HW9 KEY

34 points total, 2 points per problem part unless otherwise noted.

BIBD

```
library(car)
library(emmeans)
InData <- InData <- read.csv("C:/hess/STAT511_FA11/ASCII-comma/CH19/ex19-23.txt", quote = " ' ")
#str(InData)
InData$Person <- as.factor(InData$Person)
#table(InData$Person)
#table(InData$Treatments)
```

1. (**4pts**) t=6, r=5, b=10, k=3
2. λ = r(k-1)/(t-1) = 2

BIBD Fixed Blocks

3. ANOVA Table

```
Model1 <- lm(AreaRed ~ Person + Treatments, data = InData)
Anova(Model1, type = 3)
```

```
## Anova Table (Type III tests)
##
## Response: AreaRed
##              Sum Sq Df F value    Pr(>F)
## (Intercept) 2207.43  1 72.9953 3.796e-07 ***
## Person       512.79  9  1.8841 0.1336294
## Treatments  1747.06  5 11.5543 0.0001033 ***
## Residuals    453.61 15
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

4. (**4pts**) CLD Display

```
emout1 <- emmeans(Model1, pairwise ~ Treatments)
CLD(emout1$emmeans)
```

```
##  Treatments emmean  SE df lower.CL upper.CL .group
##  E            31.6 2.7 15     25.8     37.3  1
##  D            35.5 2.7 15     29.8     41.3  1
##  B            37.5 2.7 15     31.8     43.3  1
##  A            41.4 2.7 15     35.6     47.1  12
##  F            51.5 2.7 15     45.8     57.3   23
##  C            55.2 2.7 15     49.5     61.0    3
##
## Results are averaged over the levels of: Person
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 6 estimates
## significance level used: alpha = 0.05
```

```
detach("package:emmeans")
```

5. HSD Hand Calculation

```
qtukey(0.95, 6, 15)*sqrt( (3*453.61/15)/ (6*2))
```

```
## [1] 12.63357
```

```
qtukey(0.95, 6, 15)*3.8885/sqrt(2)
```

```
## [1] 12.63361
```

Interpretation (not required for credit): The emmeans differ between A and C, B and C, B and F, C and D, C and E, D and F, E and F are significant (greater than HSD0.05), same as the emmeans output.

BIBD Random Blocks

6. ANOVA Table

```
library(lme4)
library(lmerTest)
library(pbkrtest)
library(emmeans)
Model2 <- lmer(AreaRed ~ (1|Person) + Treatments, data = InData)
anova(Model2, ddf = "Kenward-Roger")
```

```
## Type III Analysis of Variance Table with Kenward-Roger's method
##            Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Treatments 1843.4  368.68     5 18.857  11.976 2.557e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

7. (**4pts**) CLD Display

```
emout2 <- emmeans(Model2, pairwise ~ Treatments)
CLD(emout2$emmeans)
```

```
##  Treatments emmean   SE df lower.CL upper.CL .group
##  E            33.1 2.85 24     27.2     38.9  1
##  D            34.9 2.85 24     29.0     40.8  1
##  B            36.1 2.85 24     30.2     42.0  1
##  A            41.8 2.85 24     36.0     47.7  12
##  F            50.8 2.85 24     44.9     56.7   23
##  C            56.1 2.85 24     50.2     62.0    3
##
## Degrees-of-freedom method: kenward-roger
## Confidence level used: 0.95
## P value adjustment: tukey method for comparing a family of 6 estimates
## significance level used: alpha = 0.05
```

```
detach("package:emmeans")
```

8. Comparing the two approaches:
   The ranking of the treatments is the same.
   The conclusions about significant differences is the same.

Varieties Fixed

9. ANOVA Table

```
library(emmeans)
library(car)
Varieties <- read.csv("C:/hess/STAT512/HW_2019/HW9/Varieties.csv")
#str(Varieties)
Model1 <- lm(Yield ~ Var, data = Varieties)
anova(Model1)
```

```
## Analysis of Variance Table
##
## Response: Yield
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Var        6 667.62 111.270  18.255 7.017e-06 ***
## Residuals 14  85.33   6.095
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

10. H0: $\mu_1 = \mu_2 = \mu_3 = \mu_4 = \mu_5 = \mu_6$
    OR
    H0: $\alpha_1 = \alpha_2 = \alpha_3 = \alpha_4 = \alpha_5 = \alpha_6$
    OR
    H0: population means for all varieties are the same.

11. emmeans

```
emmeans(Model1,  ~ Var)
```

```
##  Var emmean   SE df lower.CL upper.CL
##  A     18.3 1.43 14     15.3     21.4
##  B     31.0 1.43 14     27.9     34.1
##  C     22.7 1.43 14     19.6     25.7
##  D     25.0 1.43 14     21.9     28.1
##  E     33.7 1.43 14     30.6     36.7
##  F     17.3 1.43 14     14.3     20.4
##  G     22.7 1.43 14     19.6     25.7
##
## Confidence level used: 0.95
```

```
detach("package:emmeans")
```

Varieties Random

12. Random Effects

```
library(lme4)
library(lmerTest)
Model2 <- lmer(Yield ~ (1|Var), data = Varieties)
summary(Model2)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Yield ~ (1 | Var)
##    Data: Varieties
##
```

```
## REML criterion at convergence: 113.4
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.52307 -0.39126  0.01374  0.51853  1.36196
##
## Random effects:
##  Groups   Name        Variance Std.Dev.
##  Var      (Intercept) 35.039   5.919
##  Residual              6.097   2.469
## Number of obs: 21, groups:  Var, 7
##
## Fixed effects:
##             Estimate Std. Error     df t value Pr(>|t|)
## (Intercept)   24.381      2.301  6.005    10.6 4.14e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

13. Test of Variance
    H0: $\sigma^2_{var} = 0$.

```
rand(Model2)
```

```
## ANOVA-like table for random-effects: Single term deletions
##
## Model:
## Yield ~ (1 | Var)
##           npar  logLik    AIC    LRT Df Pr(>Chisq)
## <none>       3 -56.689 119.38
## (1 | Var)    2 -66.184 136.37 18.988  1  1.315e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

14. BLUPS

```
ranef(Model2)$Var + 24.381
```

```
##   (Intercept)
## A    18.66491
## B    30.63720
## C    22.76069
## D    24.96611
## E    33.15768
## F    17.71972
## G    22.76069
```