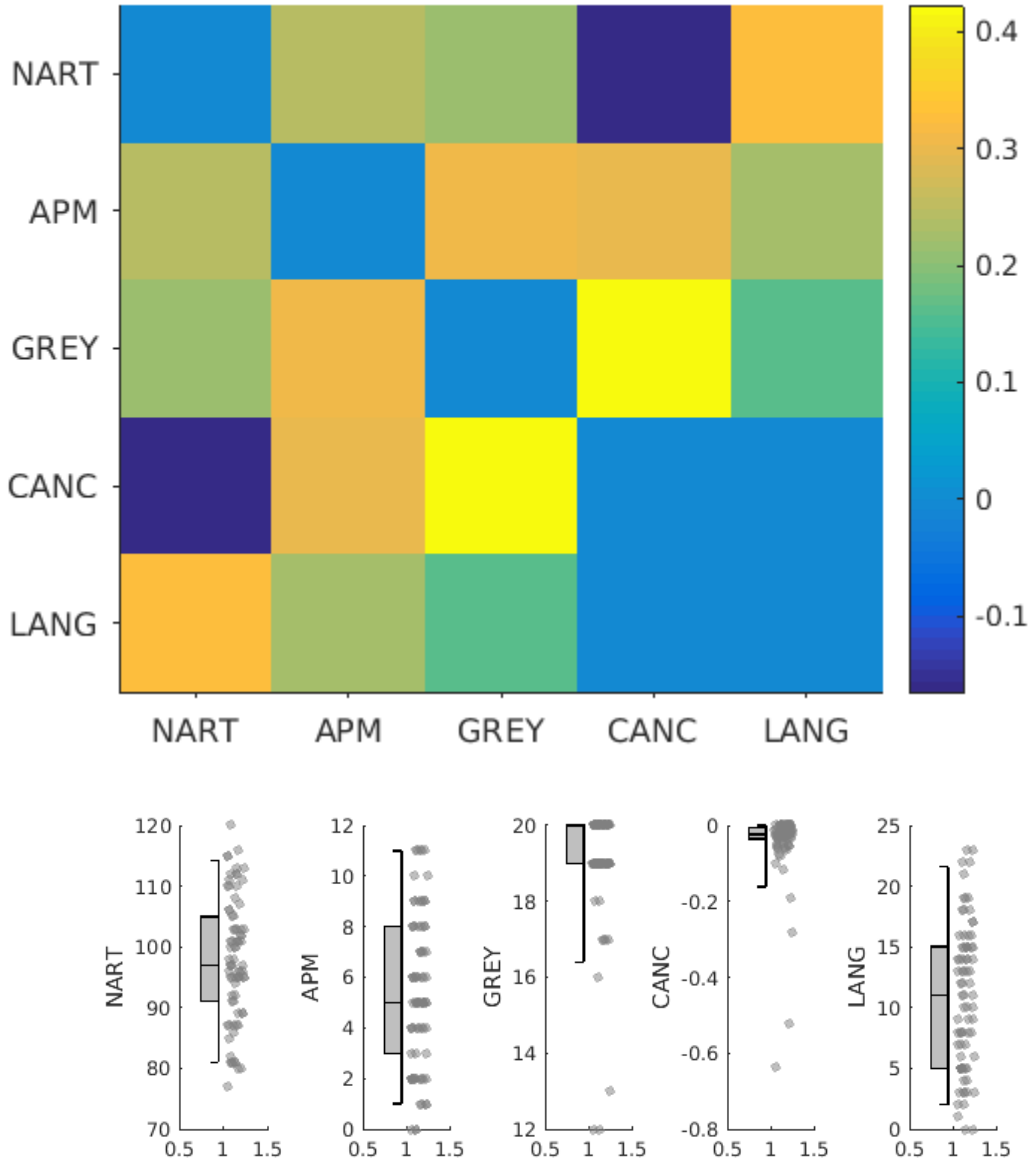


Behaviour

The behaviour in the analysis includes: The NART: often taken as a measure of premorbid IQ, but also seen as a measure of crystallized intelligence. The APM: Raven's matrices common fluid intelligence test. The VOSP: Letter completion task - a basic perception test The Bell's Cancellation Task: a common spatial neglect attention test Naming language task: a simple language test

```
figure
title('Correlation between Vars');
vars = {'NART','APM','GREY','CANC','LANG'};
t = corr(behav.data(:,4:end));
t(logical(eye(size(t))))=0;
imagesc(t);
colorbar
set(gca,'XTick',1:5,'XTickLabel', vars);
set(gca,'YTick',1:5,'YTickLabel', vars);
set(gca,'FontName', 'Helvetica','FontSize',
 12,'Box','off','TickDir','out','ygrid','off');

figure('pos',[1000 600 750 250]);
title('Distribution of variables');
for i = 1:5
    subplot(1,5,i)
    box_and_scatterplot(behav.data(:,i+3),1,1,15,...
        [.5 .5 .5],.5); hold on
    ylabel(vars{i});
```

