Ch 11. Question 9.

Solution 1. *For part (a):*

to check the design is BIBD(balanced incomplete block design), we need to check the following:

1. *the design is binary, i.e., each treatment label appear either once or not at all in a block. It is easy to see this is satisfied.*

2. *we see that each pair of label appears together in $\lambda = 2$ blocks.*

So the design is really BIBD.

For part (b):

The randomization goes by two parts:

1. *randomly assign the subjects to the blocks*

2. *within each block(subject), randomize the order in which the 3 levels of treatment factors are given to the subject.*

for part (c):

There might be potential interaction between the block(subjects) and the treatment(drugs). If it is the case, then the treatment model (11.3.1) would not be adequate.

For part (d):

becareful here that treatment $i = 2$ is really represented by label 1. (treatment 1 is labeld by 0).

```
T <- c(385, 582, 329, 674)
B<- c(417, 507, 469, 577)
n_2 <- c(1, 1, 0, 1)
Q_2 <- T[2] - sum(n_2*B)/3
Q_2

## [1] 81.66667
```

so we have verified that $Q_2 = 81.667$.

For part (e):

For any contrast $\sum_i c_i \tau_i$ under the BIBD model, we have $100(1 - \alpha)\%$ confidence interval as:

$$\sum_i c_i \tau_i \in \left(\frac{k}{\lambda v} \sum_i c_i Q_i \pm \frac{q_{v,bk-b-v+1,\alpha}}{\sqrt{2}} \sqrt{\sum c_i^2 (\frac{k}{\lambda v}) msE} \right)$$

So for $\tau_3 - \tau_2$, we have:

```
k <-3
lambda <- 2
v <- 4
b <- 4
Q <- c(-79.333, 81.667, -158.667, 156.333)
msE <- 3.683
contrast <- c(0, -1, 1, 0)
CI.lower <- k/(lambda*v)*(Q[3] - Q[2]) -
  qtukey(0.05, v, df = b*k-b-v+1, lower.tail = FALSE)*sqrt(k/(lambda*v)*msE)
CI.upper <- k/(lambda*v)*(Q[3] - Q[2]) +
  qtukey(0.05, v, df = b*k-b-v+1, lower.tail = FALSE)*sqrt(k/(lambda*v)*msE)
cat('The 95% confidence interval for (', contrast, ') is [',
    CI.lower, ',', CI.upper, ']')

## The 95% confidence interval for ( 0 -1 1 0 ) is [ -96.25789 , -83.99261 ]
```

Since it does not include 0, *we conclude that there is a difference between treatment* 3 *(labeled as drug number* 2*) and treatment* 2 *(labeled as drug number* 1*).*

For part (f):

We want to test the hypothesis that:

$$H_0 : \tau_1 = \tau_2 = \tau_3 = \tau_4$$

against

$$H_1 : \tau_i \neq \tau_j, \text{ for some } i \neq j$$

```
k <-3
lambda <- 2
v <- 4
ssTadj <- k/(lambda*v)*62578.335
msE <- 3.683
F <- (ssTadj/(v - 1))/msE
p <- pf(F, v-1, b*k-b-v+1, lower.tail=FALSE)
cat('The p value is', p)

## The p value is 3.506291e-08
```

we see that our p value for the test is smaller than $\alpha = 0.05$, *so we reject the null hypothesis and conclude that the drugs do have different treatment effect.*