HW 10

Ted Henson

4/17/2020

Chapter 13, questions 1 and 3 (pp. 294-295), but omitting 1(h).

Question 1

a)

```
library(faraway)
data(ohio)
length(unique(ohio$id))
```

```
## [1] 537
```

```
nrow(unique(ohio[, c('id', 'smoke')])))
```

```
## [1] 537
```

No, all mothers had the same smoking status throughout because all of the children's mothers had the same status for each child.

b)

```
library(ggplot2)
library(tidyverse)
```

```
## -- Attaching packages ----------------------- tidyverse 1.3.0 --
```

```
## v tibble  2.1.3      v dplyr   0.8.4
## v tidyr   1.0.2      v stringr 1.4.0
## v readr   1.3.1      v forcats 0.4.0
## v purrr   0.3.3
```

```
## -- Conflicts -------------------------- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
ohio = ohio %>% group_by(id) %>% mutate(years = sum(resp))
sum.table = ohio %>% group_by(smoke,
                              years) %>% summarise(num.wheeze = n())
sum.table = sum.table %>% group_by(smoke) %>% mutate(prop.wheeze = num.wheeze / sum(num.wheeze))
sum.table
```

```
## # A tibble: 10 x 4
## # Groups:   smoke [2]
##    smoke years num.wheeze prop.wheeze
##    <int> <int>      <int>       <dbl>
```

```
## 1     0     0        948    0.677
## 2     0     1        260    0.186
## 3     0     2        100    0.0714
## 4     0     3         48    0.0343
## 5     0     4         44    0.0314
## 6     1     0        472    0.631
## 7     1     1        128    0.171
## 8     1     2         76    0.102
## 9     1     3         44    0.0588
## 10    1     4         28    0.0374
```
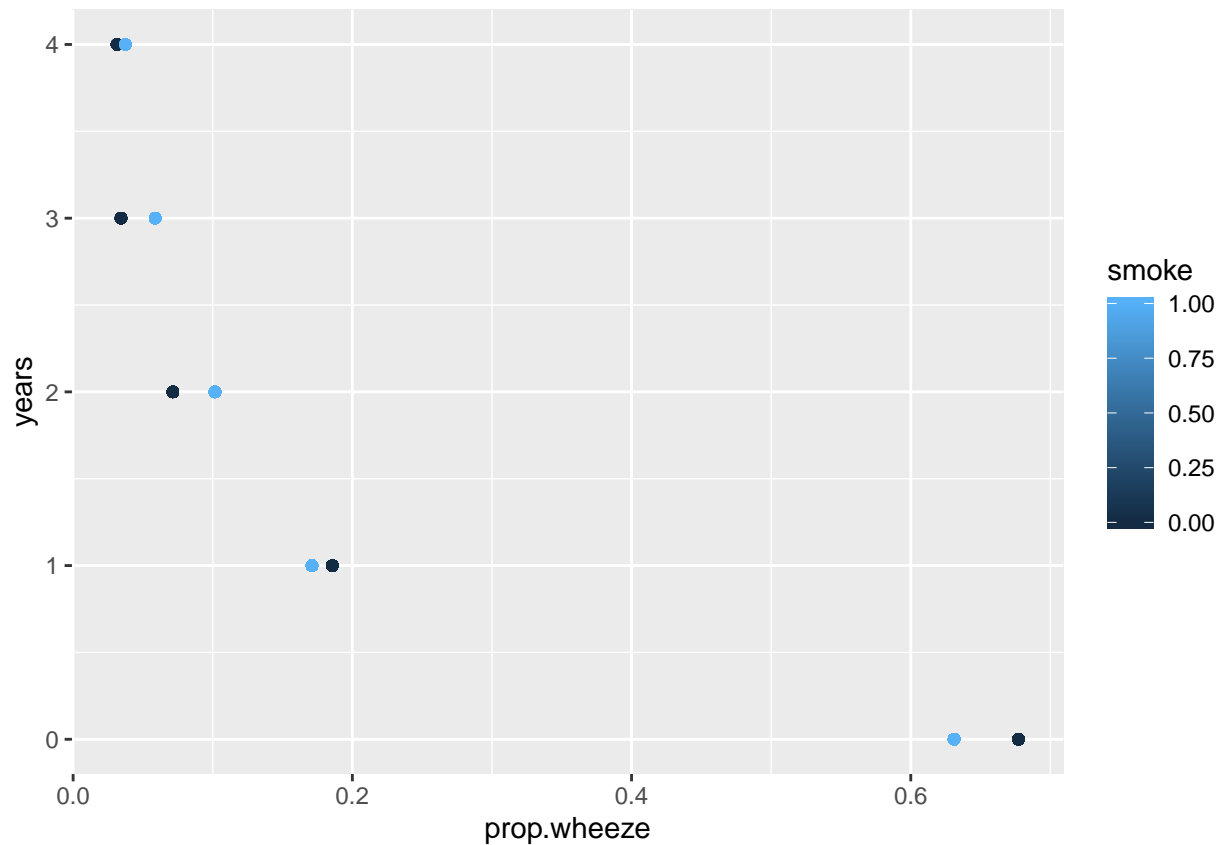
c)

```
ohio = left_join(ohio, sum.table)
```

```
## Joining, by = c("smoke", "years")
```

```
smokers = ohio %>% dplyr::filter(smoke == 1)
non.smokers = ohio %>% dplyr::filter(smoke == 0)

ggplot(ohio, aes(prop.wheeze, years,
                 col = smoke)) + geom_point()
```

d)

```r
ohio  = ohio %>% group_by(id) %>% mutate(total = sum(resp) / 4)
ohio = unique(ohio)
mod = glm(total ~ smoke, data = ohio, family = 'quasibinomial')
summary(mod)
```

```
##
## Call:
## glm(formula = total ~ smoke, family = "quasibinomial", data = ohio)
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.6205  -0.5477  -0.5477   0.2931   1.9856
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.82124    0.05534 -32.911  < 2e-16 ***
## smoke        0.27156    0.08842   3.071  0.00216 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasibinomial family taken to be 0.5139862)
##
##     Null deviance: 1045.3  on 2147  degrees of freedom
## Residual deviance: 1040.5  on 2146  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

This does not prove that there is a smoking effect because it could be due to random chance. The graph plotting years by smoking did not show any obvious difference.

e)

