STAT512 – Exam 2
Spring 2018

Honor Pledge: I have not given, received, or used any unauthorized assistance on this exam.

Signature:_____

Printed Name: KEY

Instructions:

- **Open book, open notes, calculator required. No computers or cell phones.**
- **Time limit is 1 hour 50 minutes - strictly enforced!**
- If an answer is in the computer output, use it; don't calculate it by hand.
- Show your work where appropriate. Put your final answer in the box (if provided).
- Make explanations brief and legible.
- All questions are worth 4 points except where noted. Maximum score is 100.
- Computer input/output is provided at the end of the exam.
- The exam contains a total of 13 pages (including computer input/output).
- If you run out of space, you may use the blank area on page 6.

Questions 1 through 2: An experiment was done to investigate the material hardness (**Y**) of 4 **trts** (A,B,C,D). The experiment took a total of 4 **days** to complete, because a group of 4 units are sprayed and left to dry in a ventilated hood overnight and tested the following day. It was thought that **position** (1,2,3,4) in the hood may affect the resulting hardness (Y) of the material. Suppose now that random assignments were made such that each treatment was represented exactly once on each day (1,2,3,4) and each position (1,2,3,4). There are a total of 4 trts * 4 reps =16 observations.

	Day1	Day2	Day3	Day4
Pos1	A	D	C	B
Pos2	B	A	D	C
Pos3	C	B	A	D
Pos4	D	C	B	A

1. What is the name for this design? Circle one answer.

CRD RCB (Latin Square) Split-Plot

2. Provide R code to fit an appropriate model. (I am just looking for a single line of R code.)

lm(Y ~ Trt + Day + Pos)

Questions 3 through 13 (Feed Trial): A study was done to investigate a new vitamin supplement for cattle. A successful supplement would increase **ADG** (average daily gain) in cattle. Three **Feed** formulations (A, B, C) and two levels of **Suppl** (0 or 1) were considered. Feeds are expected to be different, so the research question focused on the effect of Suppl for each Feed. A total of 24 pens of cattle were randomly assigned to one of 6 treatment combinations (2 Suppl x 3 Feed), ADG was recorded at the end of the study. The R input and output are labeled **Feed Trial.** Use $\alpha = 0.05$. → such that there are exactly 4 pens for each trt combo

Questions 3 through 7: The following questions use **just the Model1** results.

3. Considering the **emmeans1 $emmeans** output, a colleague notices that that SE is the same for each of the treatment combinations (SE = 0.072). Briefly explain why the SE is the same.

   Model based SE assuming equal variance (and we have a balanced design)

   Note: Need more than balanced design

4. Considering the **emmeans1** and **emmeans2 $contrasts** output, both are comparing levels of Suppl. Briefly explain the difference between the two sets of comparisons (for someone with little knowledge of statistics).

   emmeans1 compares Supple 0 vs 1 at each level of Feed.
   emmeans2 compares Supple 0 vs 1 averaging over levels of Feed.

5. Calculate the **F test statistic** corresponding to the main effect of **Suppl.**

$$F = \frac{MS\ Supple}{MS\ Resid} = \frac{(0.459/1)}{(0.373/18)} = 22.15$$

F=22.15

6. What is the **p-value** corresponding to the test of main effect of **Suppl**? Hint: This information appears elsewhere in the output.

   emmeans2 $contrasts output.

   0.0002

7. A colleague notices that the Feed:Suppl interaction is not significant (F = 2.301, p = 0.1288). He says that since the interaction is not significant, based on the "Factorial Principle" that it is wrong to present the **emmeans1** comparisons and only the **emmeans2** comparisons should be considered. Do you agree? Briefly discuss.

   When interaction is not significant we can increase power by focusing on main effect comparisons (emmeans2) but it is OK to look at interaction comparisons (emmeans1). Think about research questions.

Questions 8 through 10 (Feed Trial continued): The following questions compare **Models 1 and 2**.

