Hypothesis Testing Lab

Screenshots of the codes and explanations

```
% Wilcoxon signed rank test
clc:
clear all;
close all:
% see Wilcoxon Test Lab Session PPT page 4 to complete the code
% and adjust to which samples that will be used
% load csv file
group1 = load ('groupSample1.mat');
group2 = load ('groupSample2.mat');
group3 = load ('groupSample3.mat'); %small size sample
group4 = load ('groupSample4.mat'); %small size sample
group5 = load ('groupSample5.mat'); %large size sample
group6 = load ('groupSample6.mat'); %large size sample
% change struct into array
group1 = cell2mat(struct2cell(group1));
group2 = cell2mat(struct2cell(group2));
group3 = cell2mat(struct2cell(group3));
group4 = cell2mat(struct2cell(group4));
group5 = cell2mat(struct2cell(group5));
group6 = cell2mat(struct2cell(group6));
```

First, we start by loading the files containing the data we need for our analysis. Second, we address the issue of data types. We've encountered errors, specifically with structs, which have hindered our ability to perform calculations involving "-". To resolve this, especially for the signrank step, we've changed the data into arrays. This conversion simplifies the data structure and ensures compatibility for the testing process.

```
% see Wilcoxon Test Lab Session PPT page 5 to complete the code
[p_exa,h_exa,stats_exa] = signrank(group1,group2,'tail','both','alpha',0.05,
[p_appr,h_appr,stats_appr] = signrank(group1,group2,'tail','both','alpha',0.05,'method','approximate');
% performing wilcoxon signed rank test based (small sample size)
% method : exact
%[p,h,stats] = signrank(group1,group2,'method','%methodExact')
[p_small_exa,h_small_exa,stats_small_exa] = signrank(group3,group4,'tail','both','alpha',0.05,'method','exact');
% method : approximate
%[p2,h2,stats2]= signrank(group1,group2,'method','%methodApproximate')
[p_small_appr,h_small_appr,stats_small_appr] = signrank(group3,group4,'tail','both','alpha',0.05,'method','approximate');
% performing wilcoxon signed rank test based (large sample size)
% method : exact
%[p3,h3,stats3] = signrank(group1,group2,'method','%methodExact')
[p_large_exa,h_large_exa,stats_large_exa] = signrank(group5,group6,'tail','both','alpha',0.05,'method','exact');
% method : approximate
%[p4,h4,stats4] = signrank(group1,group2,'method','%methodApproximate')
[p_large_appr,h_large_appr,stats4_large_appr] = signrank(group5,group6,'tail','both','alpha',0.05,'method','approximate');
```

Next, we perform the ranking test methods.

 Result of exact and approximate (p-value[p] and decision[h]) from small and large sample size

```
h_appr

✓ h exa

✓ h_large_appr 0

h_large_exa
            0
 __h_small_appr
 h_small_exa
            0
             0.0273
🚻 p_appr
 p_exa
             0.0313
 p_large_exa 0.8485
p small appr 0.0458
 p small exa 0.0625
```

table of all the result:

	decision[h]	p-value[p]
Group 1+2 exact	1 (p<0.5)	0.0313
Group 1+2 appropriate	1	0.0273
Group 3+4 (small) exact	0	0.0625
Group 3+4 (small) appropriate	1	0.0458
Group 5+6 (large) exact	0	0.8485
Group 5+6 (large) appropriate	0	0.8371

• Comparison between exact and approximate methods

From the table above, it indicates two discoveries. Firstly, the exact methods consistently yield higher p-values compared to approximate methods. Secondly, the p-value ratio tends to be higher for larger datasets than for smaller ones, as shown in the table.

Analyze if there are different hypothesis results from different sample sizes
 Using different test methods, such as the T-test, may yield different results. In the
 video, we learned that the T-test employs a different decision criterion for ranking
 p-values as non-significant, potentially leading to different conclusions. Moreover, the
 T-test may not produce reliable results when dealing with datasets containing a lot of
 outliers.