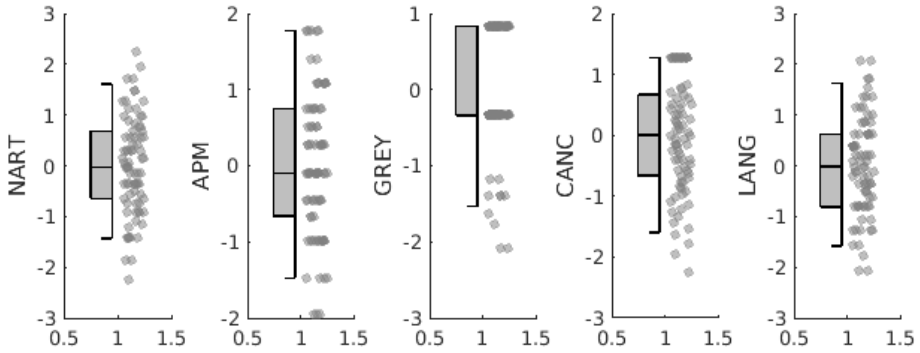
```
end
```

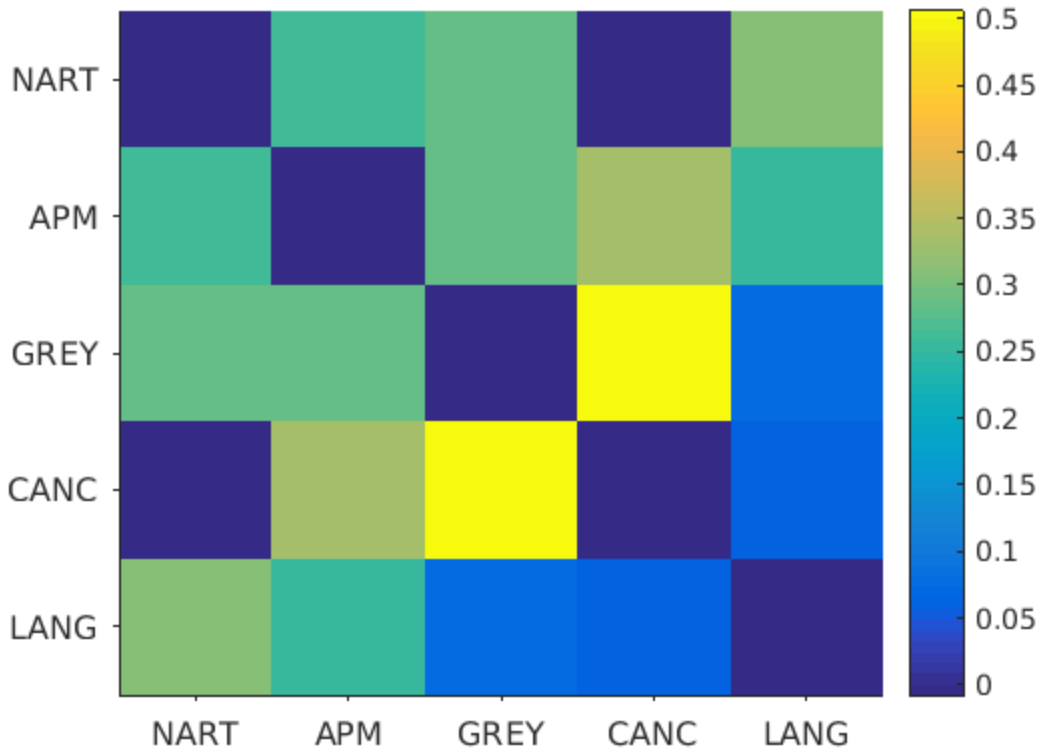


you can see that the VOSP and BC task are highly skewed. This is not unexpected as most people will not show spatial neglect, for example. I propose for the CCA we normalize these variables so as to not unfairly weight outliers. Below I demonstrate the transformation Smith et al., used in their HCP CCA paper but am happy to do something else. We can replicate the analyses in non-transformed data.

```
x = normal_transform(behav.data);

figure('pos',[1000 600 750 250]);
title('transformed variables');

for i = 1:5
    subplot(1,5,i)
    box_and_scatterplot(x(:,i+3),1,1,15,...
```

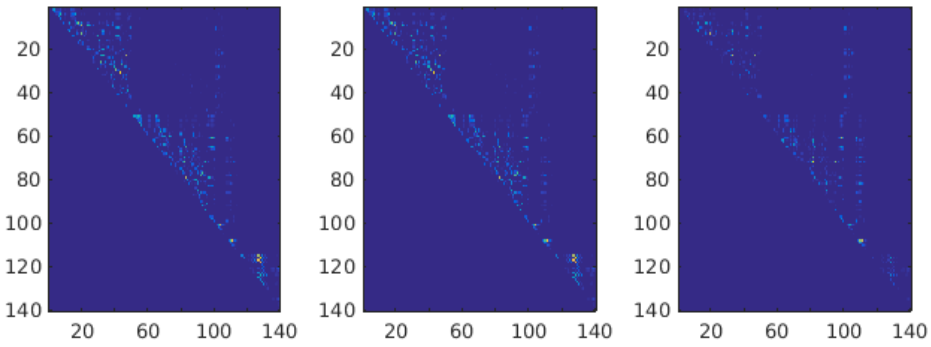
```
        [.5 .5 .5],.5); hold on
    ylabel(vars{i});
end

figure
title('Correlation between transformed Vars');
vars = {'NART','APM','GREY','CANC','LANG'};