```r
library(MASS)
```

```
##
## Attaching package: 'MASS'
```

```
## The following object is masked from 'package:dplyr':
##
##     select
```

```r
modpq=glmmPQL(resp~age + smoke,random=~1|id,
              family=binomial, data=ohio)
```

```
## iteration 1
```

```
## iteration 2
```

```
## iteration 3
```

```
## iteration 4
```

```
## iteration 5
```

```
## iteration 6
```

```
## iteration 7
```

```
## iteration 8
```

```
summary(modpq)
```

```
## Linear mixed-effects model fit by maximum likelihood
##   Data: ohio
##    AIC BIC logLik
##     NA  NA     NA
##
## Random effects:
##  Formula: ~1 | id
##         (Intercept)  Residual
## StdDev:    2.057175 0.6355563
##
## Variance function:
##   Structure: fixed weights
##   Formula: ~invwt
## Fixed effects: resp ~ age + smoke
##                   Value  Std.Error   DF   t-value p-value
## (Intercept) -2.7658365 0.14218299 1610 -19.452654  0.0000
## age         -0.1815756 0.04365164 1610  -4.159652  0.0000
## smoke        0.3251839 0.23131699  535   1.405793  0.1604
##  Correlation:
##       (Intr) age
## age    0.197
## smoke -0.591 -0.003
##
## Standardized Within-Group Residuals:
##        Min         Q1        Med         Q3        Max
## -2.6145143 -0.2829352 -0.2583719 -0.2154580  3.4443795
##
## Number of Observations: 2148
## Number of Groups: 537
```

Age has a significant effect whereas we do not have significant evidence by the p value to conclude that smoking has an effect.

f)

```
library(lme4)
```

```
## Loading required package: Matrix
```

```
##
## Attaching package: 'Matrix'
```

```
## The following objects are masked from 'package:tidyr':
##
##     expand, pack, unpack
```

```
modgh=glmer(resp~age + smoke + (1|id),
            nAGQ=25,family=binomial,ohio)
summary(modgh)
```

```
## Generalized linear mixed model fit by maximum likelihood (Adaptive
```

```
##   Gauss-Hermite Quadrature, nAGQ = 25) [glmerMod]
##  Family: binomial  ( logit )
## Formula: resp ~ age + smoke + (1 | id)
##    Data: ohio
##
##      AIC      BIC   logLik deviance df.resid
##   1603.3   1626.0   -797.6   1595.3     2144
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.3730 -0.2011 -0.1773 -0.1487  2.5076
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  id     (Intercept) 4.687    2.165
## Number of obs: 2148, groups:  id, 537
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept) -3.10153    0.21905 -14.159  < 2e-16 ***
## age         -0.17563    0.06768  -2.595  0.00946 **
## smoke        0.39857    0.27310   1.459  0.14444
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##       (Intr) age
## age    0.244
## smoke -0.493 -0.008
```

The fit and the p values were almost identical.

g)

```r
library(INLA)
```

```
## Warning: package 'INLA' was built under R version 3.6.3
```

```
## Loading required package: sp
```

```
## Loading required package: parallel
```

```
## Loading required package: foreach
```

```
##
## Attaching package: 'foreach'
```

```
## The following objects are masked from 'package:purrr':
##
##     accumulate, when
```

```
## This is INLA_20.03.17 built 2020-03-17 07:56:40 UTC.
## See www.r-inla.org/contact-us for how to get help.
```

```r
formula=resp~smoke +age +f(id,model='iid')
result=inla(formula,family='binomial',data=ohio)

# some of these variables are self-contained arrays or tables, for example
```

```
result$summary.fixed
```

```
##                   mean         sd  0.025quant    0.5quant  0.975quant        mode
## (Intercept) -2.9926148 0.20198593 -3.41021139 -2.9848420 -2.61864794 -2.9689392
## smoke        0.3916691 0.23957133 -0.07770196  0.3910664  0.86383006  0.3898967
## age         -0.1665735 0.06284433 -0.29056761 -0.1663700 -0.04382792 -0.1659583
##                      kld
## (Intercept) 8.978664e-05
## smoke       8.853180e-07
## age         7.628634e-07
```

```
result$summary.hyperpar
```

```
##                      mean         sd 0.025quant  0.5quant 0.975quant      mode
## Precision for id 0.2752962 0.04625775  0.1962147 0.2712994   0.377395 0.2635789
# others are complocated objects in their own right, for example
```

```
names(result$marginals.fixed)
```

```
## [1] "(Intercept)" "smoke"       "age"
```

The model shows that across the distribution age is negatively associated with resp and smoke has a high
degree of variability so we cannot conclude that it is related to resp.

i)

```
library(geepack)
```

```
## Warning: package 'geepack' was built under R version 3.6.3
```

```
##
## Attaching package: 'geepack'
```

```
## The following object is masked _by_ '.GlobalEnv':
##
##     ohio
```

```
## The following object is masked from 'package:faraway':
##
##     ohio
```

```
modgeep=geeglm(resp~ age + smoke,id=id,
              corstr='ar1',scale.fix=T,data=ohio,family=binomial)
```