8. Briefly explain the difference between Models 1 and 2.

Model 1 includes Feed:Supp1 interaction
Model 2 only includes main effects.

9. Is there any advantage to using Model2 (as compared to Model1)? Discuss. Hint: Think in terms of power, but there may be other approaches.

Not much advantage.
* Slight increase in dfResid from 18 → 20
but also increase in MSResid from 0.0207 → 0.0234
SE=0.059 → SE=0.062

10. Is there any disadvantage to using Model2 (as compared to Model1)? Discuss. Hint: Consider the emmeans3 and emmeans4 results.

Cannot estimate interaction contrasts!
Actually increase SE for main effect of Supp1 (see above)

Questions 11 through 13 (Feed Trial continued): Now return to **Model 1** and consider the following scenarios.

11. Suppose (just for this question), that the data had not been balanced. For example, 2 (out of 6) treatment combinations had 3 pens (instead of 4) for a total of 22 pens for the study. What modifications to the R code would be required?

No changes required.
Already using Type 3 tests and emmeans.

12. Suppose (just for this question), that the investigators had recorded the initial weight (Weight0) of each pen and wanted to include Weight0 as a covariate in the model. Provide R code to fit an appropriate model. (I am just looking for a single line of R code.)

lm(ADG ~ Feed * Supp + Weight0)

Gave full credit for Feed*Supp*Weight, but additive covariate typical.

13. Each pen included 5 cows. In our analysis, the ADG value is really the average over the 5 individual cows. It is known that ADG for cows within the same pen will be correlated. Suppose (just for this question), that we had the ADG values for each of the 120 cows (6 Trts * 4 Pens/Trt * 5 cows/Pen) and the data contained a column giving PenID (1-24). Provide R code to fit an appropriate model. (I am just looking for a single line of R code).

Pens nested within Feed*Supp

lmer(ADG ~ Feed * Supp + (1|PenID))

-4 for fixed Pen

24

Questions 14 through 19 (Germination): A study was done to investigate the effect of temperature on germination rate of seeds for a certain variety of wheat. Temperature (**Temp**) ranged between 5 and 30 degrees (Celsius). At each level of temperature 40 seeds were tested (**Ntest** = 40) and the number that germinated (**Ngerm**) were recorded. The goal of the analysis is to model the probability of germination as a function of temperature. The R input and output are labeled **Germination**.

14. Briefly explain the difference between **Models 1 and 2.** Note: I am looking for more than the R function!

Model 1 linear regression
Model 2 logistic regression

15. For **Model1**, identify and interpret the slope. Be specific.

A 1° increase in Temp is associated with 0.013 (additive) increase in predicted probability (or proportion) germination

16. For **Model2**, identify and interpret the "slope". Be specific.

A 1° increase in Temp is associated with exp(0.055) = 1.056 (or 5.6%) multiplicative increase in the predicted odds of germination

17. Comparing the plots of **both models**, does one model seem to fit better? Or is there any evidence of "lack of fit" for either model?

Both models provide similar predicted values (over observed range of Temp).
No lack of fit

18. Looking at the predicted values for **both models**, we get similar predicted values at Temp = 18 but noticeably different predicted values at Temp = 60. Explain why the predicted values are so different at Temp = 60. Be specific. (I am looking for more than that we are using two different models).

Temp	PredMod1	PredMod2
18	0.527	0.529
60	**1.085**	**0.918**

Model 2 allows a non-linear response.
Curvature beyond the range of data.

19. Do you feel "confident" in the prediction at Temp = 60 for either model? Briefly discuss.

No Model 1 gives predicted prop/prob > 1 (which makes no sense).
But even Model 2 we are extrapolating beyond the ranges of the data.