t = corr(x(:,4:end));
t(logical(eye(size(t))))=0;
imagesc(t);
colorbar
set(gca,'XTick',1:5,'XTickLabel', vars);
set(gca,'YTick',1:5,'YTickLabel', vars);
set(gca,'FontName', 'Helvetica','FontSize',
 12,'Box','off','TickDir','out','ygrid','off');
```



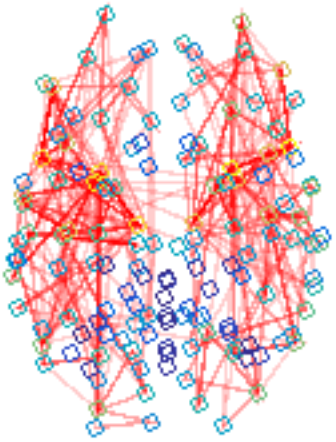


Lesion brain plot

```
figure('pos',[1000 600 750 250]);
subplot(1,3,1)
imagesc(sum(Cpre,3));
subplot(1,3,2)
imagesc(sum(Cpost,3));
subplot(1,3,3)
imagesc(sum(Cpre-Cpost,3));

figure('pos',[1000 600 250 250]);
MAT = Cpre-Cpost;
MAT = sum(MAT>0,3);

draw_connectome(MAT,COG,20,500);
set(gca,'FontName', 'Helvetica','FontSize', 10,'Box','off',...
'TickDir','out','ygrid','off','XLim',[-100 100],'YLim',[-110,90]);
title('Top 500 lesioned connections')
set(gca,'xtick',[],'xcolor',[1,1,1],'ytick',[],'ycolor',[1,1,1]);
```



Top 500 lesioned connections



Published with MATLAB® R2015b