```
summary(modgeep)
```

```
##
## Call:
## geeglm(formula = resp ~ age + smoke, family = binomial, data = ohio,
##     id = id, corstr = "ar1", scale.fix = T)
##
##  Coefficients:
##             Estimate  Std.err     Wald Pr(>|W|)
## (Intercept) -1.90262  0.11533  272.174   <2e-16 ***
## age         -0.11490  0.04544    6.394   0.0115 *
## smoke        0.23340  0.18137    1.656   0.1981
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation structure = ar1
## Scale is fixed.
##
##   Link = identity
##
## Estimated Correlation Parameters:
##       Estimate Std.err
## alpha   0.5007 0.03799
## Number of clusters:   537  Maximum cluster size: 4
```

The model agrees with the previous models that smoking is not significant, but age is. The alpha of .5 with a small standard error shows that there is a high liklihood of autocorrelation within children: a child who already wheezes is likely to continue to wheeze.
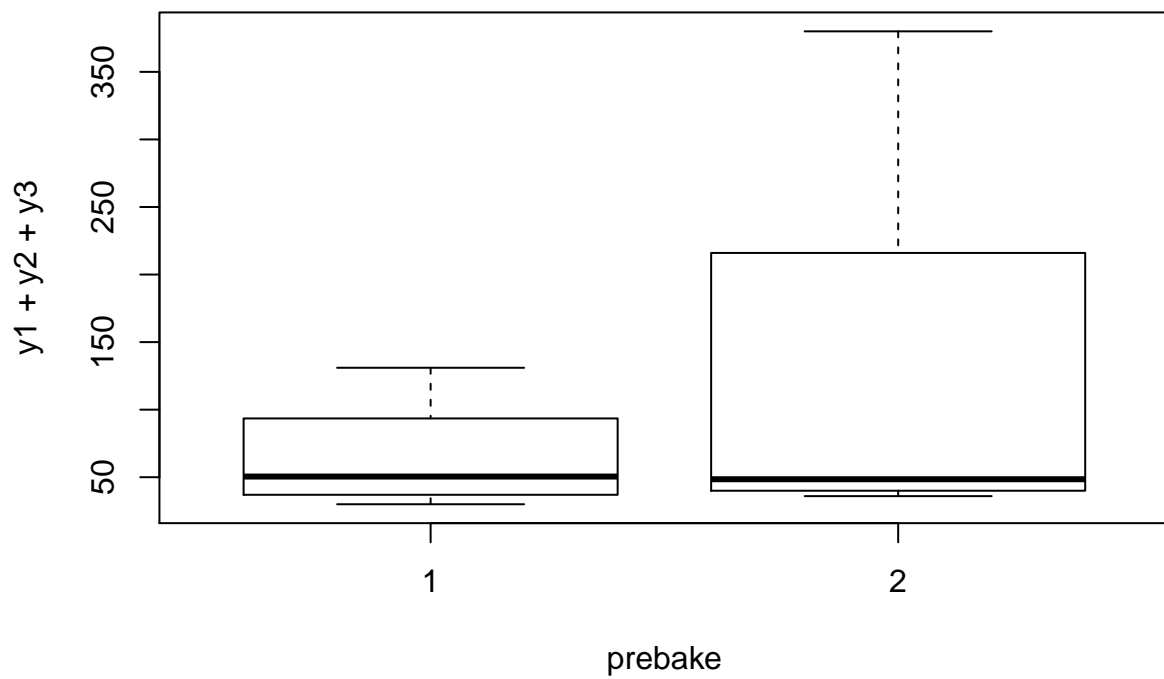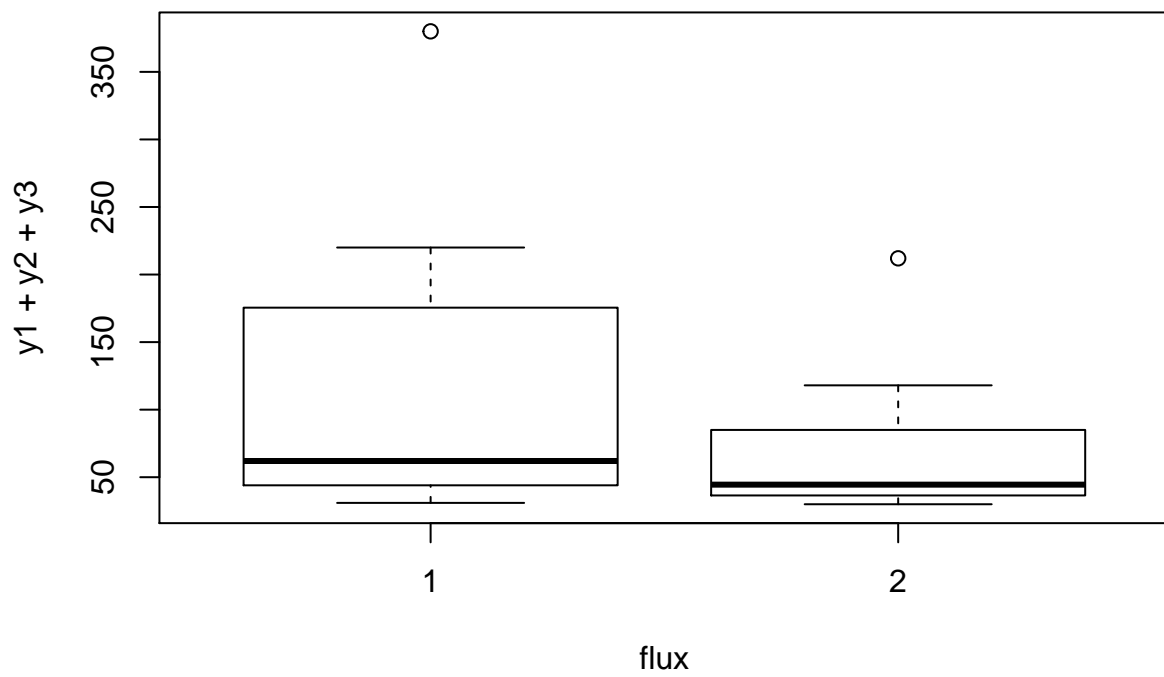
Question 3

a)
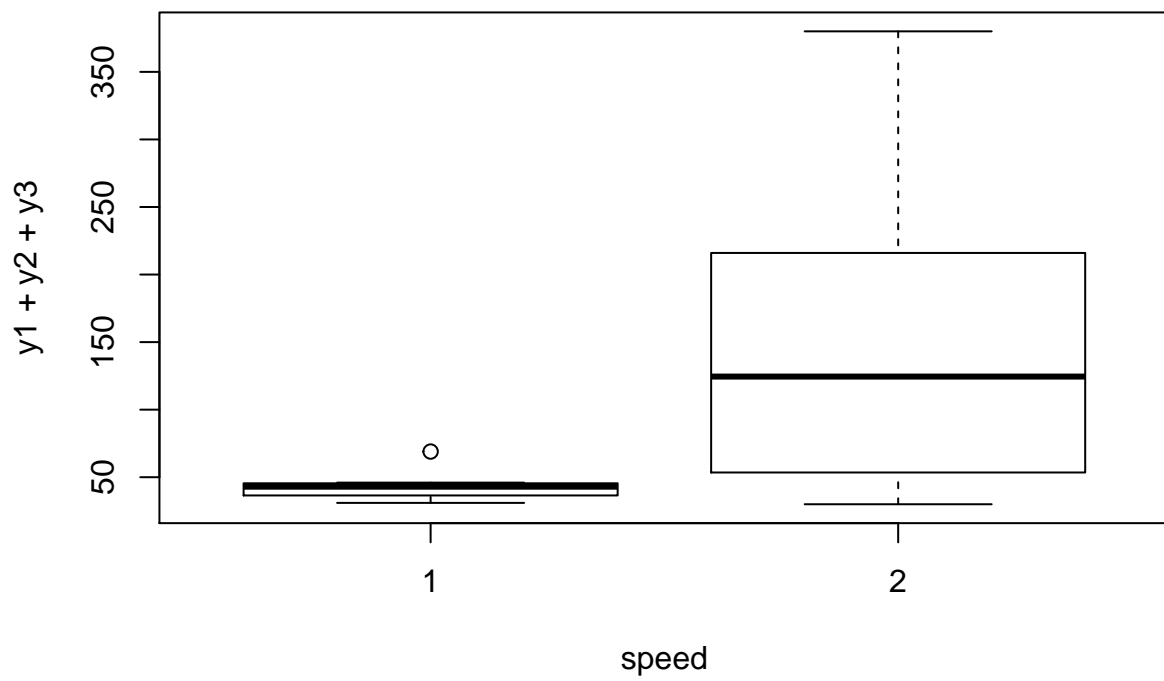
```
data(wavesolder)
head(wavesolder)
```