Questions 20 through 25: An RCB analysis was done using R. There are a total of 3 Trts * 5 Blocks =15 observations. See ANOVA table below.

```
Anova Table (Type III tests)

            Sum Sq Df F value    Pr(>F)
(Intercept) 333.55  1 733.732 3.716e-09 ***
Block         5.75  4   3.161    0.0778 .
Trt          53.27  2  58.587 1.668e-05 ***
Residuals     3.64  8
```

20. Calculate the SE for the difference between Trt means. Show your work to receive full credit.

$$SE = \sqrt{\frac{2 \cdot MSResid}{n}} = \sqrt{\frac{2 \cdot (3.64/8)}{5}} = 0.426$$

-2 for wrong "n"

0.426

21. Could a Block*Trt interaction have been included in this model? Discuss. Hint: Think about df.

No. The interaction would require 8 df. This would leave 0 df for Resid.

Note: Need more than just reduce df reduces power.

22. Suppose (just for this question) that Block had been dropped from the model, would dfResid be higher or lower? **(2 pts)**

(Higher) Lower

23. Suppose (just for this question) that Block had been dropped from this model, would SSResid be higher or lower? **(2 pts)**

(Higher) Lower

24. All other things held equal, will a model with higher dfResid have higher or lower power? **(2 pts)**

(Higher) Lower

25. All other things held equal, will a model with higher MSResid have higher or lower power? **(2 pts)**

Higher (Lower)

Questions continue on the next page....

Questions 26 through 27: An experiment was done to compare Yield (**Y**) for 5 **Varieties** * 3 **Herbicides** = 15 treatment combinations. Four **Blocks** of fifteen plots were laid out in a field. Within each block, five **Varieties** (A,B,C,D,E) were randomly assigned to North-South columns. Within each column, three **Herbicide** treatments (1,2,3) were randomly assigned. There are a total of 15 trts * 4 blocks = 60 observations. The layout for block 1 is shown below (but remaining blocks are not shown!).

D2	A2	E1	B3	C1
D3	A1	E2	B1	C3
D1	A3	E3	B2	C2

26. What is the name for this design? Circle one answer.

CRD RCB Latin Square (Split-Plot)

Var = Whole Plot Factor
Herb = Sub Plot Factor

27. Provide R code for analysis. (I am just looking for a single line of R code.)

lmer(Y ~ Var * Herb + (1|Block) + (1|Block:Var))

