multilevel1

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#example 1

Data Access and changing the names of columns which we are interested in.

```r
data1 <-  read.table("bacteria.dat")
colnames(data1) <- c("date","site","humi","temp","b1","b2","b3","b4","b5","b6","f1","f2","f3","f4","f5"
data <- data1[-1,]
head(data)
```

```
##    date site humi temp b1 b2 b3 b4 b5 b6 f1 f2 f3 f4 f5 f6
## 2 08.03    1   31   13 17 17 19 10 17 21 10  4  1  0  4  1
## 3 08.03    2   32    9 10  6  2 16  7  2 12  6  7  4  2  2
## 4 08.03    3   28    8  5  0  3  2  8  1  7  1  0  3  4  0
## 5 08.03    4   28    9  2  1  4  4  4  0 10  3  3 16  6  0
## 6 08.03    5   28   11  8 11 11  2  3  8  2  1  4 13 10  3
## 7 08.03    6   29   10  2  1  0  2  1  1  0  1  0  2  2  0
```

#example 2

Data manipulation

```r
data$b1 <- as.numeric(data$b1)
data$b2 <- as.numeric(data$b2)
data$b3 <- as.numeric(data$b3)
data$b4 <- as.numeric(data$b4)
data$b5 <- as.numeric(data$b5)
data$b6 <- as.numeric(data$b6)


data$bac <- data$b1+data$b2 + data$b3 +data$b4 + data$b5 +data$b6
data$f1 <- as.numeric(data$f1)
data$f2 <- as.numeric(data$f2)
data$f3 <- as.numeric(data$f3)
data$f4 <- as.numeric(data$f4)
data$f5 <- as.numeric(data$f5)
data$f6 <- as.numeric(data$f6)
data$fun <- data$f1+data$f2 + data$f3 +data$f4 + data$f5 +data$f6


data$humi <- as.numeric(data$humi)
data$temp <- as.numeric(data$temp)
```

#example 3

finding the best linear model. - bac ~ humi + temp + site In this model humidity and tempearture are insignificant with r-sqaure around 0.25. - bac ~ humi + temp + humi * temp + site In this model R squared improves to 0.26 but humidity, temp and product humi*temp are all insignificant. - bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site In this model temperature becomes significant with its second power highly significant and the signifciance of the product Humi*temp also increases, but humiditry is still insignificant. R square improves to 0.32. -bac ~ humi + temp + poly(humi * temp, 2) + site Both powers of the product are insignificant. -bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site This remains our best model covering wide parameters and amongst all the highest r-squared of 0.32.

```r
str(data)
```

```
## 'data.frame':    178 obs. of  18 variables:
##  $ date: Factor w/ 27 levels "02.05","03.01",..: 8 8 8 8 8 8 8 20 20 20 ...
##  $ site: Factor w/ 8 levels "1","2","3","4",..: 1 2 3 4 5 6 7 1 2 3 ...
##  $ humi: num  8 9 5 5 5 6 1 25 23 21 ...
##  $ temp: num  12 36 35 36 10 9 9 33 34 35 ...
##  $ b1  : num  9 3 20 12 23 12 2 3 19 24 ...
##  $ b2  : num  9 16 1 2 4 2 1 4 2 3 ...
##  $ b3  : num  8 9 13 14 4 1 1 18 2 13 ...
##  $ b4  : num  3 5 6 10 6 6 2 3 1 10 ...
##  $ b5  : num  9 18 19 14 13 2 2 14 2 8 ...
##  $ b6  : num  8 6 2 1 15 2 1 14 2 4 ...
##  $ f1  : num  3 5 17 3 11 1 1 13 13 3 ...
##  $ f2  : num  12 14 2 10 2 2 8 10 8 8 ...
##  $ f3  : num  2 16 1 11 13 1 9 16 2 18 ...
##  $ f4  : num  1 13 12 6 5 10 12 15 5 16 ...
##  $ f5  : num  16 10 16 18 3 10 16 19 21 11 ...
##  $ f6  : num  2 7 1 1 8 1 1 15 8 11 ...
##  $ bac : num  46 57 61 53 65 25 9 56 28 62 ...
##  $ fun : num  36 65 49 49 42 25 47 88 57 67 ...
```

```r
table(data$site)
```

```
##
##    1    2    3    4    5    6    7 site
##   25   26   25   25   25   26   26    0
```

```r
table(droplevels(data$site))
```

```
##
##  1  2  3  4  5  6  7
## 25 26 25 25 25 26 26
```

```r
data$site <- factor(data$site)
class(data$site)
```

```
## [1] "factor"
```

```r
levels(data$site)
```

```
## [1] "1" "2" "3" "4" "5" "6" "7"
```

```r
data$humi <- as.numeric(data$humi)
data$temp <- as.numeric(data$temp)
str(data)
```

```
## 'data.frame':    178 obs. of  18 variables:
##  $ date: Factor w/ 27 levels "02.05","03.01",..: 8 8 8 8 8 8 8 20 20 20 ...
##  $ site: Factor w/ 7 levels "1","2","3","4",..: 1 2 3 4 5 6 7 1 2 3 ...
##  $ humi: num  8 9 5 5 5 6 1 25 23 21 ...
##  $ temp: num  12 36 35 36 10 9 9 33 34 35 ...
##  $ b1  : num  9 3 20 12 23 12 2 3 19 24 ...
##  $ b2  : num  9 16 1 2 4 2 1 4 2 3 ...
##  $ b3  : num  8 9 13 14 4 1 1 18 2 13 ...
##  $ b4  : num  3 5 6 10 6 6 2 3 1 10 ...
##  $ b5  : num  9 18 19 14 13 2 2 14 2 8 ...
##  $ b6  : num  8 6 2 1 15 2 1 14 2 4 ...
```

```
## $ f1  : num   3 5 17 3 11 1 1 13 13 3 ...
## $ f2  : num   12 14 2 10 2 2 8 10 8 8 ...
## $ f3  : num   2 16 1 11 13 1 9 16 2 18 ...
## $ f4  : num   1 13 12 6 5 10 12 15 5 16 ...
## $ f5  : num   16 10 16 18 3 10 16 19 21 11 ...
## $ f6  : num   2 7 1 1 8 1 1 15 8 11 ...
## $ bac : num   46 57 61 53 65 25 9 56 28 62 ...
## $ fun : num   36 65 49 49 42 25 47 88 57 67 ...
```

```
#View(data)
```

```
model1 <- lm(bac ~ humi+temp+site, data = data)
model1
```

```
##
## Call:
## lm(formula = bac ~ humi + temp + site, data = data)
##
## Coefficients:
## (Intercept)          humi          temp         site2         site3
##     66.8020       -0.1146        0.2433      -15.5513      -15.3397
##        site4         site5         site6         site7
##    -17.0510      -23.9843      -34.2093      -27.7960
```

```
summary(model1)
```

```
##
## Call:
## lm(formula = bac ~ humi + temp + site, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -46.134 -11.663  -1.282  11.987  41.189
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  66.80196    5.71966  11.679  < 2e-16 ***
## humi         -0.11457    0.07885  -1.453  0.14805
## temp          0.24333    0.15005   1.622  0.10673
## site2       -15.55133    5.12538  -3.034  0.00279 **
## site3       -15.33969    5.18287  -2.960  0.00352 **
## site4       -17.05100    5.18498  -3.289  0.00123 **
## site5       -23.98430    5.18248  -4.628 7.32e-06 ***
## site6       -34.20931    5.14403  -6.650 3.88e-10 ***
## site7       -27.79595    5.13098  -5.417 2.05e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.27 on 169 degrees of freedom
## Multiple R-squared:  0.2568, Adjusted R-squared:  0.2216
## F-statistic: 7.298 on 8 and 169 DF,  p-value: 2.607e-08
```

```
model2 <- lm(bac ~ humi+temp+humi*temp+ site, data = data)
model2
```

```
##
```

```
## Call:
## lm(formula = bac ~ humi + temp + humi * temp + site, data = data)
##
## Coefficients:
## (Intercept)          humi          temp         site2         site3
##    59.81910       0.07221       0.64228     -16.18926     -15.82071
##        site4         site5         site6         site7     humi:temp
##    -17.97150     -24.34218     -34.78775     -28.33145      -0.01093
```

```
summary(model2)
```

```
##
## Call:
## lm(formula = bac ~ humi + temp + humi * temp + site, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -44.13  -11.64   -1.68   12.19   40.96
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)   59.819095   7.851304   7.619 1.78e-12 ***
## humi           0.072209   0.164268   0.440 0.660805
## temp           0.642280   0.342457   1.876 0.062458 .
## site2        -16.189259   5.138785  -3.150 0.001931 **
## site3        -15.820711   5.185819  -3.051 0.002653 **
## site4        -17.971500   5.223179  -3.441 0.000732 ***
## site5        -24.342179   5.179493  -4.700 5.40e-06 ***
## site6        -34.787747   5.153128  -6.751 2.29e-10 ***
## site7        -28.331451   5.137380  -5.515 1.30e-07 ***
## humi:temp     -0.010926   0.008435  -1.295 0.196971
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.24 on 168 degrees of freedom
## Multiple R-squared:  0.2641, Adjusted R-squared:  0.2247
## F-statistic:   6.7 on 9 and 168 DF,  p-value: 3.536e-08
```

```
model3 <- lm(bac ~ poly(humi, 2) + poly(temp,2)+humi*temp+ site,data = data)
model3
```

```
##
## Call:
## lm(formula = bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp +
##     site, data = data)
##
## Coefficients:
##    (Intercept)  poly(humi, 2)1  poly(humi, 2)2  poly(temp, 2)1
##       79.17265        70.38062         5.43401       130.23487
## poly(temp, 2)2            humi            temp           site2
##      -69.76962              NA              NA       -16.76460
##          site3           site4           site5           site6
##      -15.70999       -18.49009       -25.08393       -34.45091
##          site7       humi:temp
##      -27.90807        -0.01986
```

```r
summary(model3)
```

```
##
## Call:
## lm(formula = bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp +
##     site, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -42.759 -10.368  -0.169  11.462  41.875
##
## Coefficients: (2 not defined because of singularities)
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    79.172650   6.245602  12.677  < 2e-16 ***
## poly(humi, 2)1 70.380620  42.132678   1.670 0.096714 .
## poly(humi, 2)2  5.434009  18.106977   0.300 0.764472
## poly(temp, 2)1 130.234871 44.627491   2.918 0.004008 **
## poly(temp, 2)2 -69.769622 18.900872  -3.691 0.000302 ***
## humi                  NA         NA      NA       NA
## temp                  NA         NA      NA       NA
## site2         -16.764603   4.974693  -3.370 0.000935 ***
## site3         -15.709987   5.015609  -3.132 0.002051 **
## site4         -18.490092   5.060068  -3.654 0.000346 ***
## site5         -25.083926   5.010103  -5.007 1.40e-06 ***
## site6         -34.450907   5.006562  -6.881 1.16e-10 ***
## site7         -27.908075   4.984373  -5.599 8.75e-08 ***
## humi:temp      -0.019863   0.008574  -2.317 0.021747 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.62 on 166 degrees of freedom
## Multiple R-squared:  0.3213, Adjusted R-squared:  0.2764
## F-statistic: 7.145 on 11 and 166 DF,  p-value: 6.918e-10
```

```r
model4 <- lm(bac ~ humi+temp + poly(humi*temp,2)+ site, data = data)
model4
```

```
##
## Call:
## lm(formula = bac ~ humi + temp + poly(humi * temp, 2) + site,
##     data = data)
##
## Coefficients:
##          (Intercept)                  humi                  temp
##             62.45120              -0.04671               0.37866
## poly(humi * temp, 2)1  poly(humi * temp, 2)2                 site2
##            -27.49443             -32.81605             -16.21393
##                site3                 site4                 site5
##            -15.70694             -17.92107             -24.85277
##                site6                 site7
##            -34.25367             -27.94750
```

```r
summary(model4)
```

```
##
```

```
## Call:
## lm(formula = bac ~ humi + temp + poly(humi * temp, 2) + site,
##     data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -44.263 -10.674  -0.718  11.974  40.769
##
## Coefficients:
##                         Estimate Std. Error t value Pr(>|t|)
## (Intercept)             62.45120   12.78141   4.886 2.40e-06 ***
## humi                    -0.04671    0.17935  -0.260 0.794868
## temp                     0.37866    0.37802   1.002 0.317937
## poly(humi * temp, 2)1  -27.49443   52.18416  -0.527 0.598981
## poly(humi * temp, 2)2  -32.81605   20.35052  -1.613 0.108732
## site2                  -16.21393    5.11451  -3.170 0.001813 **
## site3                  -15.70694    5.16178  -3.043 0.002722 **
## site4                  -17.92107    5.19857  -3.447 0.000716 ***
## site5                  -24.85277    5.16471  -4.812 3.32e-06 ***
## site6                  -34.25367    5.13944  -6.665 3.69e-10 ***
## site7                  -27.94750    5.11863  -5.460 1.70e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.15 on 167 degrees of freedom
## Multiple R-squared:  0.2754, Adjusted R-squared:  0.232
## F-statistic: 6.347 on 10 and 167 DF,  p-value: 3.099e-08
```

```r
humi1 <- (data$humi)^2
temp1 <- (data$temp)^2
mylm <- lm(bac ~ poly(humi,2)+poly(temp,2)+ humi*temp+ site,data = data)
mylm
```

```
##
## Call:
## lm(formula = bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp +
##     site, data = data)
##
## Coefficients:
##    (Intercept)  poly(humi, 2)1  poly(humi, 2)2  poly(temp, 2)1
##       79.17265        70.38062         5.43401       130.23487
## poly(temp, 2)2            humi            temp           site2
##      -69.76962              NA              NA       -16.76460
##          site3           site4           site5           site6
##      -15.70999       -18.49009       -25.08393       -34.45091
##          site7       humi:temp
##      -27.90807        -0.01986
```

```r
summary(mylm)
```

```
##
## Call:
## lm(formula = bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp +
##     site, data = data)
##
```