```
##    y1 y2 y3 prebake flux speed preheat cooling agitator temp
## 1 13 30 26       1    1     1       1       1        1    1
## 2  4 16 11       1    1     1       2       2        2    2
## 3 20 15 20       1    1     2       1       1        2    2
## 4 42 43 46       1    1     2       2       2        1    1
## 5 14 15 17       1    2     1       1       2        1    2
## 6 10 17 16       1    2     1       2       1        2    1
```
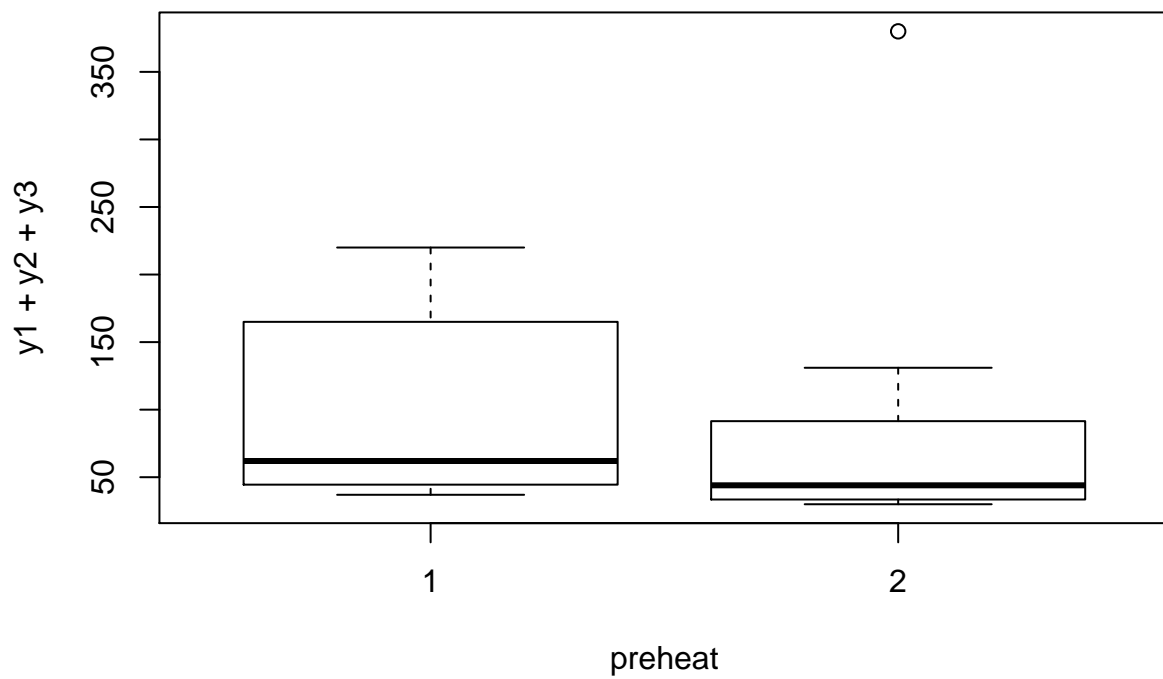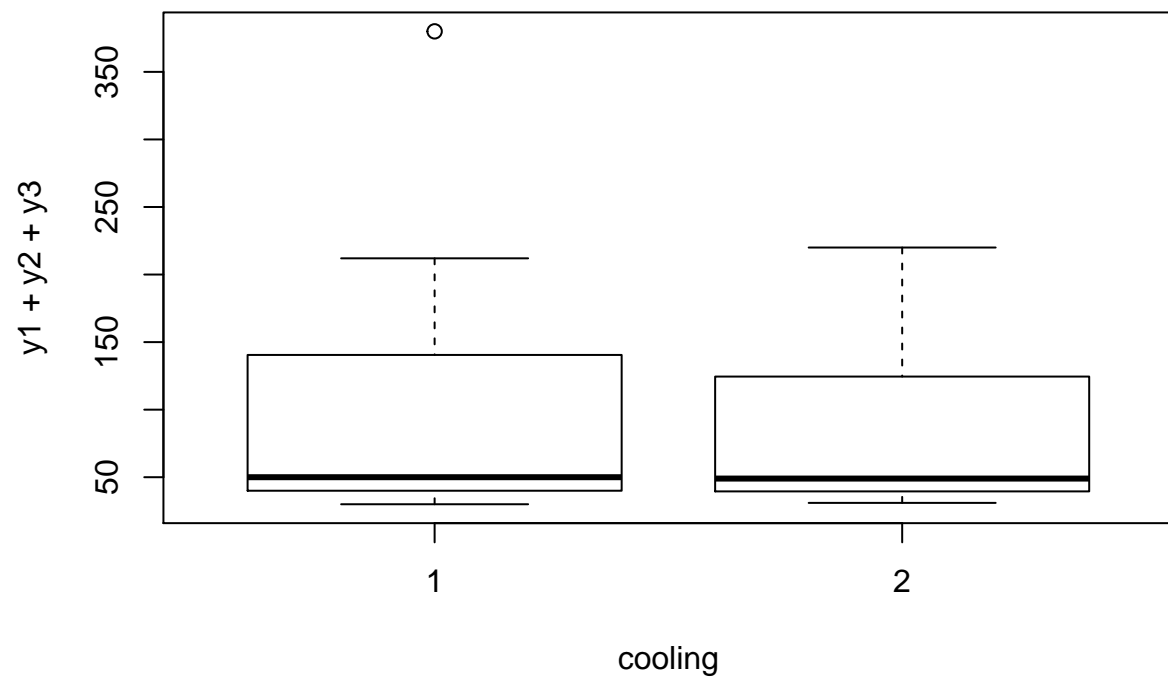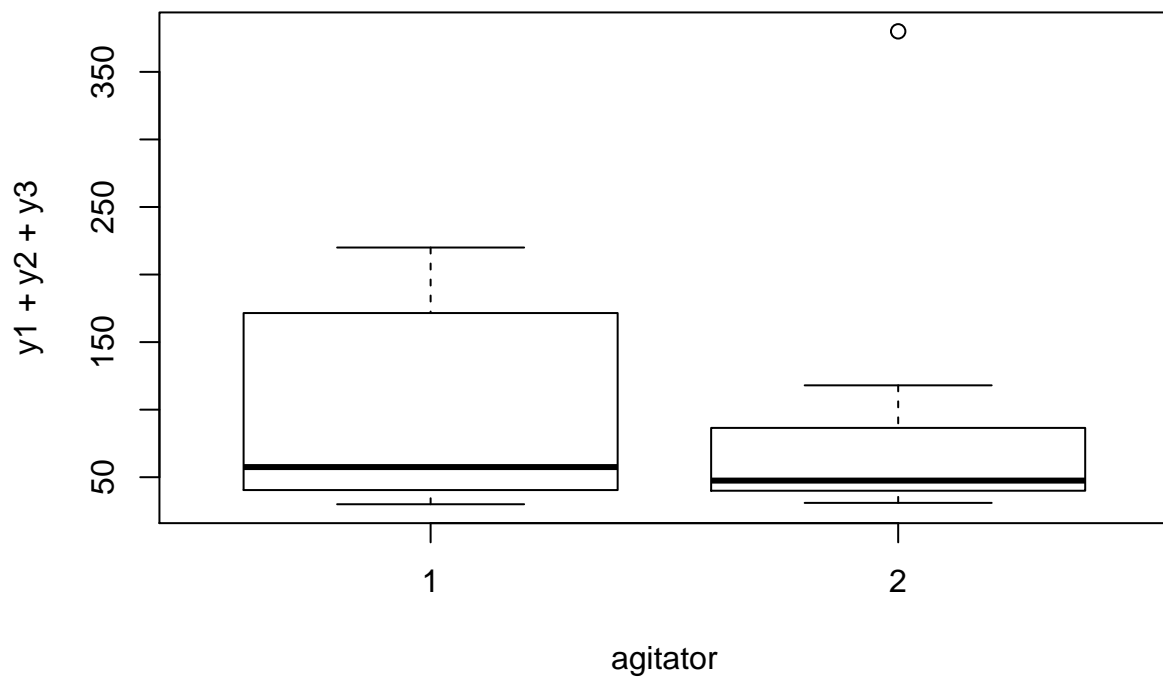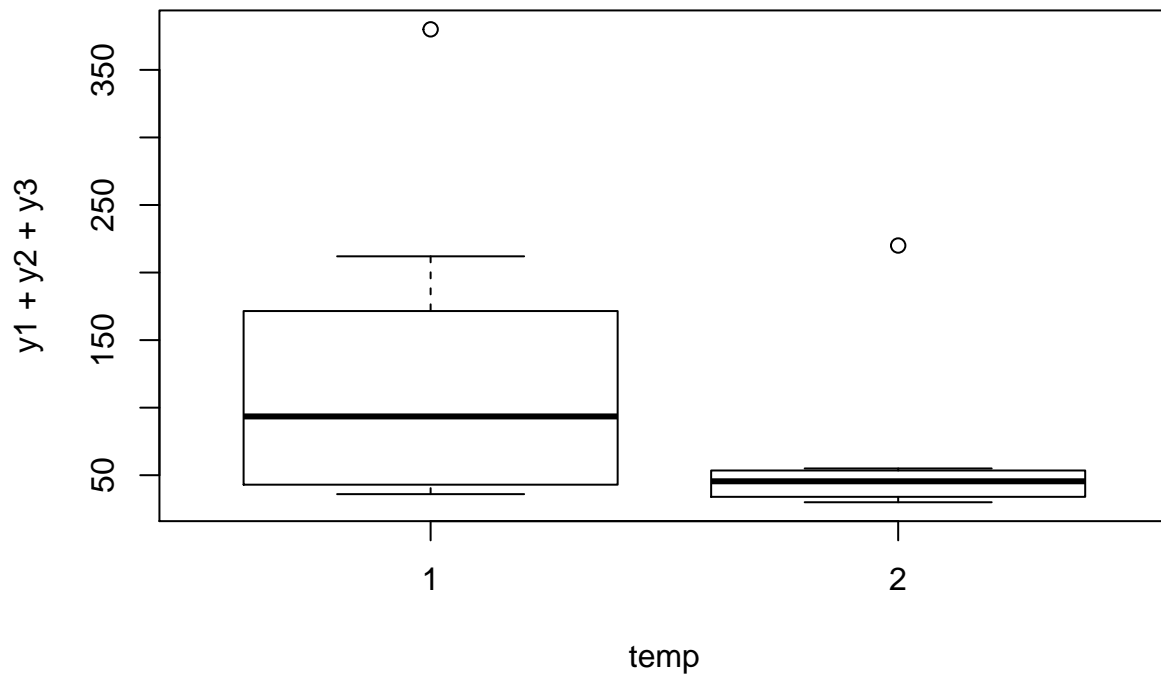
```
plot(y1+y2+y3 ~ ., data = wavesolder)
```

b)

