

```
%%% Bootstrap Problem Set
```

```
[X,Y]=GetSample(10);    % the data provided
```

```
%%% (1a) bootstrap, two sample comparison
```

```
N=10;
```

```
numsims=100000;    % simulate many times
```

```
d=nan(numsims,1);
```

```
for i=1:numsims
```

```
    Xboot=X(ceil(N*rand(N,1)));    % the bootstrap / sampling from data w/ replacement
```

```
    Yboot=Y(ceil(N*rand(N,1)));
```

```
    d(i)=mean(Xboot)-mean(Yboot);
```

```
end
```

```
figure
```

```
hist(d,40);
```

```
title('1a');
```

```
d_stdest=std(d)        % ex. 0.63
```

```
lower_CI=prctile(d,5)   % ex. -1.74
```

```
median=prctile(d,50)    % ex. -0.70
```

```
upper_CI=prctile(d,95)  % ex. 0.34
```

```
% Here bootstrap yields a distribution of d that looks relatively wide
```

```
% (centered somewhere at -0.7 with a bootstrap std of 0.635)
```

```
% Moreover the 95% CI on d comfortably includes 0, which is poor evidence that d is nonzero.
```

```
% Though for formal hypothesis testing, we should use permutation test instead of the bootstrap.
```

```
%%% (1b) (paired samples)
```

```
for i=1:numsims
```

```
    paired_indices=ceil(N*rand(N,1));
```

```
    Xboot=X(paired_indices);
```

```
    Yboot=Y(paired_indices);
```

```
    d(i)=mean(Xboot)-mean(Yboot);
```

```
end
```

```
figure
```

```
hist(d,40);
```

```
title('1b');
```

```
d_stdest=std(d)        % ex. 0.15
```

```
lower_CI=prctile(d,5)   % ex. -0.95
```

```
median=prctile(d,50)    % ex. -0.70
```

```
upper_CI=prctile(d,95)  % ex. -0.4457
```

```
% Here bootstrap yields a distribution of d that is considerably narrower
```

```
% than in (1a). Now the 95% CI comfortably excludes 0, which suggests that d is nonzero
```

```
% and thus that there is a significant difference between the two groups.
```

```
%%% (2a) permutation test, two sample comparison (not paired)
```

```
% in contrast to re-sampling from each respective sets of samples as in
```

```
% problem (1), we'll now be jumbling the sets in each simulation and
```

```
% calculating d
```

```
d_data=mean(X)-mean(Y)    % ex. -0.70
```

```
dperm=nan(numsims,1);
```

```
Z=[X;Y];
```

```

for i=1:numsims
    Zperm=Z(randperm(length(Z)));
    dperm(i)=mean(Zperm(1:length(X)))-mean(Zperm((length(X)+1):length(Z)));
end

figure
hist(dperm,40);
title('2a');

lower_CI=prctile(dperm,5)    % ex. -1.10
median=prctile(dperm,50)    % ex. -0.00
upper_CI=prctile(dperm,95)  % ex. 1.10

% the 95% CI generated by the permutation test contains the difference we
% observe from the data (-0.70) -- thus the difference is not large enough to reject
% the null hypothesis.

%%% (2b) permutation test, paired two sample comparison

% for paired data, we'll permute the group identity within each pair

d_data_2b=mean(X)-mean(Y)    % ex. -0.70
dperm=nan(numsims,1);
Z=[X Y];                    % here concatenate into columns to visualize "pairing"
Zperm=[];

for i=1:numsims
    for j=1:10                % flipping columns randomly
        if rand>0.5
            Zperm(j,:)=Z(j,:);
        else
            Zperm(j,:)=fliplr(Z(j,:));
        end
    end
    dperm(i)=mean(Zperm(:,1))-mean(Zperm(:,2));
end

figure
hist(dperm,40);
title('2b');

lower_CI=prctile(dperm,5)    % ex. -0.46
median=prctile(dperm,50)    % ex. 0.00
upper_CI=prctile(dperm,95)  % ex. 0.44

% with this identical but paired data, the 95% CI generated by the permutation test does not
% contain
% the difference we observe from the data (-0.70) -- thus the difference is
% large enough to reject the null hypothesis.

%%% (3) power analysis: unpaired vs. paired permutation tests

numsims=500;
numdatasets=200;

% unpaired

Zperm=[];
N_vals=[10 20];
diff_vals=[0.12 0.25 0.5 1 2];
power=nan(2,5);

for n=1:2
    for k=1:5
        reject_count=0;        % initialize count

```

```

for j=1:numdatasets
    [X,Y]=GetSample(N_vals(n),diff_vals(k));
    Z=[X;Y];
    d=mean(X)-mean(Y);
    dperm=nan(1,numsim);
    for i=1:numsim
        Zperm=Z(randperm(length(Z)));
        dperm(i)=mean(Zperm(1:length(X)))-mean(Zperm((length(X)+1):length(Z)));
    end
    if d<prctile(dperm,5) || d>prctile(dperm,95)    %% hypothesis test
        reject_count=reject_count+1;
    end
end
power(n,k)=reject_count/numdatasets;
end
end

```

```

figure
hold on
plot(diff_vals,power(1,:), 'b')
plot(diff_vals,power(2,:), 'r')
set(gca, 'FontSize', 14);
h = xlabel('true difference');
set(h, 'FontSize', 16);
h = ylabel('statistical power (beta)');
set(h, 'FontSize', 16);
h = title('unpaired data, permutation test power (red: N=10, blue: N=20)');
set(h, 'FontSize', 16);

```

% paired

```

Zperm=[];
N_vals=[10 20];
diff_vals=[0.12 0.25 0.5 1 2];
power=nan(2,5);

```

```

for n=1:2
    for k=1:5
        reject_count=0;    %% initialize count
        for j=1:numdatasets
            [X,Y]=GetSample(N_vals(n),diff_vals(k));
            Z=[X Y];
            d=mean(X)-mean(Y);
            dperm=nan(1,numsim);
            for i=1:numsim
                for j=1:10    %% for paired test, flipping columns randomly
                    if rand>0.5
                        Zperm(j,:)=Z(j,:);
                    else
                        Zperm(j,:)=fliplr(Z(j,:));
                    end
                end
                dperm(i)=mean(Zperm(:,1))-mean(Zperm(:,2));
            end
            if d<prctile(dperm,5) || d>prctile(dperm,95)    %% hypothesis test
                reject_count=reject_count+1;
            end
        end
        power(n,k)=reject_count/numdatasets;
    end
end
end

```

```

figure
hold on
plot(diff_vals,power(1,:), 'b')
plot(diff_vals,power(2,:), 'r')

```

```

set(gca, 'FontSize', 14);
h = xlabel('true difference');
set(h, 'FontSize', 16);
h = ylabel('statistical power (beta)');
set(h, 'FontSize', 16);
h = title('paired data, permutation test power (red: N=10, blue: N=20)');
set(h, 'FontSize', 16);

```

```

%% The paired test is more powerful. For differences around 0.75 (and smaller), the
%% paired test provides practically a significant boost in power. Within
%% each group, the larger sample size boosts power, though less so for the
%% paired data. For the unpaired data, the difference in power is from
%% unlikely (less than 0.5) to likely (more than 0.5) at around a true
%% difference of 0.8.

```