6

```
## Residuals:
##     Min      1Q  Median      3Q     Max
## -42.759 -10.368  -0.169  11.462  41.875
##
## Coefficients: (2 not defined because of singularities)
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)     79.172650   6.245602  12.677  < 2e-16 ***
## poly(humi, 2)1  70.380620  42.132678   1.670 0.096714 .
## poly(humi, 2)2   5.434009  18.106977   0.300 0.764472
## poly(temp, 2)1 130.234871  44.627491   2.918 0.004008 **
## poly(temp, 2)2 -69.769622  18.900872  -3.691 0.000302 ***
## humi                  NA         NA      NA       NA
## temp                  NA         NA      NA       NA
## site2          -16.764603   4.974693  -3.370 0.000935 ***
## site3          -15.709987   5.015609  -3.132 0.002051 **
## site4          -18.490092   5.060068  -3.654 0.000346 ***
## site5          -25.083926   5.010103  -5.007 1.40e-06 ***
## site6          -34.450907   5.006562  -6.881 1.16e-10 ***
## site7          -27.908075   4.984373  -5.599 8.75e-08 ***
## humi:temp       -0.019863   0.008574  -2.317 0.021747 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.62 on 166 degrees of freedom
## Multiple R-squared:  0.3213, Adjusted R-squared:  0.2764
## F-statistic: 7.145 on 11 and 166 DF,  p-value: 6.918e-10
```

```r
mylm1 <- lm(bac~poly(temp,2)+site+humi*temp, data=data)
mylm1
```

```
##
## Call:
## lm(formula = bac ~ poly(temp, 2) + site + humi * temp, data = data)
##
## Coefficients:
##    (Intercept)  poly(temp, 2)1  poly(temp, 2)2           site2
##       69.52412        130.78711       -70.23745       -16.67819
##          site3           site4           site5           site6
##      -15.64071        -18.38253       -25.03447       -34.29697
##          site7            humi            temp       humi:temp
##      -27.77797         0.28791              NA        -0.02016
```

```r
summary(mylm1)
```

```
##
## Call:
## lm(formula = bac ~ poly(temp, 2) + site + humi * temp, data = data)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -42.885 -10.467  -0.324  11.628  42.150
##
## Coefficients: (1 not defined because of singularities)
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    69.524124   4.474812  15.537  < 2e-16 ***
```
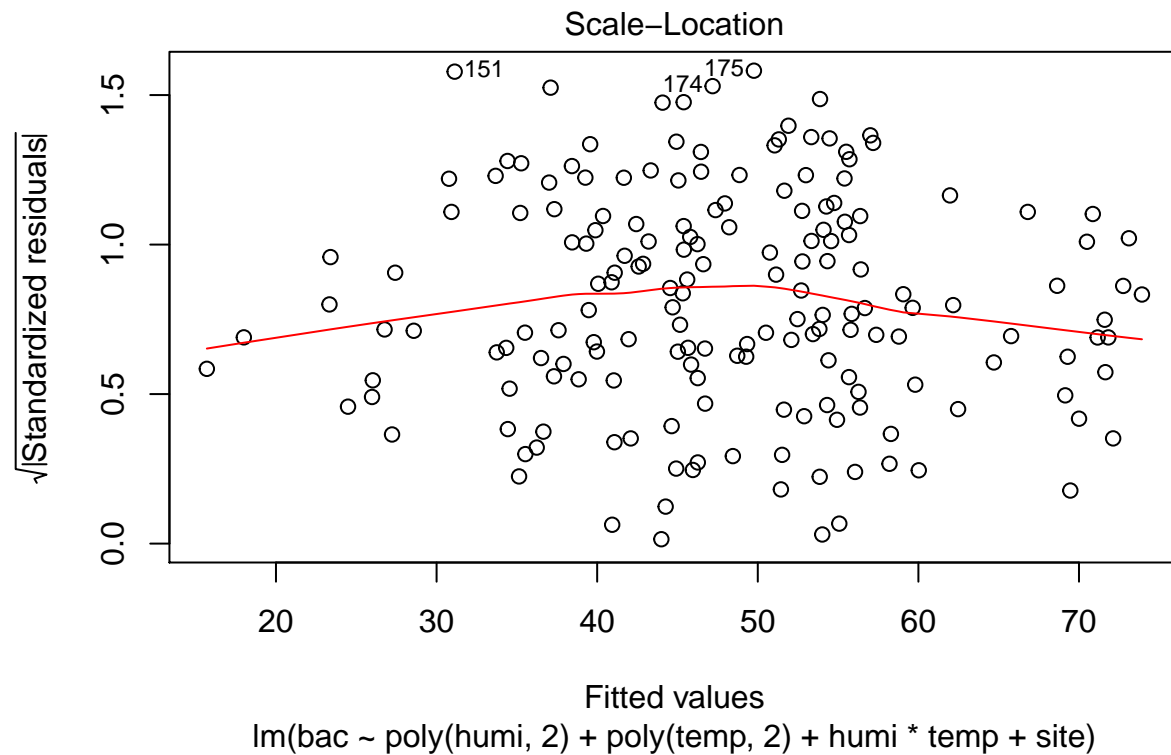
```
## poly(temp, 2)1 130.787108   44.467894    2.941 0.003734 **
## poly(temp, 2)2 -70.237452   18.785089   -3.739 0.000254 ***
## site2           -16.678186    4.952803   -3.367 0.000942 ***
## site3           -15.640707    4.996625   -3.130 0.002062 **
## site4           -18.382530    5.033589   -3.652 0.000348 ***
## site5           -25.034471    4.993732   -5.013 1.36e-06 ***
## site6           -34.296972    4.966630   -6.905 9.98e-11 ***
## site7           -27.777966    4.951936   -5.610 8.26e-08 ***
## humi              0.287914    0.168454    1.709 0.089280 .
## temp                    NA          NA       NA       NA
## humi:temp        -0.020160    0.008494   -2.373 0.018757 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 17.57 on 167 degrees of freedom
## Multiple R-squared:  0.321,  Adjusted R-squared:  0.2803
## F-statistic: 7.894 on 10 and 167 DF,  p-value: 2.461e-10
```

#Checking for linearity,normality and constant variance.