```r
mod1 = glm(y1 ~ prebake + flux + speed + preheat + cooling + agitator + temp, data = wavesolder,
           family = 'poisson')
summary(mod1)
```

```
##
## Call:
## glm(formula = y1 ~ prebake + flux + speed + preheat + cooling +
##     agitator + temp, family = "poisson", data = wavesolder)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.918  -0.504  -0.225   0.128   3.899
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)  2.697835   0.166016   16.25  < 2e-16 ***
## prebake2     0.619214   0.105453    5.87  4.3e-09 ***
## flux2       -0.363287   0.102864   -3.53  0.00041 ***
## speed2       1.052762   0.113521    9.27  < 2e-16 ***
## preheat2    -0.073369   0.102202   -0.72  0.47283
## cooling2    -0.000534   0.102552   -0.01  0.99585
## agitator2    0.209704   0.100813    2.08  0.03751 *
## temp2       -0.953866   0.110919   -8.60  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

14

```
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 266.562  on 15  degrees of freedom
## Residual deviance:  23.198  on  8  degrees of freedom
## AIC: 115.6
##
## Number of Fisher Scoring iterations: 4
```

```r
mod2 = glm(y2 ~ prebake + flux + speed + preheat + cooling + agitator + temp, data = wavesolder,
          family
          = 'poisson')
summary(mod2)
```

```
##
## Call:
## glm(formula = y2 ~ prebake + flux + speed + preheat + cooling +
##     agitator + temp, family = "poisson", data = wavesolder)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -7.522  -2.004   0.188   2.436   4.796
##
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)   2.9944     0.1443   20.75  < 2e-16 ***
## prebake2      0.9077     0.0901   10.08  < 2e-16 ***
## flux2        -0.9361     0.0919  -10.19  < 2e-16 ***
## speed2        1.3943     0.1017   13.71  < 2e-16 ***
## preheat2     -0.2402     0.0874   -2.75    0.006 **
## cooling2     -0.1351     0.0874   -1.55    0.122
## agitator2    -0.4243     0.0882   -4.81  1.5e-06 ***
## temp2        -0.1975     0.0873   -2.26    0.024 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 679.88  on 15  degrees of freedom
## Residual deviance: 176.35  on  8  degrees of freedom
## AIC: 267.9
##
## Number of Fisher Scoring iterations: 6
```

```r
mod3 = glm(y3 ~ prebake + flux + speed + preheat + cooling + agitator + temp, data = wavesolder,
          family = 'poisson')
summary(mod3)
```

```
##
## Call:
## glm(formula = y3 ~ prebake + flux + speed + preheat + cooling +
##     agitator + temp, family = "poisson", data = wavesolder)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
```

```
## -2.681  -0.998  -0.269   0.741   5.116
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)    3.3257     0.1444   23.03  < 2e-16 ***
## prebake2       0.2783     0.0946    2.94   0.0033 **
## flux2         -0.2496     0.0945   -2.64   0.0082 **
## speed2         1.1558     0.1048   11.03  < 2e-16 ***
## preheat2      -0.0147     0.0942   -0.16   0.8761
## cooling2      -0.5195     0.0957   -5.43  5.7e-08 ***
## agitator2      0.1203     0.0911    1.32   0.1865
## temp2         -1.2831     0.1083  -11.85  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##     Null deviance: 466.296  on 15  degrees of freedom
## Residual deviance:  55.457  on  8  degrees of freedom
## AIC: 150.3
##
## Number of Fisher Scoring iterations: 5
```

```r
mod1 = glm(y1 ~ prebake + flux + speed + preheat + cooling + agitator + temp, data = wavesolder,
           family = 'quasipoisson')
summary(mod1)
```

```
##
## Call:
## glm(formula = y1 ~ prebake + flux + speed + preheat + cooling +
##     agitator + temp, family = "quasipoisson", data = wavesolder)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -1.918  -0.504  -0.225   0.128   3.899
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.697835   0.333978    8.08  4.1e-05 ***
## prebake2     0.619214   0.212141    2.92   0.0193 *
## flux2       -0.363287   0.206934   -1.76   0.1172
## speed2       1.052762   0.228372    4.61   0.0017 **
## preheat2    -0.073369   0.205601   -0.36   0.7304
## cooling2    -0.000534   0.206305    0.00   0.9980
## agitator2    0.209704   0.202808    1.03   0.3314
## temp2       -0.953866   0.223138   -4.27   0.0027 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 4.047)
##
##     Null deviance: 266.562  on 15  degrees of freedom
## Residual deviance:  23.198  on  8  degrees of freedom
## AIC: NA
##
```

```
## Number of Fisher Scoring iterations: 4
```

```r
mod2 = glm(y2 ~ prebake + flux + speed + preheat + cooling + agitator + temp, data = wavesolder,
           family
           = 'quasipoisson')
summary(mod2)
```

```
##
## Call:
## glm(formula = y2 ~ prebake + flux + speed + preheat + cooling +
##     agitator + temp, family = "quasipoisson", data = wavesolder)
##
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
## -7.522  -2.004   0.188   2.436   4.796
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)    2.994      0.652    4.59   0.0018 **
## prebake2       0.908      0.407    2.23   0.0563 .
## flux2         -0.936      0.415   -2.26   0.0541 .
## speed2         1.394      0.459    3.03   0.0162 *
## preheat2      -0.240      0.395   -0.61   0.5599
## cooling2      -0.135      0.395   -0.34   0.7410
## agitator2     -0.424      0.399   -1.06   0.3183
## temp2         -0.198      0.395   -0.50   0.6301
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 20.41)
##
##     Null deviance: 679.88  on 15   degrees of freedom
## Residual deviance: 176.35  on  8   degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 6
```

```r
mod3 = glm(y3 ~ prebake + flux + speed + preheat + cooling + agitator + temp, data = wavesolder,
           family = 'quasipoisson')
summary(mod3)
```

```
##
## Call:
## glm(formula = y3 ~ prebake + flux + speed + preheat + cooling +
##     agitator + temp, family = "quasipoisson", data = wavesolder)
##
## Deviance Residuals:
##     Min      1Q  Median      3Q     Max
## -2.681  -0.998  -0.269   0.741   5.116
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   3.3257     0.4526    7.35    8e-05 ***
## prebake2      0.2783     0.2965    0.94   0.3754
## flux2        -0.2496     0.2961   -0.84   0.4238
```

```
## speed2          1.1558      0.3284      3.52    0.0079 **
## preheat2        -0.0147      0.2954     -0.05    0.9615
## cooling2        -0.5195      0.3000     -1.73    0.1216
## agitator2        0.1203      0.2855      0.42    0.6845
## temp2           -1.2831      0.3394     -3.78    0.0054 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 9.826)
##
##     Null deviance: 466.296  on 15  degrees of freedom
## Residual deviance:  55.457  on  8  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 5
```

The first model is inadequate because of overdispersion. The second model includes an overdispersion paramater which eliminates the significance of many of the variables the intial model thought were significant.
c)

```
mod = glm(y1+y2+y3 ~ prebake + flux + speed + preheat + cooling + agitator + temp, data = wavesolder,
          family = 'quasipoisson')
summary(mod)
```

```
##
## Call:
## glm(formula = y1 + y2 + y3 ~ prebake + flux + speed + preheat +
##     cooling + agitator + temp, family = "quasipoisson", data = wavesolder)
##
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max
## -5.875  -2.197  -0.037   2.486   6.427
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.1414     0.4081   10.15  7.6e-06 ***
## prebake2       0.6512     0.2594    2.51   0.0364 *
## flux2         -0.5767     0.2593   -2.22   0.0568 .
## speed2         1.2287     0.2915    4.22   0.0029 **
## preheat2      -0.1665     0.2548   -0.65   0.5318
## cooling2      -0.1619     0.2533   -0.64   0.5407
## agitator2     -0.0897     0.2510   -0.36   0.7299
## temp2         -0.6982     0.2640   -2.64   0.0295 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for quasipoisson family taken to be 22.73)
##
##     Null deviance: 1126.79  on 15  degrees of freedom
## Residual deviance:  168.05  on  8  degrees of freedom
## AIC: NA
##
## Number of Fisher Scoring iterations: 4
```

