# Answer Keys to Homework#6

### Problem 1

For RCBD, we can form 9 blocks by considering all combinations of the three cars and three drivers, and then randomize the four gasoline additives inside each block. In comparison to the Latin square design which requires four cars and four drivers, RCBD is more flexible. However, Latin square design usually demands much less number of runs.

We can increase the power for RCBD by including more cars or more drivers or both. For the Latin square design, we can follow the four different ways of replicating Latin squares as talked in Lecture 7 but including as less number of new blocks as possible.

### Problem 2

(a) The hypotheses are

	$H_0$ :	There is no difference between the four assembly methods,
vs	$H_1$ :	or symbolically, $\tau_A = \tau_B = \tau_C = \tau_D$ . There is a difference between the four assembly methods,
		or symbolically, $\tau_A, \tau_B, \tau_C$ and $\tau_D$ are not all equal.

Let's look at the ANOVA table output from SAS (I replaced the line for the model SS by lines for the two block SS and the treatment SS).

		Sum of			
Source	DF	Squares	Mean Square	F Value	Pr > F
ord	3	18.50000000	6.16666667	3.52	0.0885
opt	3	51.50000000	17.16666667	9.81	0.0099
trt	3	72.50000000	24.16666667	13.81	0.0042
Error	6	10.5000000	1.7500000		
Corrected Total	15	153.0000000			

Since *p*-value for treatment effect is small (= 0.0042), I conclude that there is a difference between the four assembly methods.

(b) The treatment effects  $\tau_j, j = A, B, C, D$  are estimated by

$$\hat{\tau}_j = \bar{y}_{\cdot j \cdot} - \bar{y}_{\cdots}, \qquad j = A, B, C, D.$$

The overall mean  $\bar{y}_{...}$  and the treatment group means  $\bar{y}_{.j.}$  can be obtained from the SAS output of PROC GLM.

R-Square	Coeff Var	Root MSE	y Mean
0.931373	12.90610	1.322876	10.25000
	trt	y LSMEAN	
	1	7.5000000	
	2	9.2500000	
	3	13.2500000	
	4	11.0000000	

Plugging in these values, I get the four treatment effect estimates as below

$\hat{ au}_A$	$\hat{ au}_B$	$\hat{ au}_C$	$\hat{ au}_D$
-2.75	-1.00	3.00	0.75

(c) The critical distance for Tukey's pairwise comparisons method is

$$CD = q_{\alpha,p,(p-2)(p-1)}\sqrt{MS_E/p} = q_{0.05,4,6}\sqrt{1.75/4} = 3.24.$$

The four treatment means are ordered as 13.25 > 11.00 > 9.25 > 7.50(C > D > B > A). After computing differences following this order and comparing them with the critical distance, I reach the following conclusion.

- The pairs of assembly methods which have significantly different effects are (C, B), (C, A), (D, A).
- The pairs of assembly methods whose effects are not significantly different are (C, D), (D, B), (B, A).

(d) The diagnostic plots in Figure ?? are: normal probability Q-Q plot, plot of residuals versus assembly methods (treatment), plot of residuals versus assembly orders (row block), plot of residuals versus operators (column block), and plot of residuals versus predicted values. The normal Q-Q plot shows that the normality assumption is valid. And there are no potential outliers or influential points in the plots. Only the plot of residuals against predicted values shows some curvilinearity, but this is not enough to question on the additivity assumption since our sample size is small.

#### Problem 3

(a) This is a  $4 \times 4$  Graeco-Latin square design. It superimposes on the Latin square of 4 assembly methods another Latin square of 4 workplaces. And these two Latin squares are orthogonal to each other, that is, each assembly method in the first Latin square is paired with each workplace in the second Latin square exactly once.

(b) The ANOVA table from SAS is as follows (again, I replaced the line for the model SS by lines for the block SS and the treatment SS).

		Sum of			
Source	DF	Squares	Mean Square	F Value	Pr > F
ord	3	0.50000000	0.16666667	0.02	0.9960
opt	3	19.0000000	6.33333333	0.69	0.6157
trt	3	95.50000000	31.83333333	3.47	0.1669
wp	3	7.5000000	2.5000000	0.27	0.8429
Error	3	27.5000000	9.1666667		
Corrected Total	15	150.0000000			

The *p*-value for the treatment effect is large (= 0.1669), so I conclude that the four assembly methods are not different.

(c) My conclusion here is inconsistent with that from Problem 1. First, our data are different from those in Problem 1 and seem to have less variation due to assembly methods (treatment SS here, 7.5, is only about 1/10 of that in Problem 1, 72.5). Second, the Graeco-Latin square design reduces the degree of freedom for  $MS_E$  from 6 to 3, which may cause the F test for the treatment effect less sensitive.



Normal Q-Q Plot

Figure 1: Diagnostic Plots

## Problem 4

We need to compute  $\Phi = \sqrt{pD^2/(2p\sigma^2)} = \sqrt{D^2/(2\sigma^2)}$ . The degrees of freedom for error are (p-2)(p-1). The degrees of freedom in the numerator is p-1. In other words, we use the formula  $\Phi = \sqrt{nD^2/(2a\sigma^2)}$  and replace n and a by the appropriate values. That will be the case for any design that we use in the future.