PS4

2024-09-18

Stat 5000 Homework #4 Fall 2024 due Fri, Sep 27th @ 11:59 pm Name: Collaborators:

Directions: Type or clearly handwrite your solutions to each of the following exercises. Partial credit cannot be given unless all work is shown. You may work in groups provided that each person takes responsibility for understanding and writing out the solutions. Additionally, you must give proper credit to your collaborators by providing their names on the line below (if you worked alone, write "No Collaborators"):

1.

Consider the dataset from Homework #1 about survival times (in days) of guinea pigs that were randomly assigned either to a control group or to a treatment group that received a dose of tubercle bacilli (a bacterium that causes tuberculosis). These data are found in the guinea_pigs.csv file located in our course's shared folder on SAS Studio. Suppose the researchers want to test the hypothesis that the mean (or median/distribution of) survival times are the same for controls and the guinea pigs infected with tubercle bacilli against the one-sided alternative that infection with tubercle Bacilli tends to decrease survival times.

- 1. Perform a two-sample t-test assuming two independent random samples from normal distributions with equal variances in SAS Studio. Report (i) the observed t-statistic and (ii) the p-value.
- 2. Perform a two-sample Welch t-test assuming two independent random samples from normal distributions with unequal variances (using the Satterthwaite approximation) in SAS Studio. Report (i) the observed t^* -statistic and (ii) the p-value.

T-test for Difference in Mean Times - Survival Time

The TTEST Procedure

Variable: Time

Treatment	Method	N	Mean	Std Dev	Std Err	Minimum	Maximum
Bacilli		58	242.5	117.9	15.4851	76.0000	598.0
Control		64	345.2	222.2	27.7767	18.0000	735.0
Diff (1-2)	Pooled		-102.7	180.4	32.6978		
Diff (1-2)	Satterthwaite		-102.7		31.8015		

Treatment	Method	Mean	95% CL Mean		Std Dev	95% CL Std De	
Bacilli		242.5	211.5	273.5	117.9	99.6997	144.4
Control		345.2	289.7	400.7	222.2	189.3	269.1
Diff (1-2)	Pooled	-102.7	-167.4	-37.9448	180.4	160.1	206.5
Diff (1-2)	Satterthwaite	-102.7	-165.8	-39.5736			

Method	Variances	DF	t Value	Pr > t
Pooled	Equal	120	-3.14	0.0021
Satterthwaite	Unequal	97.803	-3.23	0.0017

Equality of Variances							
Method	Num DF	Den DF	F Value	Pr > F			
Folded F	63	57	3.55	<.0001			

Figure 1: Figure 1

Variable: Time

Treatment	Method	N	Mean	Std Dev	Std Err	Minimum	Maximum
Bacilli		58	242.5	117.9	15.4851	76.0000	598.0
Control		64	345.2	222.2	27.7767	18.0000	735.0
Diff (1-2)	Pooled		-102.7	180.4	32.6978		
Diff (1-2)	Satterthwaite		-102.7		31.8015		

Figure 2: Figure 1

3. Perform a randomization/permutation test using 20,000 new random assignments of guinea pigs to treatment groups in SAS Studio. Report (i) the observed difference in sample means and (ii) the p-value.

GLM results for Difference in Mean Survival Times

The Multtest Procedure

Model Information						
Test for continuous variables	Mean t-test					
Degrees of Freedom Method	Pooled					
Tails for continuous tests	Two-tailed					
Strata weights	None					
P-value adjustment	Permutation					
Center continuous variables	No					
Number of resamples	20000					
Seed	500					

Contrast Coefficients						
		Treatment				
Contrast		Bacilli	Control			
Trend	Centered	-0.5	0.5			

Continuous Variable Tabulations								
Variable	le Treatment NumObs Mean Standard Deviation							
Time	Bacilli	58	242.5345	117.9309				
Time	Control	64	345.2188	222.2139				

p-Values							
Variable	Contrast	Raw	Permutation				
Time	Trend	0.0021	0.0023				

Figure 3: Figure 1

4. Perform the Wilcoxon rank-sum test in SAS Studio. Report (i) the sum of the ranks w, for the Bacilli treatment group and (ii) the p-value.