The model is perfectly normal and linear also meeting the requirements of constant variance.
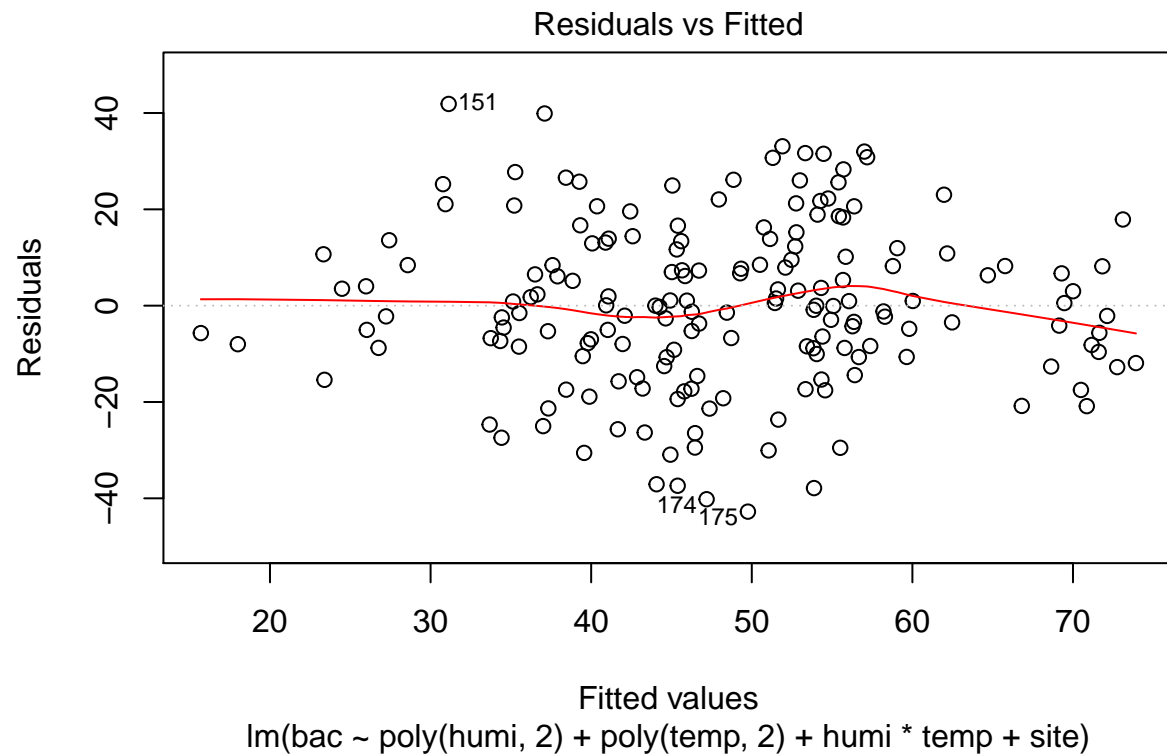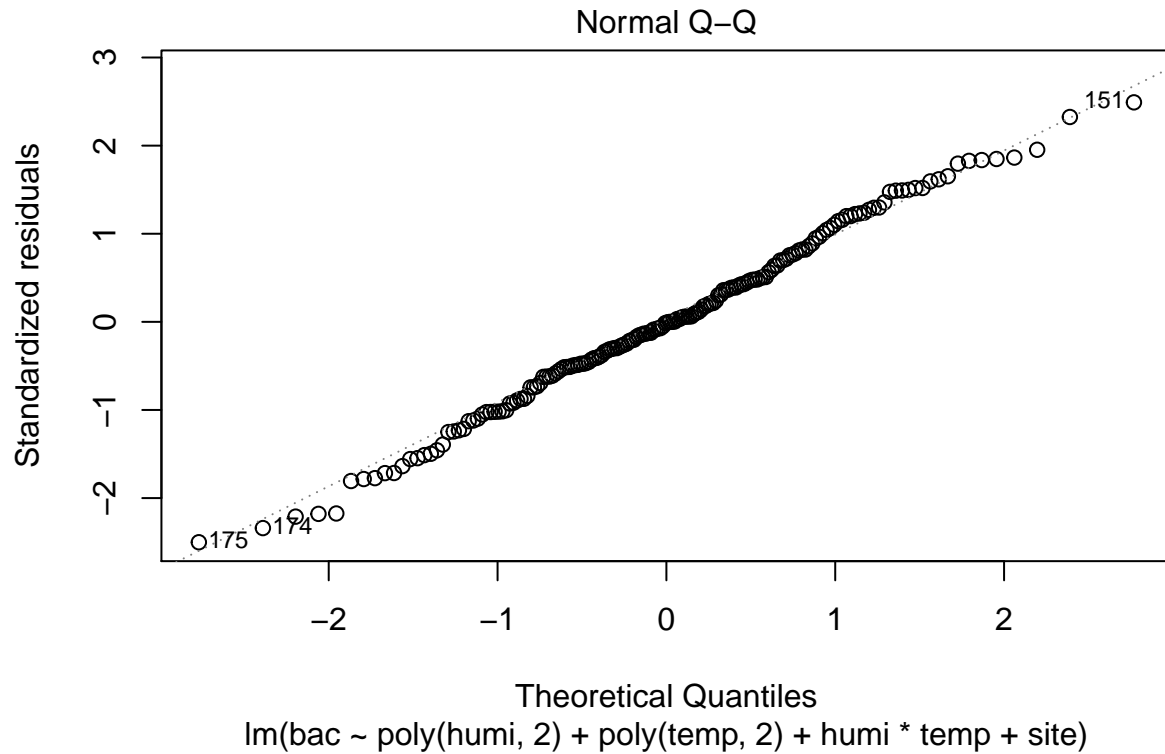
```
# homosceadcity

plot(mylm, 3)
```


Scale–Location

#checking linearity
```
plot(mylm, 1)
```

Residuals vs Fitted

Fitted values
lm(bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site)

```r
# checking normality
plot(mylm, 2)
```

Normal Q–Q

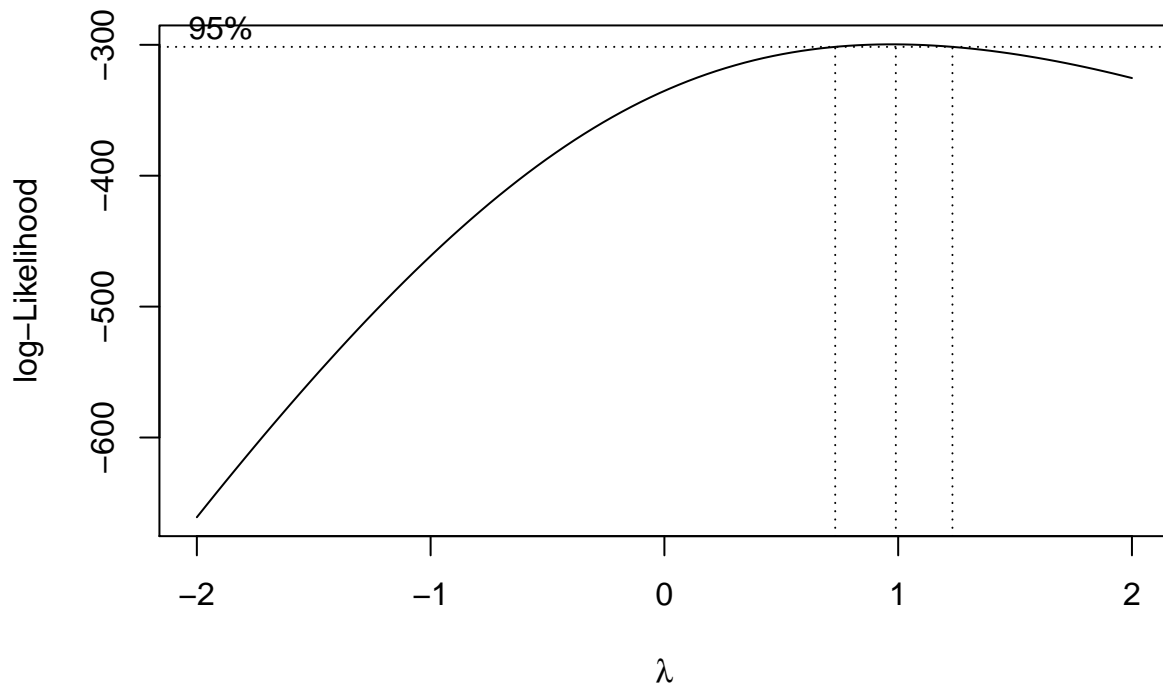lm(bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site)