This model produced significant variables similar to the quasi poisson models for the individual runs.

d)

```r
wavesolder$id = c(1:16)
wavesolder$sum = sum(wavesolder$y1,
                     wavesolder$y2,
                     wavesolder$y3)
wavesolder = gather(wavesolder,
           key = day,
           val = count,
           y1:y3)
wavesolder = wavesolder %>% arrange(id)

modgeep1=geeglm(count ~ prebake + flux + speed + preheat + cooling + agitator + temp,id = id,
                corstr='ar1',scale.fix=T,data=wavesolder,family=poisson)

summary(modgeep1)
```

```
##
## Call:
## geeglm(formula = count ~ prebake + flux + speed + preheat + cooling +
##     agitator + temp, family = poisson, data = wavesolder, id = id,
##     corstr = "ar1", scale.fix = T)
##
##  Coefficients:
##             Estimate Std.err   Wald Pr(>|W|)
## (Intercept)    3.041   0.222 187.39  < 2e-16 ***
## prebake2       0.669   0.179  13.96  0.00019 ***
## flux2         -0.600   0.164  13.33  0.00026 ***
## speed2         1.240   0.201  37.90  7.4e-10 ***
## preheat2      -0.174   0.167   1.09  0.29730
## cooling2      -0.155   0.169   0.85  0.35630
## agitator2     -0.111   0.160   0.48  0.48816
## temp2         -0.665   0.178  13.98  0.00019 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation structure = ar1
## Scale is fixed.
##
##   Link = identity
##
## Estimated Correlation Parameters:
##       Estimate Std.err
## alpha   -0.163   0.386
## Number of clusters:   16  Maximum cluster size: 3
```

With a fixed scale there is still no evidence that there is correlation between succesive duplicates.

e)

```r
modgeep1=geeglm(count ~ prebake + flux + speed + preheat + cooling + agitator + temp,id = id,
                corstr='ar1',data=wavesolder,family=poisson)

summary(modgeep1)
```

```
## 
## Call:
## geeglm(formula = count ~ prebake + flux + speed + preheat + cooling +
##     agitator + temp, family = poisson, data = wavesolder, id = id,
##     corstr = "ar1")
## 
##  Coefficients:
##              Estimate Std.err   Wald Pr(>|W|)
## (Intercept)     3.041   0.222 186.81  < 2e-16 ***
## prebake2        0.669   0.179  13.95  0.00019 ***
## flux2          -0.601   0.165  13.34  0.00026 ***
## speed2          1.240   0.202  37.80  7.8e-10 ***
## preheat2       -0.175   0.168   1.09  0.29711
## cooling2       -0.155   0.169   0.85  0.35779
## agitator2      -0.112   0.161   0.49  0.48546
## temp2          -0.663   0.178  13.89  0.00019 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Correlation structure = ar1
## Estimated Scale Parameters:
## 
##             Estimate Std.err
## (Intercept)     10.8    4.62
##   Link = identity
## 
## Estimated Correlation Parameters:
##       Estimate Std.err
## alpha    -0.17   0.337
## Number of clusters:   16  Maximum cluster size: 3
```

Even without a fixed scale there is still no evidence that there is correlation between succesive duplicates.

f)

```
modgeep1=geeglm(count ~ prebake + flux + speed + preheat + cooling + agitator + temp,id = id,
                corstr='unstructed',data=wavesolder,family=poisson)
```

```
## Warning in if (corstrv == -1) stop("invalid corstr."): the condition has length
## > 1 and only the first element will be used

## Warning in if (corstrv == 5) stop("need zcor matrix for userdefined corstr.")
## else zcor <- genZcor(clusz, : the condition has length > 1 and only the first
## element will be used

## Warning in if (corstrv == 1) return(matrix(0, 0, 0)): the condition has length >
## 1 and only the first element will be used

## Warning in if (corstrv == 6) alpha <- 1 else alpha <- rep(0, q): the condition
## has length > 1 and only the first element will be used
```

```
summary(modgeep1)
```

```
## 
## Call:
## geeglm(formula = count ~ prebake + flux + speed + preheat + cooling +
##     agitator + temp, family = poisson, data = wavesolder, id = id,
```

```
##      corstr = "unstructed")
##
##  Coefficients:
##             Estimate Std.err   Wald Pr(>|W|)
## (Intercept)   3.0428  0.2141 201.98  < 2e-16 ***
## prebake2      0.6512  0.1718  14.37  0.00015 ***
## flux2        -0.5767  0.1591  13.14  0.00029 ***
## speed2        1.2287  0.1933  40.39  2.1e-10 ***
## preheat2     -0.1665  0.1614   1.06  0.30243
## cooling2     -0.1619  0.1624   0.99  0.31898
## agitator2    -0.0897  0.1534   0.34  0.55857
## temp2        -0.6982  0.1735  16.19  5.7e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation structure = exchangeable ar1 unstructured userdefined fixed
## Estimated Scale Parameters:
##
##             Estimate Std.err
## (Intercept)     11.2    5.04
##
## Warning in if (pmatch(x$corstr, "independence", 0) == 0) {: the condition has
## length > 1 and only the first element will be used
##
##   Link = identity
##
## Estimated Correlation Parameters:
##       Estimate Std.err
## alpha  0.00831   0.217
## Number of clusters:   16  Maximum cluster size: 3
```

This model found a couple more significant variables than the poisson model did, and it produced lower p values for the significant variables.