-2 for (1|Block:Herb) instead of Block:Var

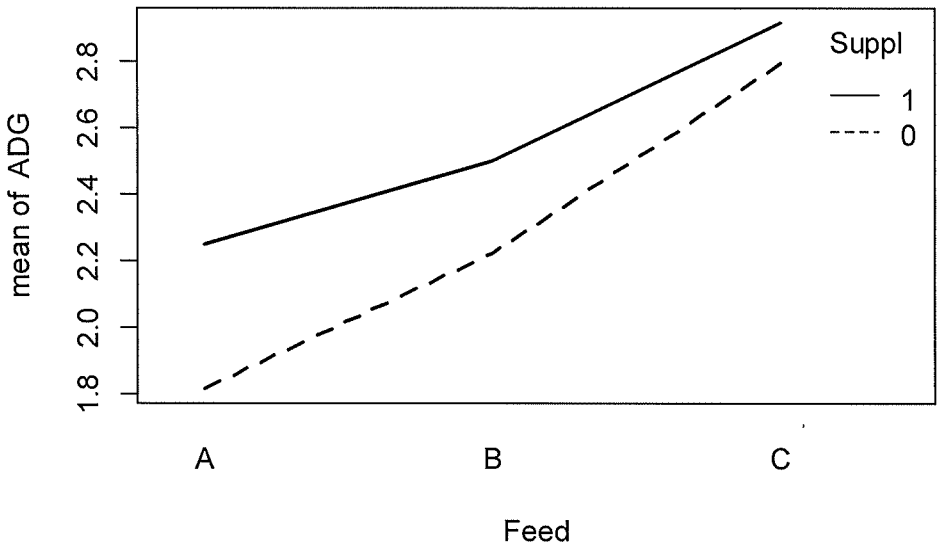
Feed Trial (Questions 3 through 13)

```
library(dplyr)
library(car)
library(emmeans)
FeedData$Suppl <- as.factor(FeedData$Suppl)
str(FeedData)
SumStats <- summarize(group_by(FeedData, Feed, Suppl),
                      n = n(),
                      mean = mean(ADG),
                      sd   = sd(ADG),
                      SE   = sd/sqrt(n))
SumStats
with(interaction.plot(Feed, Suppl, ADG, lwd = 2), data = FeedData)
#MODEL1
options(contrasts = c("contr.sum", "contr.poly"))
Model1 <- lm(ADG ~ Feed*Suppl, data = FeedData)
Anova(Model1, type = 3)
#EMMEANS1
emmeans(Model1, pairwise ~ Suppl|Feed)
#EMMEANS2
emmeans(Model1, pairwise ~ Suppl)
#MODEL2
Model2 <- lm(ADG ~ Feed + Suppl, data = FeedData)
Anova(Model2, type = 3)
#EMMEANS3
emmeans(Model2, pairwise ~ Suppl|Feed)
#EMMEANS4
emmeans(Model2, pairwise ~ Suppl)
```

```
> library(dplyr)
> library(car)
> library(emmeans)
> FeedData$Suppl <- as.factor(FeedData$Suppl)
> str(FeedData)
Classes 'tbl_df', 'tbl' and 'data.frame':   24 obs. of  4 variables:
 $ Feed : chr  "A" "A" "A" "A" ...
 $ Suppl: Factor w/ 2 levels "0","1": 1 1 1 1 2 2 2 2 1 1 ...
 $ ADG  : num  1.55 1.81 1.99 1.93 2.2 ...
> SumStats <- summarize(group_by(FeedData, Feed, Suppl),
+                       n = n(),
+                       mean = mean(ADG),
+                       sd   = sd(ADG),
+                       SE   = sd/sqrt(n))
```

Feed Trial continued (Questions 3 through 13)

```
> SumStats
# A tibble: 6 x 6
# Groups: Feed [?]
  Feed  Suppl     n  mean     sd     SE
  <chr> <fct> <int> <dbl>  <dbl>  <dbl>
1 A     0         4  1.82 0.195  0.0976
2 A     1         4  2.25 0.0449 0.0224
3 B     0         4  2.22 0.0861 0.0430
4 B     1         4  2.50 0.167  0.0833
5 C     0         4  2.79 0.147  0.0735
6 C     1         4  2.92 0.165  0.0826
> with(interaction.plot(Feed, Suppl, ADG, lwd = 2), data = FeedData)
```




```
> #MODEL1
> options(contrasts = c("contr.sum", "contr.poly"))
> Model1 <- lm(ADG ~ Feed*Suppl, data = FeedData)
> Anova(Model1, type = 3)
Anova Table (Type III tests)
Response: ADG
             Sum Sq Df  F value    Pr(>F)
(Intercept) 140.052  1 6764.833 < 2.2e-16 ***
Feed          2.752  2   66.458 4.885e-09 ***
Suppl         0.459  1
Feed:Suppl    0.095  2    2.301 0.1288688
Residuals     0.373 18
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Feed Trial continued (Questions 3 through 13)

```
> #EMMEANS1
> emmeans(Model1, pairwise ~ Suppl|Feed)
$emmeans
Feed = A:
 Suppl   emmean         SE df lower.CL upper.CL
 0     1.816961 0.07194272 18 1.665815 1.968107
 1     2.247085 0.07194272 18 2.095939 2.398231

Feed = B:
 Suppl   emmean         SE df lower.CL upper.CL
 0     2.220061 0.07194272 18 2.068915 2.371207
 1     2.498621 0.07194272 18 2.347475 2.649768