#example 4

When we compare mylm and mylmBC the results are almost similar not much of a difference. If we use log transformation r-squared goes down without much changes in significance results.

```r
# Estimate Maximum Liklihood Box-Cox transform parameters
library(MASS)
```

```
## Warning: package 'MASS' was built under R version 3.6.2
```

```r
bc.null <- boxcox(mylm)
```

```
bc.null.opt <- bc.null$x[which.max(bc.null$y)]

print(paste("ML Box-Cox estimate for null model:",bc.null.opt))
```

```
## [1] "ML Box-Cox estimate for null model: 0.98989898989899"
```

```
# lambda=0.989
mylmBC <- lm(bac^(0.989) ~ poly(humi,2)+poly(temp,2)+ humi*temp+ site,data = data)
mylmBC
```

```
##
## Call:
## lm(formula = bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + humi *
##     temp + site, data = data)
##
## Coefficients:
##    (Intercept)  poly(humi, 2)1  poly(humi, 2)2  poly(temp, 2)1
##       75.52395        66.89706         5.32351       123.79450
## poly(temp, 2)2            humi            temp           site2
##      -66.23780              NA              NA       -15.88888
##          site3           site4           site5           site6
##      -14.92328       -17.52496       -23.78003       -32.68382
##          site7       humi:temp
##      -26.47335        -0.01886
```
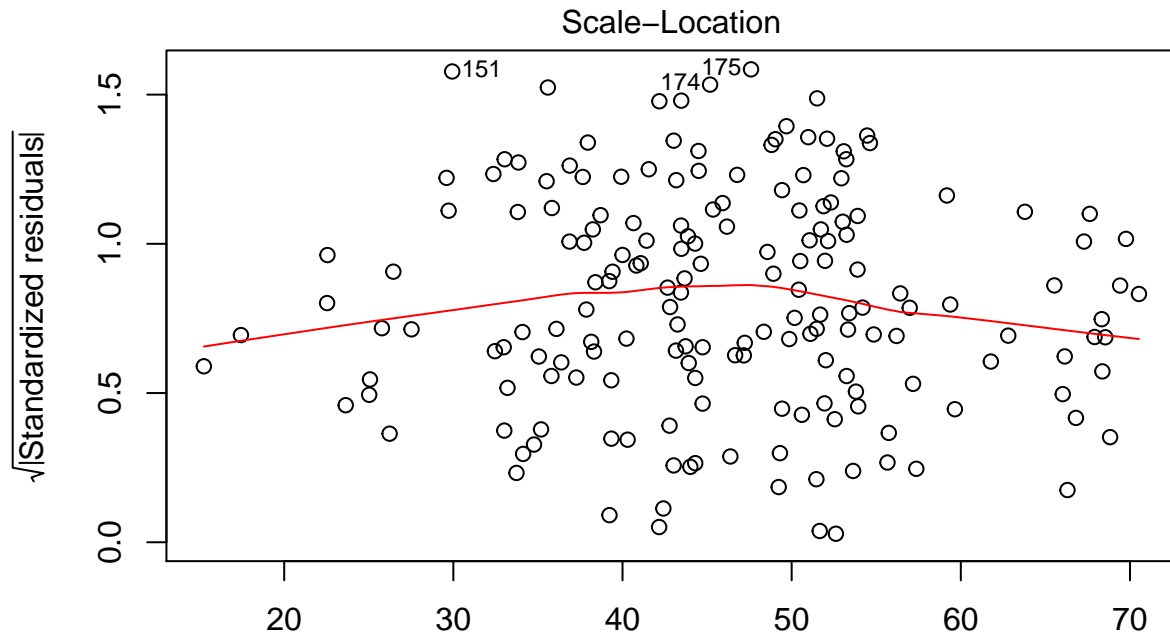
```
plot(mylmBC,1)
```

Residuals vs Fitted
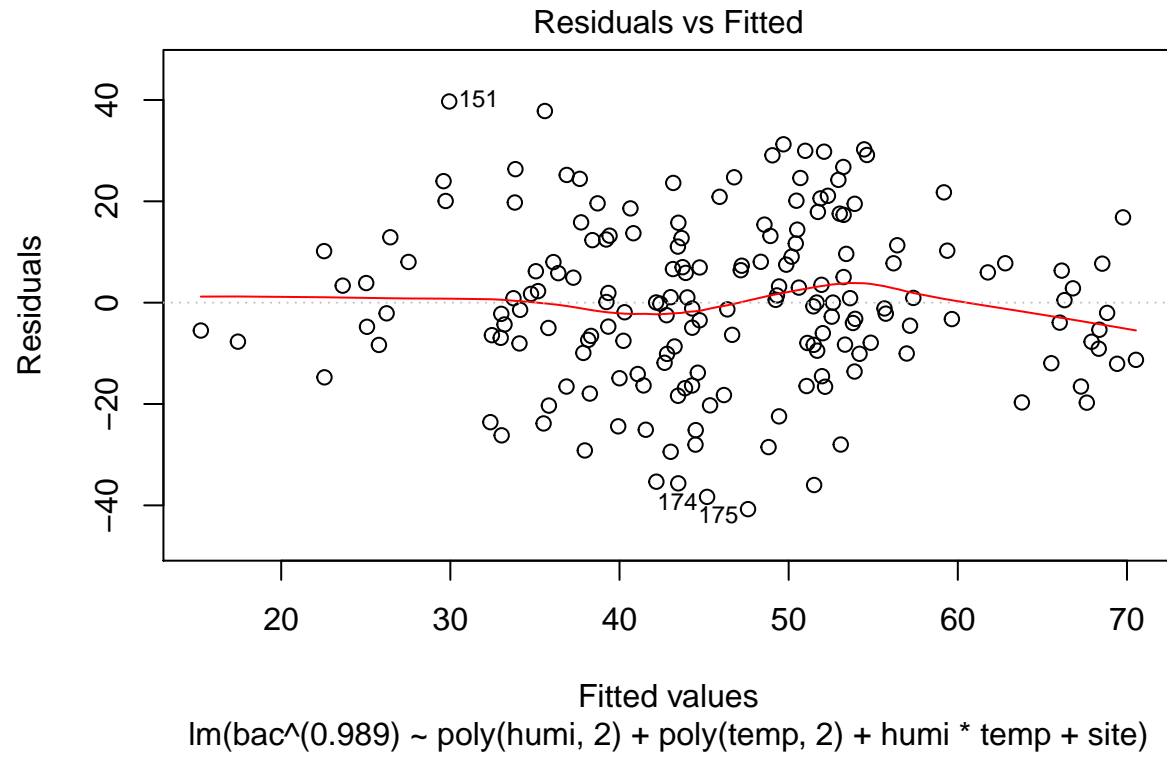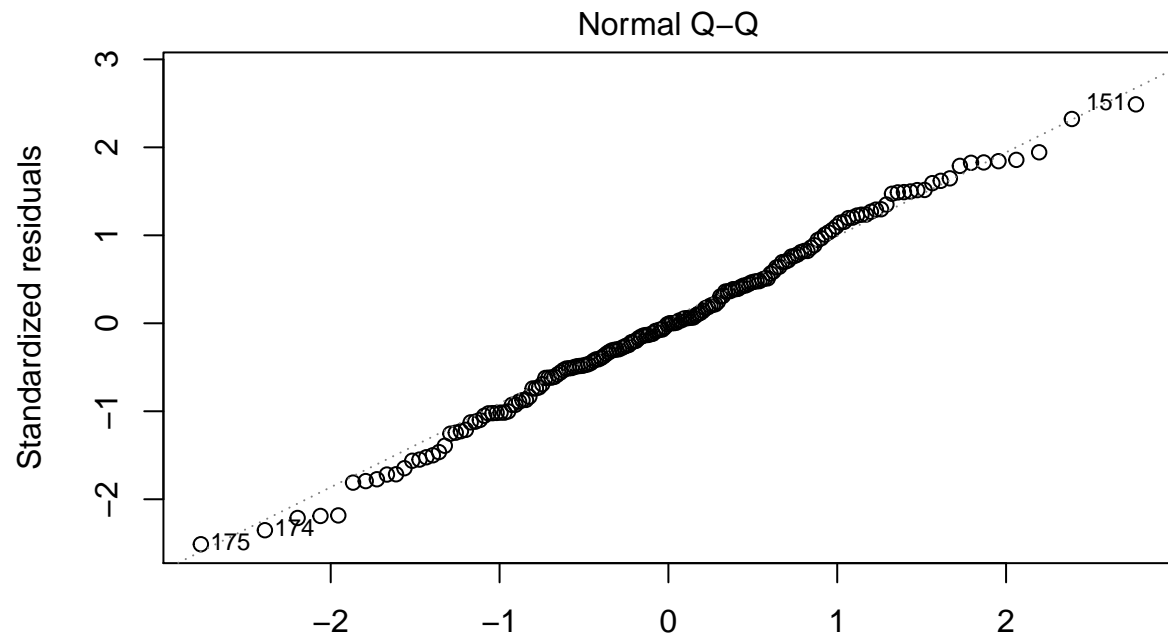
Fitted values
lm(bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site)

```
plot(mylmBC,2)
```

Normal Q–Q

lm(bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site)

```r
plot(mylmBC,3)
```

Scale-Location

lm(bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site)

```r
summary(mylmBC)
```

```
## 
## Call:
## lm(formula = bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + humi *
##     temp + site, data = data)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max
## -40.746  -9.807  -0.098  10.866  39.701
## 
## Coefficients: (2 not defined because of singularities)
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)     75.523946   5.927384  12.742  < 2e-16 ***
## poly(humi, 2)1  66.897065  39.985987   1.673 0.096208 .
## poly(humi, 2)2   5.323515  17.184413   0.310 0.757111
## poly(temp, 2)1 123.794499  42.353688   2.923 0.003952 **
## poly(temp, 2)2 -66.237802  17.937858  -3.693 0.000301 ***
## humi                  NA         NA      NA       NA
## temp                  NA         NA      NA       NA
## site2          -15.888885   4.721228  -3.365 0.000949 ***
## site3          -14.923281   4.760060  -3.135 0.002032 **
## site4          -17.524961   4.802254  -3.649 0.000352 ***
## site5          -23.780034   4.754835  -5.001 1.44e-06 ***
## site6          -32.683822   4.751474  -6.879 1.17e-10 ***
## site7          -26.473347   4.730416  -5.596 8.87e-08 ***
```
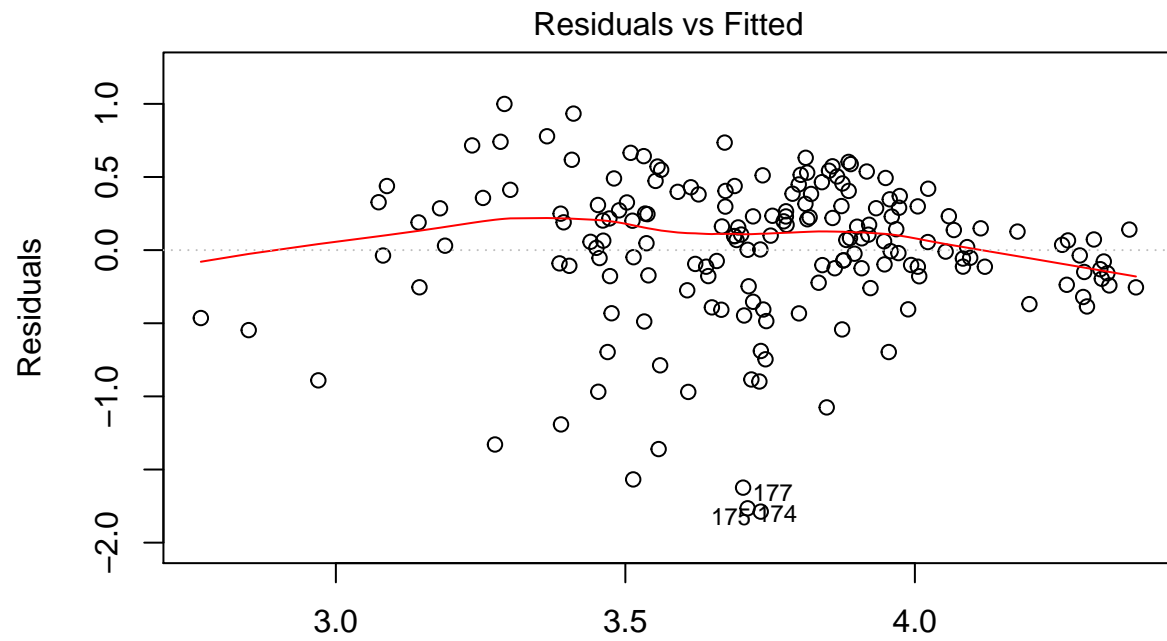
```
## humi:temp      -0.018859   0.008137  -2.318 0.021694 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 16.72 on 166 degrees of freedom
## Multiple R-squared:  0.3213, Adjusted R-squared:  0.2763
## F-statistic: 7.143 on 11 and 166 DF,  p-value: 6.962e-10
```

```
# lambda=0

bc2.mod <- lm(log(bac) ~ poly(humi,2)+poly(temp,2)+ humi*temp+ site,data = data)
bc2.mod
```

```
##
## Call:
## lm(formula = log(bac) ~ poly(humi, 2) + poly(temp, 2) + humi *
##     temp + site, data = data)
##
## Coefficients:
##    (Intercept)  poly(humi, 2)1  poly(humi, 2)2  poly(temp, 2)1
##      4.5464355       2.2136434       0.6154832       4.1065044
## poly(temp, 2)2            humi            temp           site2
##     -1.9763786              NA              NA      -0.3881101
##          site3           site4           site5           site6
##     -0.4521175      -0.4376138      -0.5830852      -0.8651738
##          site7       humi:temp
##     -0.6941739      -0.0005589
```

```
plot(bc2.mod,1)
```

Residuals vs Fitted

Fitted values
lm(log(bac) ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site)

```
plot(bc2.mod,2)
```

Normal Q–Q

Standardized residuals

Theoretical Quantiles
lm(log(bac) ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site)

```
plot(bc2.mod,3)
```

Scale–Location

Fitted values
lm(log(bac) ~ poly(humi, 2) + poly(temp, 2) + humi * temp + site)
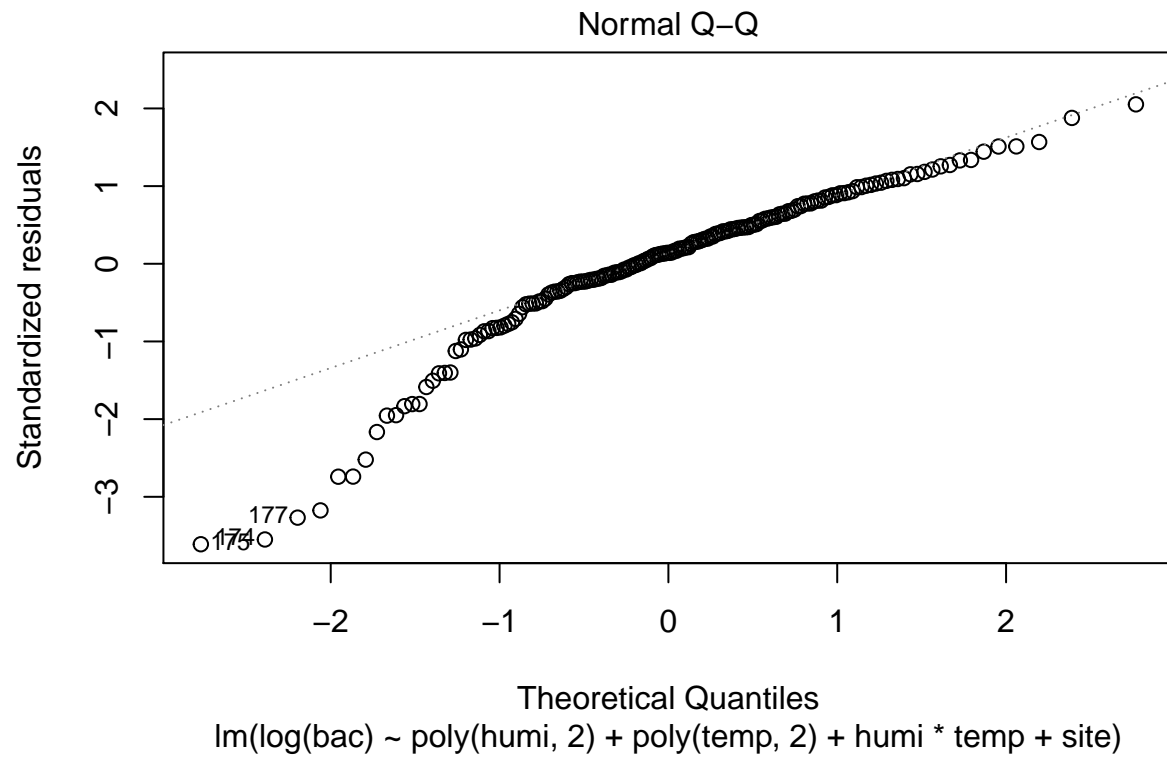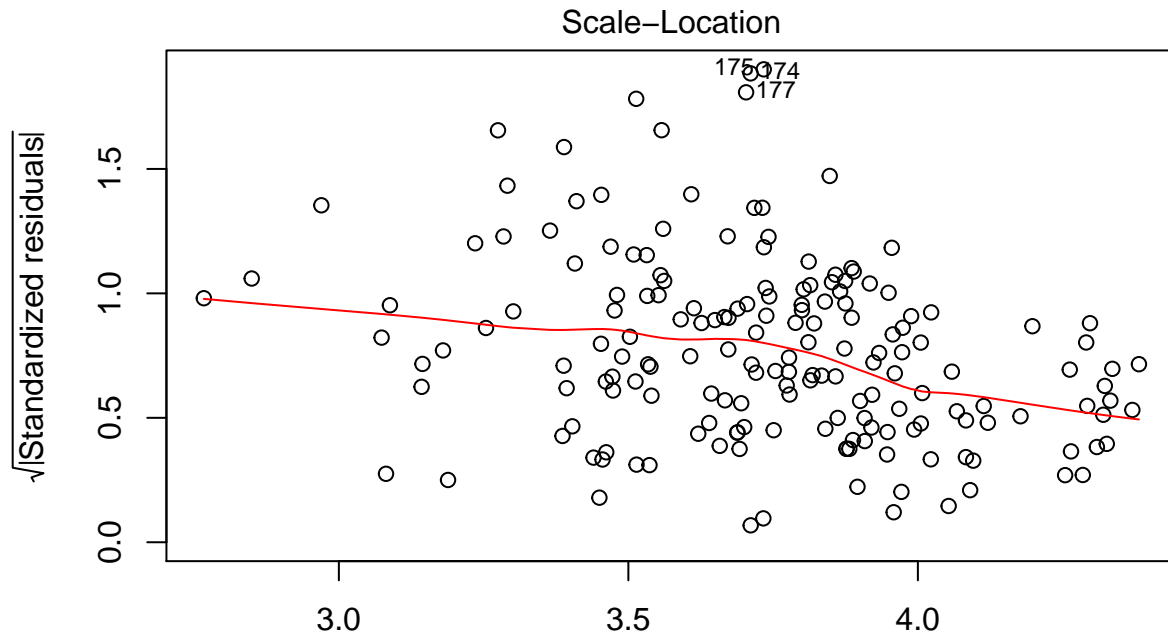
```r
summary(bc2.mod)
```

```
## 
## Call:
## lm(formula = log(bac) ~ poly(humi, 2) + poly(temp, 2) + humi *
##     temp + site, data = data)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.78788 -0.17757  0.06937  0.30669  0.99933
## 
## Coefficients: (2 not defined because of singularities)
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.5464355  0.1808930  25.133  < 2e-16 ***
## poly(humi, 2)1 2.2136434  1.2202996   1.814 0.071481 .
## poly(humi, 2)2 0.6154832  0.5244370   1.174 0.242233
## poly(temp, 2)1 4.1065044  1.2925575   3.177 0.001775 **
## poly(temp, 2)2 -1.9763786  0.5474308  -3.610 0.000405 ***
## humi                 NA         NA      NA       NA
## temp                 NA         NA      NA       NA
## site2         -0.3881101  0.1440833  -2.694 0.007793 **
## site3         -0.4521175  0.1452684  -3.112 0.002186 **
## site4         -0.4376138  0.1465561  -2.986 0.003255 **
## site5         -0.5830852  0.1451089  -4.018 8.87e-05 ***
## site6         -0.8651738  0.1450063  -5.966 1.42e-08 ***
## site7         -0.6941739  0.1443637  -4.809 3.39e-06 ***
```

```
## humi:temp      -0.0005589  0.0002483  -2.250 0.025740 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5103 on 166 degrees of freedom
## Multiple R-squared:  0.2837, Adjusted R-squared:  0.2363
## F-statistic: 5.978 on 11 and 166 DF,  p-value: 3.556e-08
```

