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Preambles

```
clear all; close all; clc;
savePlots = 1;
```

Load the data

```
load('cbt3data.mat');
```

Initialise Km and meanKm

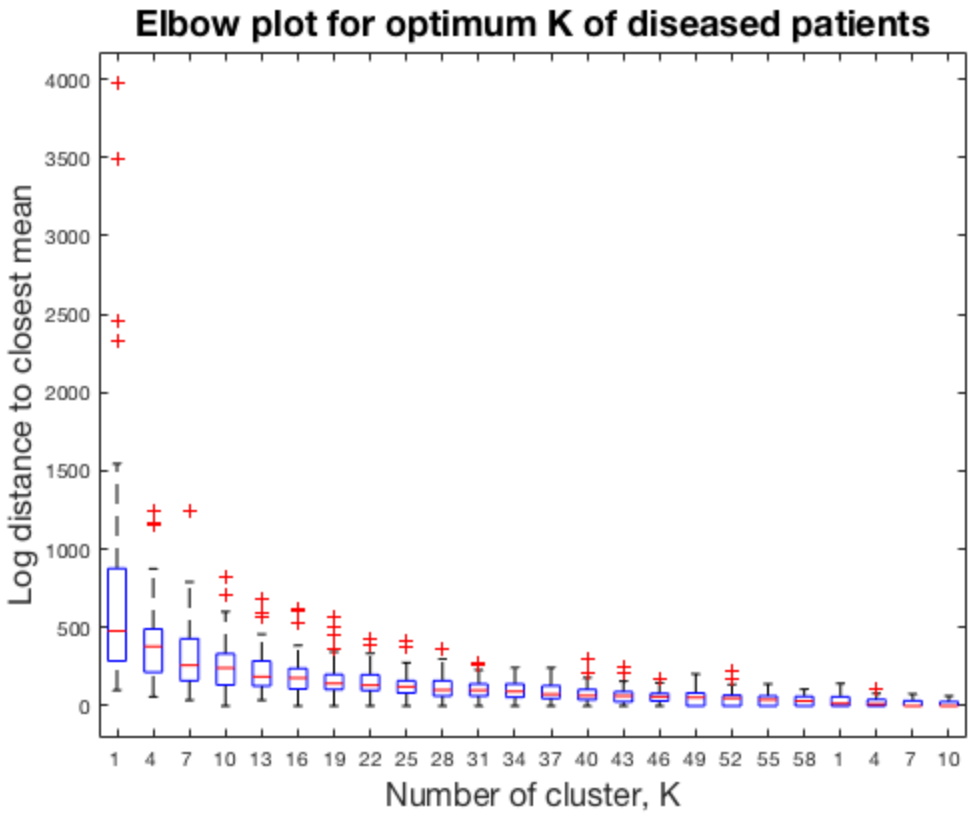
```
person_type = {'Diseased Patients';'Healthy Controls'};
D_diseased_total = [];
D_healthy_total = [];
```

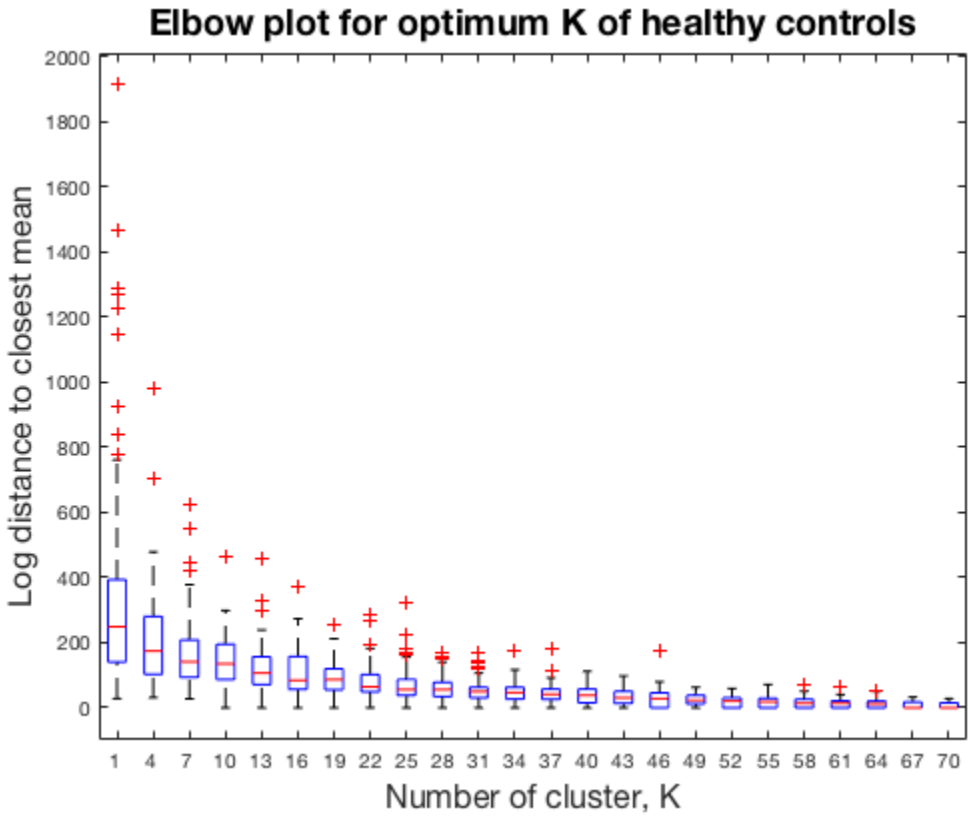
We get a community matrix for 10,20, and 30 clusters

```
for K = 1:3:70;
    tic;
    % we get the ith diseased and healthy person
    X = diseased(:,:,1)';
    Y = healthy(:,:,1)'; % we get the ith healthy person

    % For the ith person, we get the cluster index for each brain
 region
    [~,~,~,D_diseased] = kmeans(X,K, 'Replicates',100);
    [~,~,~,D_healthy] = kmeans(Y,K, 'Replicates',100);

    % We take the distance closest to a cluster
    D_diseased_min = min(D_diseased,[],2);
    D_healthy_min = min(D_healthy,[],2);

    % We store the ditances for each point to its respective mean
    D_diseased_total = [D_diseased_total, D_diseased_min];
    D_healthy_total = [D_healthy_total, D_healthy_min];

end
```

Boxplot of data

```
figure(1)
boxplot(D_diseased_total);
labels = (1:3:60);
set(gca, 'XTickLabel', labels);
% set(gca,'YScale','log')
xlabel('Number of cluster, K','fontsize',16);
ylabel('Log distance to closest mean','fontsize',16);
title('Elbow plot for optimum K of diseased patients', 'fontsize',18);
if (savePlots == 1)
    filename = ('elbowDiseased.png');
    saveas(gcf,filename);
end

figure(2)
boxplot(D_healthy_total);
labels = (1:3:90);
set(gca, 'XTickLabel', labels);
set(gca, 'XTickLabel', labels);
% set(gca,'YScale','log')
xlabel('Number of cluster, K','fontsize',16);
ylabel('Log distance to closest mean','fontsize',16);
title('Elbow plot for optimum K of healthy controls', 'fontsize',18);
if (savePlots == 1)
    filename = ('elbowHealthy.png');
    saveas(gcf,filename);
end
```


Elbow plot for optimum K of diseased patients
Log distance to closest mean
Number of cluster, K


Elbow plot for optimum K of healthy controls
Log distance to closest mean
Number of cluster, K

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