Feed = C:
 Suppl   emmean         SE df lower.CL upper.CL
 0     2.794944 0.07194272 18 2.643798 2.946090
 1     2.916420 0.07194272 18 2.765274 3.067566

$contrasts
Feed = A:
 contrast   estimate        SE df t.ratio p.value
 0 - 1    -0.4301239 0.1017424 18  -4.228  0.0005

Feed = B:
 contrast   estimate        SE df t.ratio p.value
 0 - 1    -0.2785603 0.1017424 18  -2.738  0.0135

Feed = C:
 contrast   estimate        SE df t.ratio p.value
 0 - 1    -0.1214767 0.1017424 18  -1.194  0.2480

> #EMMEANS2
> emmeans(Model1, pairwise ~ Suppl)
NOTE: Results may be misleading due to involvement in interactions
$emmeans
 Suppl   emmean         SE df lower.CL upper.CL
 0     2.277322 0.04153615 18 2.190058 2.364586
 1     2.554042 0.04153615 18 2.466778 2.641306

$contrasts
 contrast   estimate        SE df t.ratio p.value
 0 - 1    -0.2767203 0.05874098 18  -4.711  0.0002

Results are averaged over the levels of: Feed
```

Feed Trial continued (Questions 3 through 13)

```
> #MODEL2
> Model2 <- lm(ADG ~ Feed + Suppl, data = FeedData)
> Anova(Model2, type = 3)
Anova Table (Type III tests)
Response: ADG
             Sum Sq Df  F value    Pr(>F)
(Intercept) 140.052  1 5986.075 < 2.2e-16 ***
Feed          2.752  2   58.807 4.204e-09 ***
Suppl         0.459  1   19.637 0.0002567 ***
Residuals     0.468 20
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> #EMMEANS3
> emmeans(Model2, pairwise ~ Suppl|Feed)
$emmeans
Feed = A:
 Suppl   emmean         SE df lower.CL upper.CL
 0     1.893662 0.06244515 20 1.763404 2.023921
 1     2.170383 0.06244515 20 2.040124 2.300641

Feed = B:
 Suppl   emmean         SE df lower.CL upper.CL
 0     2.220981 0.06244515 20 2.090723 2.351239
 1     2.497701 0.06244515 20 2.367443 2.627960

Feed = C:
 Suppl   emmean         SE df lower.CL upper.CL
 0     2.717322 0.06244515 20 2.587064 2.847580
 1     2.994042 0.06244515 20 2.863784 3.124300

$contrasts
Feed = A:
 contrast   estimate         SE df t.ratio p.value
 0 - 1    -0.2767203 0.06244515 20  -4.431  0.0003

Feed = B:
 contrast   estimate         SE df t.ratio p.value
 0 - 1    -0.2767203 0.06244515 20  -4.431  0.0003

Feed = C:
 contrast   estimate         SE df t.ratio p.value
 0 - 1    -0.2767203 0.06244515 20  -4.431  0.0003
```

See next page...

Feed Trial continued (Questions 3 through 13)

```
> #EMMEANS4
> emmeans(Model2, pairwise ~ Suppl)
$emmeans
 Suppl   emmean         SE df lower.CL upper.CL
 0     2.277322 0.04415539 20 2.185215 2.369428
 1     2.554042 0.04415539 20 2.461936 2.646149


$contrasts
 contrast   estimate         SE df t.ratio p.value
 0 - 1    -0.2767203 0.06244515 20  -4.431  0.0003
Results are averaged over the levels of: Feed
```

Germination (Questions 14 through 19)

```
GermData$PropGerm <- GermData$Ngerm/GermData$Ntest
GermData
#Model1
Model1 <- lm(PropGerm ~ Temp, data = GermData)
summary(Model1)
#Model2
Model2 <- glm(cbind(Ngerm, Ntest-Ngerm) ~ Temp, family = binomial(link = "
logit"), data = GermData)
summary(Model2)
#Predictions (both models)
NewData <- data.frame(Temp = c(18, 60))
Predictions <- data.frame(NewData,
                          PredMod1 = predict(Model1, NewData),
                          PredMod2 = predict(Model2, NewData,
                                             type = "response"))
Predictions
```

```
> GermData$PropGerm <- GermData$Ngerm/GermData$Ntest
> GermData
  Temp Ntest Ngerm PropGerm
1    5    40    13    0.325
2   10    40    17    0.425
3   15    40    21    0.525
4   20    40    23    0.575
5   25    40    24    0.600
6   30    40    27    0.675

> #Model1
> Model1 <- lm(PropGerm ~ Temp, data = GermData)
> summary(Model1)
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 0.288333   0.026730  10.787 0.000419 ***
Temp        0.013286   0.001373   9.678 0.000638 ***

Residual standard error: 0.02871 on 4 degrees of freedom
Multiple R-squared:  0.959,     Adjusted R-squared:  0.9488
F-statistic: 93.67 on 1 and 4 DF,  p-value: 0.0006377
```

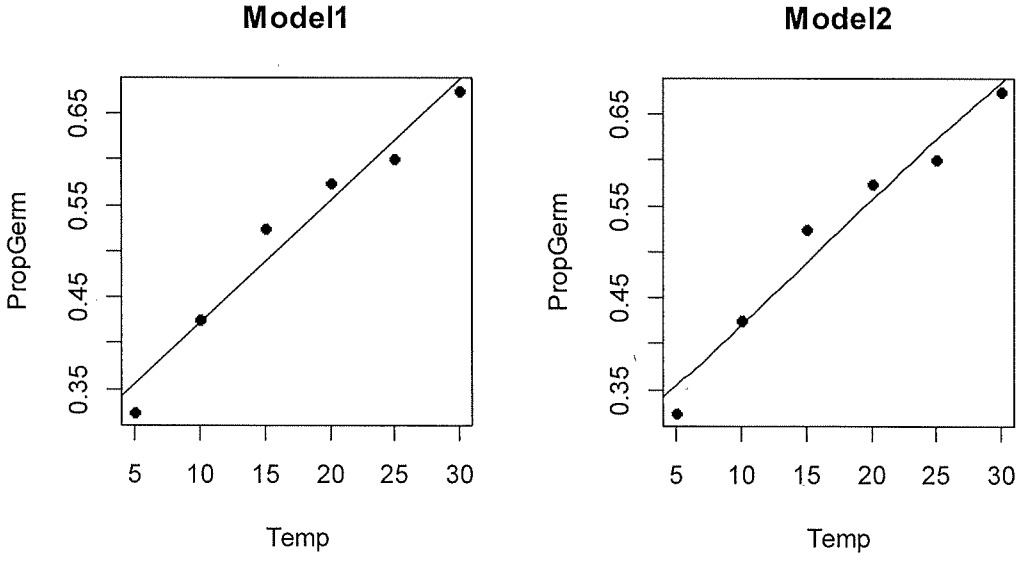
Germination continued (Questions 14 through 19)

```
> #Model2
> Model2 <- glm(cbind(Ngerm, Ntest-Ngerm) ~ Temp, family = binomial(link =
"logit"), data = GermData)
> summary(Model2)
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.87292    0.30515  -2.861 0.004228 **
Temp         0.05491    0.01585   3.464 0.000533 ***

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 13.11149  on 5  degrees of freedom
Residual deviance:  0.54339  on 4  degrees of freedom
AIC: 29.117

> #Predictions (both models)
> NewData <- data.frame(Temp = c(18, 60))
> Predictions <- data.frame(NewData,
+                 PredMod1 = predict(Model1, NewData),
+                 PredMod2 = predict(Model2, NewData, type = "response"))
> Predictions
  Temp  PredMod1  PredMod2
1   18 0.5274762 0.5288117
2   60 1.0854762 0.9184448
> #Plots (both models)
> #Model1
> plot(PropGerm ~ Temp, data = GermData, main = "Model1")
> abline(coef(Model1))
> #Model2
> TempRange <- seq(0, 35, 0.5)
> phat <- predict(Model2, list(Temp = TempRange), type = "response")
> plot(PropGerm ~ Temp, data = GermData, main = "Model2")
> lines(phat ~ TempRange)
```



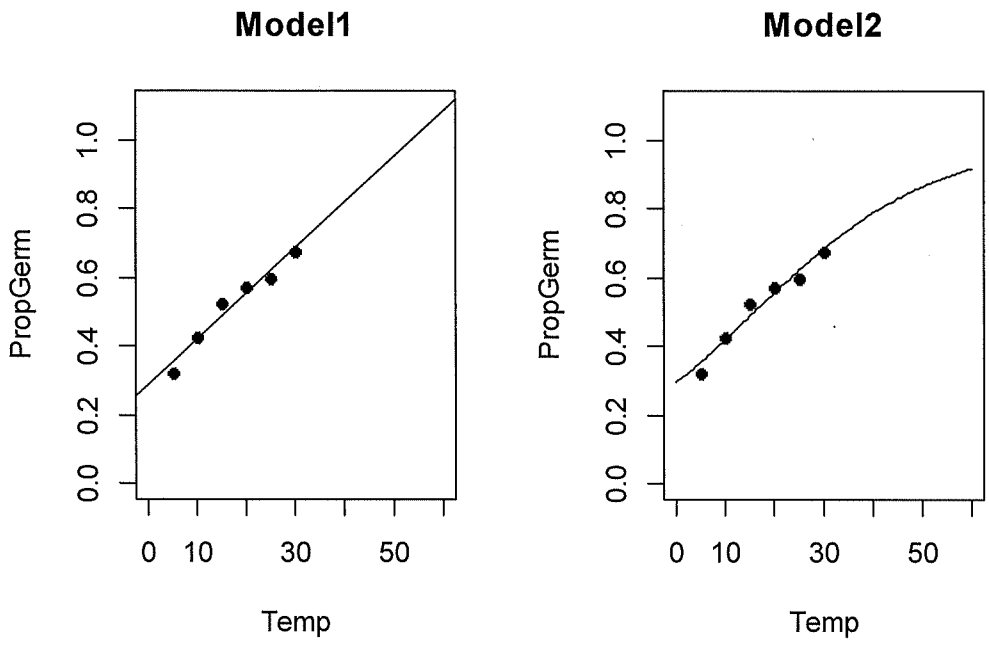
Exam 2 "Extra" Output

Note: This information was NOT provided during the original exam!

#5, 6

```
> Anova(Model1, type = 3)
Anova Table (Type III tests)
Response: ADG
             Sum Sq Df  F value    Pr(>F)
(Intercept) 140.052  1 6764.833 < 2.2e-16 ***
Feed          2.752  2   66.458 4.885e-09 ***
Suppl         0.459  1   22.192 0.0001743 ***
Feed:Suppl    0.095  2    2.301 0.1288688
Residuals     0.373 18
```

#18, 19



#20

```
> library(emmeans)
> emmeans(Model, pairwise ~ Trt)

$contrasts
 contrast  estimate        SE df t.ratio p.value
 A - B    -1.892546 0.4264264  8  -4.438  0.0055
 A - C    -4.592350 0.4264264  8 -10.769  <.0001
 B - C    -2.699804 0.4264264  8  -6.331  0.0006
```

#21

```
> Model2 <- lm(Y ~ Block*Trt, data = RCBData)
> anova(Model2)
Analysis of Variance Table
Response: Y
          Df Sum Sq Mean Sq F value Pr(>F)
Block      4  5.748  1.4370
Trt        2 53.267 26.6336
Block:Trt  8  3.637  0.4546
Residuals  0  0.000
Warning message:
In anova.lm(Model2) :
  ANOVA F-tests on an essentially perfect fit are unreliable
```