#exmaple 5 We see the word Deviance twice over in the model output. Deviance is a measure of goodness of fit of a generalized linear model. Or rather, it's a measure of badness of fit–higher numbers indicate worse fit.

R reports two forms of deviance – the null deviance and the residual deviance. The null deviance shows how well the response variable is predicted by a model that includes only the intercept (grand mean).

By looking at deviance measurements Gamma with link log has best fit.

-Fisher Scoring What about the Fisher scoring algorithm? Fisher's scoring algorithm is a derivative of Newton's method for solving maximum likelihood problems numerically. This doesn't really tell you a lot that you need to know, other than the fact that the model did indeed converge, and had no trouble doing it.

- Information Criteria The Akaike Information Criterion (AIC) provides a method for assessing the quality of your model through comparison of related models. It's based on the Deviance, but penalizes you for making the model more complicated. Much like adjusted R-squared, it's intent is to prevent you from including irrelevant predictors.

However, unlike adjusted R-squared, the number itself is not meaningful. If you have more than one similar candidate models (where all of the variables of the simpler model occur in the more complex models), then you should select the model that has the smallest AIC.

So it's useful for comparing models, but isn't interpretable on its own. mylm has lowest AIC of 1540 while glm with gauusian has 1541 and with gamma it has 1581. In the glm model using gamma family humidity for the first time becomes significant.

```
t<- as.numeric(data$temp)
data$site <- as.numeric(data$site)
class(data$site)
```

```
## [1] "numeric"
```

```
m1 <- glm(bac ~ poly(humi,2)+poly(temp,2)+ humi*temp+ site,data=data,family=gaussian(link="log") )
m1
```

```
##
## Call:  glm(formula = bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp +
##     site, family = gaussian(link = "log"), data = data)
##
## Coefficients:
##    (Intercept)  poly(humi, 2)1  poly(humi, 2)2  poly(temp, 2)1
##      4.4461131       1.2392888       0.0373254       2.4735757
## poly(temp, 2)2            humi            temp            site
##     -1.5004662              NA              NA      -0.0961627
##      humi:temp
##     -0.0003762
##
## Degrees of Freedom: 177 Total (i.e. Null);  171 Residual
## Null Deviance:      75930
## Residual Deviance: 55040     AIC: 1542
```

```
summary(m1)
```

```
## 
## Call:
## glm(formula = bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp +
##     site, family = gaussian(link = "log"), data = data)
## 
## Deviance Residuals:
##     Min      1Q   Median      3Q      Max
## -45.033  -12.935    0.425   11.479   44.471
## 
## Coefficients: (2 not defined because of singularities)
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)      4.4461131  0.1247797  35.632  < 2e-16 ***
## poly(humi, 2)1   1.2392888  0.9760846   1.270 0.205933
## poly(humi, 2)2   0.0373254  0.3845972   0.097 0.922800
## poly(temp, 2)1   2.4735757  1.0220691   2.420 0.016561 *
## poly(temp, 2)2  -1.5004662  0.4426850  -3.389 0.000869 ***
## humi                   NA         NA      NA       NA
## temp                   NA         NA      NA       NA
## site            -0.0961627  0.0145607  -6.604 4.85e-10 ***
## humi:temp       -0.0003762  0.0001998  -1.883 0.061443 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## (Dispersion parameter for gaussian family taken to be 321.8716)
## 
##     Null deviance: 75925  on 177  degrees of freedom
## Residual deviance: 55040  on 171  degrees of freedom
## AIC: 1541.8
## 
## Number of Fisher Scoring iterations: 6
```

```r
anova(mylm)
```

```
## Analysis of Variance Table
## 
## Response: bac
##               Df Sum Sq Mean Sq F value     Pr(>F)
## poly(humi, 2)  2    494  246.94  0.7955 0.4530589
## poly(temp, 2)  2   4822 2410.98  7.7671 0.0005963 ***
## site           6  17416 2902.60  9.3508 7.812e-09 ***
## humi:temp      1   1666 1665.87  5.3667 0.0217473 *
## Residuals    166  51528  310.41
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
AIC(mylm)
```

```
## [1] 1540.064
```

```r
m2 <- glm(bac ~ poly(humi,2)+poly(temp,2)+ humi*temp+ site,data=data,family=Gamma(link="log"))
summary(m2)
```

```
## 
## ## Call:
## glm(formula = bac ~ poly(humi, 2) + poly(temp, 2) + humi * temp +
##     site, family = Gamma(link = "log"), data = data)
```

```
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -1.51027  -0.28276  -0.00202   0.20325   1.10556
##
## Coefficients: (2 not defined because of singularities)
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)    4.5147509  0.1328446  33.985  < 2e-16 ***
## poly(humi, 2)1 2.0091447  0.9744539   2.062  0.04074 *
## poly(humi, 2)2 0.1961375  0.4211306   0.466  0.64199
## poly(temp, 2)1 3.3655894  1.0296911   3.269  0.00131 **
## poly(temp, 2)2 -1.7115889  0.4393926  -3.895  0.00014 ***
## humi                  NA         NA      NA       NA
## temp                  NA         NA      NA       NA
## site          -0.0968153  0.0156023  -6.205 3.99e-09 ***
## humi:temp     -0.0004981  0.0001983  -2.511  0.01295 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.1689495)
##
##     Null deviance: 47.228  on 177  degrees of freedom
## Residual deviance: 37.331  on 171  degrees of freedom
## AIC: 1581.3
##
## Number of Fisher Scoring iterations: 6
```