GLM results for Difference in Mean Survival Times The NPAR1WAY Procedure Wilcoxon Scores (Rank Sums) for Variable Time **Classified by Variable Treatment** Sum of **Expected** Std Dev Mean **Treatment S**cores Under H0 Under H0 N Score Bacilli 58 3190.50 3567.0 195.053487 55.008621 Control 64 4312.50 3936.0 195.053487 67.382813 Average scores were used for ties. Wilcoxon Two-Sample Test t Approximation **Statistic** Z Pr < ZPr > |Z| Pr < Z Pr > |Z| 3190.500 -1.9277 0.0269 0.0539 0.0281 0.0562 Z includes a continuity correction of 0.5. Kruskal-Wallis Test Chi-Square DF Pr > ChiSq 3.7258 0.0536 1

Figure 4: Figure 1

5. Compare the results from parts (a)–(d).

2.

Revisit the guinea pig study from the previous exercise. Use SAS to create diagnostic information to assess the assumptions for the traditional t-based inference procedure.

- 1. There is not enough information provided to assess independence of observations within each group. Which study design aspects would help you assess the assumption of independence between the groups.
- 2. Assess the assumption of equal variances using:
 - 1. the ratio of standard deviations;

```
knitr::include_graphics("gross.png")
```

```
191 %let a=%SYSEVALF(269.1/144.4);
192 %put &a;
1.86357340720221
```

- 2. side-by-side boxplots;
- 3. the F-test;
- 4. the Brown-Forsythe test.
- 3. Assess the assumption of normality using the following methods:
 - 1. side-by-side histograms;
 - 2. Q-Q plot(s);
 - 3. the Shapiro-Wilk test.
- 4. Based on what you learned in parts (a)–(c), complete the following exercises.
 - $1. \,$ Summarize the assessment of all three assumptions.
 - 2. Discuss which tests are the most appropriate among the 4 used in the previous exercise.
 - 3. Interpret the result, in the context of the study, for one of the tests you chose.

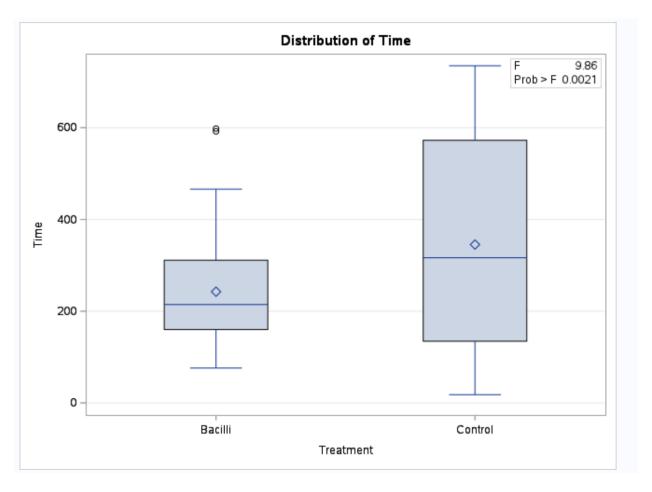


Figure 5: Figure 1

Equality of Variances							
Method	Num DF	Den DF	F Value	Pr > F			
Folded F	63	57	3.55	<.0001			

Figure 6: Figure 1

GLM results for Difference in Mean Survival Times The GLM Procedure							
Brown and Forsythe's Test for Homogeneity of Time Variance ANOVA of Absolute Deviations from Group Medians							
Source	DF	Sum of Squares	Mean Square	F Value	Pr > F		
Treatment	1	359581	359581	42.80	<.0001		
Error	120	1008165	8401.4				