#prediction regions

```r
p1<-predict(m1,data.frame(temp=t,site=6,humi=60),type="response",data=data)
```

```
## Warning in predict.lm(object, newdata, se.fit, scale = 1, type = if (type
## == : prediction from a rank-deficient fit may be misleading
```

```r
p1
```

```
##        1        2        3        4        5        6        7        8
## 39.20020 26.79531 27.94145 26.79531 38.15022 37.50825 37.50825 30.17726
##        9       10       11       12       13       14       15       16
## 29.07072 27.94145 27.94145 29.07072 29.07072 29.07072 37.50825 38.71544
##       17       18       19       20       21       22       23       24
## 39.20020 38.71544 37.50825 38.71544 38.71544 40.27853 40.27853 40.27853
##       25       26       27       28       29       30       31       32
## 39.59914 40.27853 39.91439 40.14118 40.32387 39.59914 39.59914 39.91439
##       33       34       35       36       37       38       39       40
## 39.59914 39.59914 40.32387 40.27853 39.91439 40.14118 40.27853 40.32387
##       41       42       43       44       45       46       47       48
## 40.14118 39.91601 39.91601 39.91601 39.91601 39.91601 40.14226 40.14226
##       49       50       51       52       53       54       55       56
## 39.59914 40.32387 39.91439 38.71230 39.19755 40.14118 40.27853 38.71230
##       57       58       59       60       61       62       63       64
## 38.71230 39.19755 38.14661 38.14661 38.71230 38.14661 36.78922 36.00629
##       65       66       67       68       69       70       71       72
## 32.29820 32.29820 35.16033 33.30067 33.30067 36.00629 37.50419 36.78922
##       73       74       75       76       77       78       79       80
## 36.00629 32.29820 32.29820 33.30067 38.14661 38.71230 37.50419 36.00629
```

```
##        81       82       83       84       85       86       87       88
## 37.50419 36.00629 36.00629 38.14661 38.14661 37.50419 36.00629 36.00629
##        89       90       91       92       93       94       95       96
## 35.16033 35.16033 40.32387 39.59914 40.14118 40.32387 39.59914 39.91439
##        97       98       99      100      101      102      103      104
## 40.14118 39.91601 39.60128 40.14226 40.14226 39.91601 40.14226 39.91601
##       105      106      107      108      109      110      111      112
## 40.27853 40.14118 40.32387 39.59914 39.59914 38.71230 38.71230 40.14226
##       113      114      115      116      117      118      119      120
## 40.14226 40.14226 40.14226 40.14226 39.60128 38.71544 38.71544 39.20020
##       121      122      123      124      125      126      127      128
## 39.20020 38.15022 38.71544 38.71544 27.94145 26.79531 27.94145 26.79531
##       129      130      131      132      133      134      135      136
## 37.50825 38.15022 37.50825 30.17726 40.27798 34.25662 29.07072 27.94145
##       137      138      139      140      141      142      143      144
## 26.79531 30.18378 31.26142 31.26142 36.01116 36.01116 30.18378 30.18378
##       145      146      147      148      149      150      151      152
## 36.01116 31.26142 30.18378 36.01116 30.18378 31.26142 36.79370 34.25662
##       153      154      155      156      157      158      159      160
## 40.27798 40.27798 40.27798 34.25662 34.25662 34.26218 34.26218 33.30652
##       161      162      163      164      165      166      167      168
## 33.30652 33.30652 34.26218 35.16556 33.30652 34.26218 31.26142 32.30431
##       169      170      171      172      173      174      175      176
## 31.26142 31.26142 31.26142 36.79370 36.01116 34.25662 36.79370 40.27798
##       177      178
## 34.25662 31.25508
```

```r
p2 <- predict(m2,data.frame(temp=t,site=6,humi=60),type="response",data=data)
```

```
## Warning in predict.lm(object, newdata, se.fit, scale = 1, type = if (type
## == : prediction from a rank-deficient fit may be misleading
```

```r
p2
```

```
##        1        2        3        4        5        6        7        8
## 40.54060 26.31650 27.60220 26.31650 39.29813 38.54168 38.54168 30.13078
##        9       10       11       12       13       14       15       16
## 28.87605 27.60220 27.60220 28.87605 28.87605 28.87605 38.54168 39.96610
##       17       18       19       20       21       22       23       24
## 40.54060 39.96610 38.54168 39.96610 39.96610 41.82826 41.82826 41.82826
##       25       26       27       28       29       30       31       32
## 41.04048 41.82826 41.41014 41.67538 41.88525 41.04048 41.04048 41.41014
##       33       34       35       36       37       38       39       40
## 41.04048 41.04048 41.88525 41.82826 41.41014 41.67538 41.82826 41.88525
##       41       42       43       44       45       46       47       48
## 41.67538 41.39261 41.39261 41.39261 41.39261 41.39261 41.66362 41.66362
##       49       50       51       52       53       54       55       56
## 41.04048 41.88525 41.41014 39.99996 40.56922 41.67538 41.82826 39.99996
##       57       58       59       60       61       62       63       64
## 39.99996 40.56922 39.33698 39.33698 39.99996 39.33698 37.75024 36.83807
##       65       66       67       68       69       70       71       72
## 32.55304 32.55304 35.85524 33.70544 33.70544 36.83807 38.58523 37.75024
##       73       74       75       76       77       78       79       80
## 36.83807 32.55304 32.55304 33.70544 39.33698 39.99996 38.58523 36.83807
##       81       82       83       84       85       86       87       88
```

```
## 38.58523 36.83807 36.83807 39.33698 39.33698 38.58523 36.83807 36.83807
##       89       90       91       92       93       94       95       96
## 35.85524 35.85524 41.88525 41.04048 41.67538 41.88525 41.04048 41.41014
##       97       98       99      100      101      102      103      104
## 41.67538 41.39261 41.01731 41.66362 41.66362 41.39261 41.66362 41.39261
##      105      106      107      108      109      110      111      112
## 41.82826 41.67538 41.88525 41.04048 41.04048 39.99996 39.99996 41.66362
##      113      114      115      116      117      118      119      120
## 41.66362 41.66362 41.66362 41.66362 41.01731 39.96610 39.96610 40.54060
##      121      122      123      124      125      126      127      128
## 40.54060 39.29813 39.96610 39.96610 27.60220 26.31650 27.60220 26.31650
##      129      130      131      132      133      134      135      136
## 38.54168 39.29813 38.54168 30.13078 41.83416 34.80864 28.87605 27.60220
##      137      138      139      140      141      142      143      144
## 26.31650 30.06281 31.29264 31.29264 36.78611 36.78611 30.06281 30.06281
##      145      146      147      148      149      150      151      152
## 36.78611 31.29264 30.06281 36.78611 30.06281 31.29264 37.70231 34.80864
##      153      154      155      156      157      158      159      160
## 41.83416 41.83416 41.83416 34.80864 34.80864 34.74973 34.74973 33.64365
##      161      162      163      164      165      166      167      168
## 33.64365 33.64365 34.74973 35.79962 33.64365 34.74973 31.29264 32.48878
##      169      170      171      172      173      174      175      176
## 31.29264 31.29264 31.29264 37.70231 36.78611 34.80864 37.70231 41.83416
##      177      178
## 34.80864 31.35896
```

```r
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.6.3
```

```r
df <- data.frame(data$temp,p1,p2)
g <- ggplot(df, aes(data$temp))
g <- g + geom_line(aes(y=p1), colour="red")
g <- g + geom_line(aes(y=p2), colour="green")
g
```
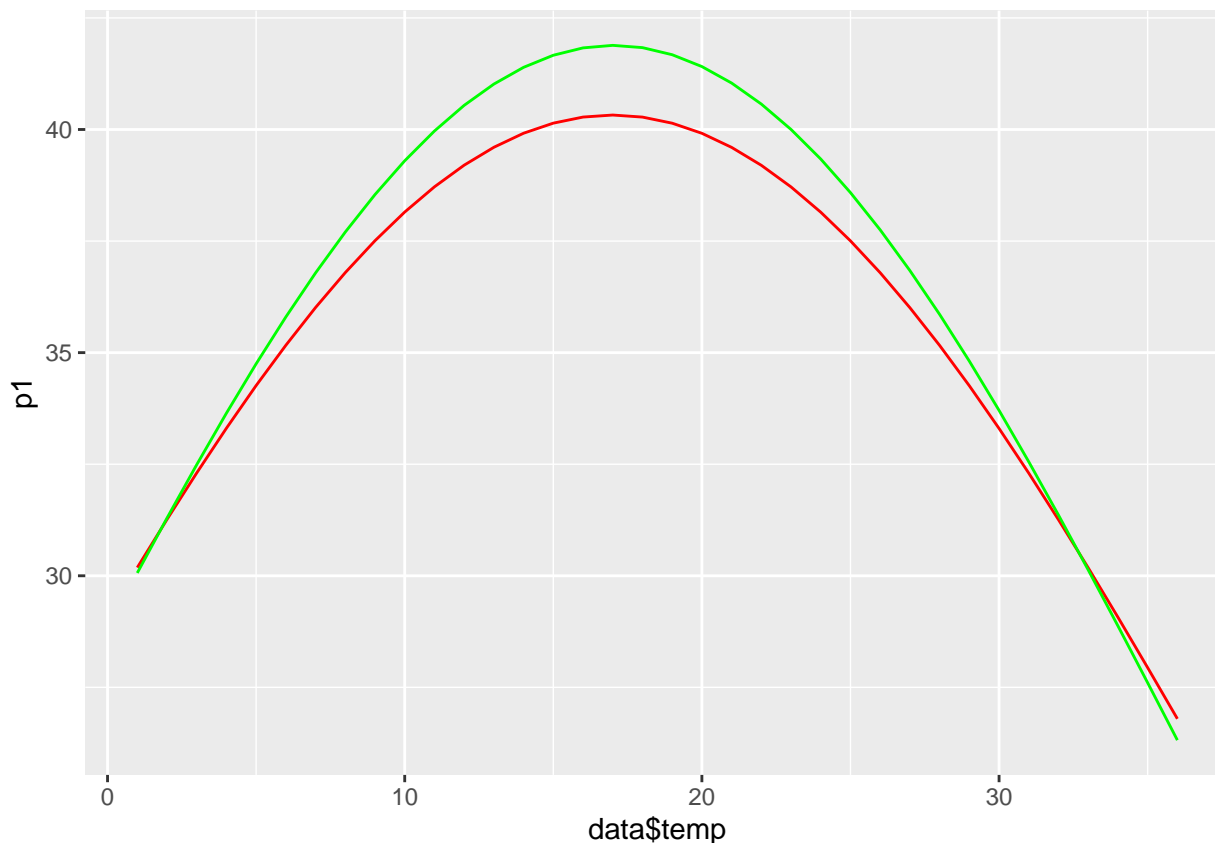
#example 6

When it comes to signifciance using a mutli-level model dosent help. All the paramtres are becomin insignificant. It is better to have two lvels of site and date as comapared to other levels.

```
data$date <- as.factor(data$date)
class(data$date)
```

```
## [1] "factor"
```

```
library(lme4)
```

```
## Warning: package 'lme4' was built under R version 3.6.3
```

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

```
M1 <- glmer(bac^(0.989) ~ poly(humi,2)+poly(temp,2)+ humi*temp+(site|date),data = data,family=gaussian()
```

```
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
```

```
## Warning: Some predictor variables are on very different scales: consider
## rescaling
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl =
## control$checkConv, : Model failed to converge with max|grad| = 1.18063 (tol
## = 0.002, component 1)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, : Model is nearly uniden
##   - Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
##   - Rescale variables?
```

```
summary(M1)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: gaussian  ( log )
## Formula:
## bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + humi * temp + (site |
##     date)
##    Data: data
##
##      AIC      BIC   logLik deviance df.resid
##   1871.5   1903.3   -925.7   1851.5      168
##
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -2.35942 -0.59964  0.06067  0.60784  2.89524
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  date     (Intercept) 28.69    5.356
##           site        20.64    4.544    -0.94
##  Residual             177.32   13.316
## Number of obs: 178, groups:  date, 26
##
## Fixed effects:
##                 Estimate Std. Error t value Pr(>|z|)
## (Intercept)    4.1951144  0.1091191  38.445  < 2e-16 ***
## poly(humi, 2)1 0.6543954  0.8976815   0.729  0.46601
## poly(humi, 2)2 -0.3126783 0.3947925  -0.792  0.42836
## poly(temp, 2)1 1.0008215  0.9829871   1.018  0.30861
## poly(temp, 2)2 -0.9785761 0.3688638  -2.653  0.00798 **
## humi:temp      -0.0001879 0.0001798  -1.045  0.29599
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) ply(h,2)1 ply(h,2)2 ply(t,2)1 ply(t,2)2
## poly(hm,2)1  0.832
## poly(hm,2)2 -0.039 -0.168
## ply(tmp,2)1  0.860  0.854    -0.056
## ply(tmp,2)2 -0.227 -0.315    -0.023    -0.297
## humi:temp   -0.958 -0.891     0.086    -0.912     0.278
## fit warnings:
## fixed-effect model matrix is rank deficient so dropping 2 columns / coefficients
## Some predictor variables are on very different scales: consider rescaling
## convergence code: 0
## Model failed to converge with max|grad| = 1.18063 (tol = 0.002, component 1)
## Model is nearly unidentifiable: very large eigenvalue
##  - Rescale variables?
## Model is nearly unidentifiable: large eigenvalue ratio
##  - Rescale variables?
```

```
M2 <- glmer(bac^(0.989) ~ poly(humi,2)+poly(temp,2)+ (humi*temp|date),data = data,family=gaussian(link=
```

```
## Warning in (function (fn, par, lower = rep.int(-Inf, n), upper =
## rep.int(Inf, : failure to converge in 10000 evaluations
```

```
## boundary (singular) fit: see ?isSingular
```

```
summary(M2)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
## Family: gaussian ( log )
## Formula: bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + (humi * temp |
##    date)
##   Data: data
##
##      AIC      BIC   logLik deviance df.resid
##   2220.6   2271.5  -1094.3   2188.6      162
##
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -2.39063 -0.72314 -0.03185  0.65901  3.02383
##
## Random effects:
##  Groups   Name        Variance  Std.Dev. Corr
##  date     (Intercept) 5.447e-04  0.02334
##           humi        2.440e+00  1.56201 -0.98
##           temp        1.343e+01  3.66423 -0.59  0.44
##           humi:temp   1.990e-02  0.14107  0.96 -0.91 -0.75
##  Residual             1.877e+02 13.69861
## Number of obs: 178, groups:  date, 26
##
## Fixed effects:
##                 Estimate Std. Error t value Pr(>|z|)
## (Intercept)       3.4781     0.5824   5.972 2.35e-09 ***
## poly(humi, 2)1    9.8740     2.8167   3.506 0.000456 ***
## poly(humi, 2)2   -0.4009     2.9081  -0.138 0.890354
## poly(temp, 2)1   -8.9447     6.2075  -1.441 0.149596
## poly(temp, 2)2    1.8826     1.1633   1.618 0.105589
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) ply(h,2)1 ply(h,2)2 ply(t,2)1
## poly(hm,2)1 -0.561
## poly(hm,2)2  0.626 -0.211
## ply(tmp,2)1  0.645 -0.650    -0.065
## ply(tmp,2)2  0.280  0.212     0.361    -0.224
## convergence code: 0
## boundary (singular) fit: see ?isSingular
## failure to converge in 10000 evaluations
```

```
M3 <- glmer(bac^(0.989) ~ poly(humi,2)+poly(temp,2)+ (humi*temp|date)+(site|date),data=data,family=gaus
```

```
## Warning in optwrap(optimizer, devfun, start, rho$lower, control =
## control, : convergence code 1 from bobyqa: bobyqa -- maximum number of
```

```
## function evaluations exceeded

## Warning in (function (fn, par, lower = rep.int(-Inf, n), upper =
## rep.int(Inf, : failure to converge in 10000 evaluations

## boundary (singular) fit: see ?isSingular
```

```r
summary(M3)
```

```
## Warning in vcov.merMod(object, use.hessian = use.hessian): variance-covariance matrix computed from
## not positive definite or contains NA values: falling back to var-cov estimated from RX

## Warning in vcov.merMod(object, correlation = correlation, sigm = sig): variance-covariance matrix co
## not positive definite or contains NA values: falling back to var-cov estimated from RX

## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: gaussian  ( log )
## Formula: bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + (humi * temp |
##     date) + (site | date)
##    Data: data
##
##      AIC      BIC   logLik deviance df.resid
##   2435.1   2495.5  -1198.5   2397.1      159
##
## Scaled residuals:
##     Min       1Q   Median       3Q      Max
## -2.08561 -0.59555  0.02311  0.63233  3.04673
##
## Random effects:
##  Groups   Name        Variance  Std.Dev. Corr
##  date     (Intercept) 2.967e+03 54.4742
##           humi        1.418e+01  3.7655  -0.77
##           temp        1.161e+01  3.4067  -0.87  0.98
##           humi:temp   8.555e-02  0.2925   0.58 -0.96 -0.88
##  date.1   (Intercept) 8.076e+02 28.4192
##           site        7.293e+00  2.7005  -0.68
##  Residual             1.114e+02 10.5553
## Number of obs: 178, groups:  date, 26
##
## Fixed effects:
##                Estimate Std. Error t value Pr(>|z|)
## (Intercept)       3.105      6.696   0.464  0.64284
## poly(humi, 2)1   20.340     50.349   0.404  0.68623
## poly(humi, 2)2  -10.309      3.793  -2.718  0.00657 **
## poly(temp, 2)1   33.373     41.535   0.803  0.42170
## poly(temp, 2)2   -1.471      2.294  -0.641  0.52131
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) ply(h,2)1 ply(h,2)2 ply(t,2)1
## poly(hm,2)1  0.649
## poly(hm,2)2  0.037 -0.064
## ply(tmp,2)1  0.634  0.989    -0.163
## ply(tmp,2)2  0.018 -0.009     0.163    -0.055
## convergence code: 0
```

```
## boundary (singular) fit: see ?isSingular
## failure to converge in 10000 evaluations
M4 <- glmer(bac^(0.989) ~ poly(humi,2)+poly(temp,2)+ (humi*temp|date),data =data,family=Gamma(link="log

## Warning in optwrap(optimizer, devfun, start, rho$lower, control =
## control, : convergence code 1 from bobyqa: bobyqa -- maximum number of
## function evaluations exceeded

## boundary (singular) fit: see ?isSingular
summary(M4)

## Generalized linear mixed model fit by maximum likelihood (Laplace
##    Approximation) [glmerMod]
##  Family: Gamma  ( log )
## Formula: bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + (humi * temp |
##     date)
##    Data: data
##
##      AIC      BIC   logLik deviance df.resid
##   1599.9   1650.8   -783.9   1567.9      162
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.9703 -0.6185  0.0625  0.5443  3.2056
##
## Random effects:
##  Groups   Name        Variance  Std.Dev.  Corr
##  date     (Intercept) 2.845e-01 0.5333454
##           humi        1.419e-04 0.0119129 -0.99
##           temp        9.740e-04 0.0312097 -1.00  0.99
##           humi:temp   8.634e-07 0.0009292  0.97 -0.97 -0.98
##  Residual             1.707e-01 0.4132078
## Number of obs: 178, groups:  date, 26
##
## Fixed effects:
##               Estimate Std. Error t value Pr(>|z|)
## (Intercept)    3.82800    0.06222  61.524   <2e-16 ***
## poly(humi, 2)1  0.41694    0.98997   0.421   0.6736
## poly(humi, 2)2 -0.39178    0.69535  -0.563   0.5731
## poly(temp, 2)1  0.49674    1.04986   0.473   0.6361
## poly(temp, 2)2 -1.86176    0.77437  -2.404   0.0162 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) ply(h,2)1 ply(h,2)2 ply(t,2)1
## poly(hm,2)1  0.486
## poly(hm,2)2  0.183   0.363
## ply(tmp,2)1  0.404   0.620     0.301
## ply(tmp,2)2  0.155  -0.179     0.122     0.021
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

```
M5 <-glmer(bac^(0.989) ~ poly(humi,2)+poly(temp,2)+ (site|date),data = data,family=Gamma(link="log"))
summary(M5)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Gamma  ( log )
## Formula: bac^(0.989) ~ poly(humi, 2) + poly(temp, 2) + (site | date)
##    Data: data
##
##      AIC      BIC   logLik deviance df.resid
##   1564.8   1593.5   -773.4   1546.8      169
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.17153 -0.57775 -0.01368  0.52429  2.05888
##
## Random effects:
##  Groups   Name        Variance Std.Dev. Corr
##  date     (Intercept) 0.038833 0.19706
##           site        0.006723 0.08199  -0.84
##  Residual             0.142481 0.37747
## Number of obs: 178, groups:  date, 26
##
## Fixed effects:
##               Estimate Std. Error t value Pr(>|z|)
## (Intercept)    3.95080    0.09085  43.486   <2e-16 ***
## poly(humi, 2)1 -0.24063    0.75170  -0.320    0.749
## poly(humi, 2)2 -0.10699    0.70576  -0.152    0.880
## poly(temp, 2)1  0.99522    0.68405   1.455    0.146
## poly(temp, 2)2 -0.89765    0.64543  -1.391    0.164
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) ply(h,2)1 ply(h,2)2 ply(t,2)1
## poly(hm,2)1 -0.172
## poly(hm,2)2 -0.024 -0.094
## ply(tmp,2)1 -0.251  0.322     0.095
## ply(tmp,2)2  0.090 -0.187    -0.155    -0.214
```