Figure 7: Figure 1

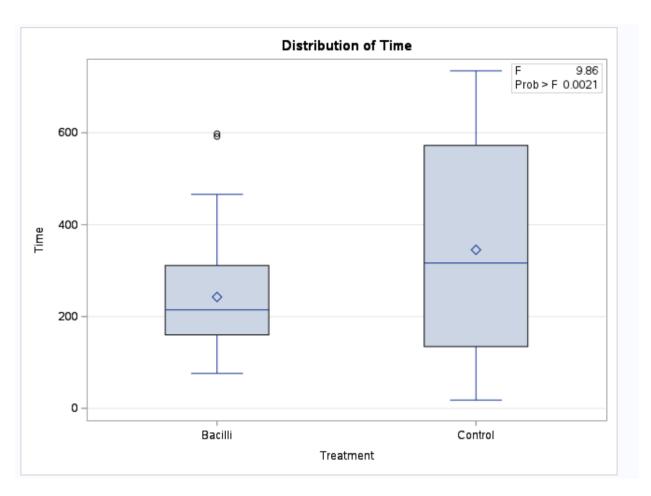


Figure 8: Figure 1

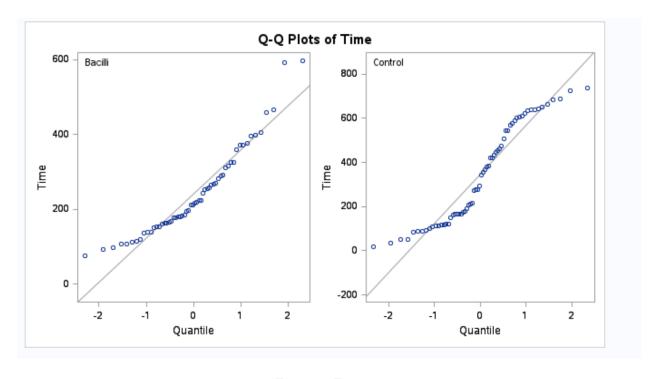


Figure 9: Figure 1

Tests for Normality							
Test	St	Statistic p Value					
Shapiro-Wilk	W	0.91559	Pr < W	0.0006			
Kolmogorov-Smirnov	D	0.128064	Pr > D	0.0188			
Cramer-von Mises	W-Sq	0.212674	Pr > W-Sq	<0.0050			
Anderson-Darling	A-Sq	1.317813	Pr > A-Sq	<0.0050			

Figure 10: Figure 1

3.

Researchers have data consisting of the annual adjusted gross incomes (income) for 100 randomly sampled individuals from two adjacent zip codes (zip). What type of statistical analysis should you use to compare the incomes in the two zip codes?

1. The output below was created to diagnose the assumption of normality for this data.

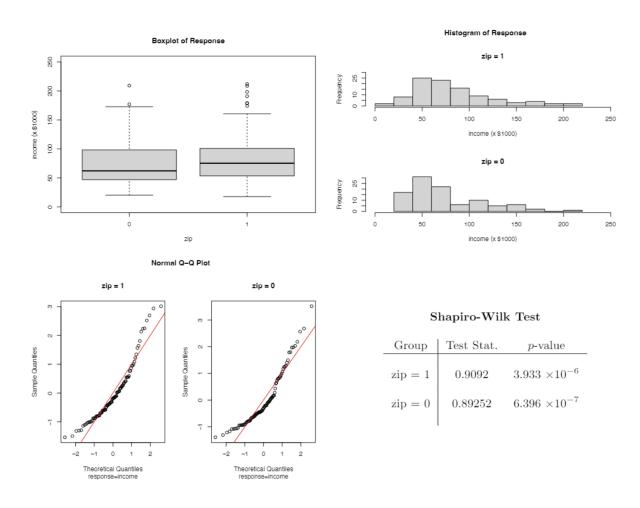


Figure 11: Figure 1

Describe three aspects (minimum) that indicate the normality assumption is violated.

- 2. Using the information you gathered in part (a), which transformation should be explored to achieve normality? Choose one: logarithm, square-root, arcsine, or power/Box-Cox.
- 3. One of these transformations has been applied and the resulting diagnostic output is provided below.

Did the transformation succeed in remediating the non-normality?

Histogram of Transformed Response Boxplot of Transformed Response zip = 1 ū f(income) f(income) Ξ zip = 0 9 zip Normal Q-Q Plot zip = 1 zip = 0 Shapiro-Wilk Test Group Test Stat. p-value Sample Quantiles Sample Quantiles zip = 10.990370.6942 zip = 00.986630.4129 -1 0 -1 Theoretical Quantiles response=f(income) Theoretical Quantiles response=f(income)

Figure 12: Figure 2

4.

Given the additional output (shown below) to diagnose the equal variance assumption, how should you proceed with the data analysis?

• Summary statistics: $s_0 = 0.4899$, $s_1 = 0.5067$, ratio = 1.0342

• F-test: statistic = 1.0696, p-value = 0.3692

 Brown-Forsythe test: statistic = 0.0125, p-value = 0.9109

Total: 50 points # correct: %: