Forestry Example

 CZ

Fall, 2014

Forestry Example

The objective of the experiment was to predict total needle area (TNA) of a seedling based on

- trunk size: caliper (CAL)
- height (HT)
- product (interaction) of CAL and HT (HTCAL)

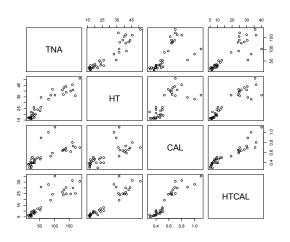
```
> dat <- read.table("forestry.txt", header=TRUE)</pre>
> head(dat)
     TNA HT CAL HTCAL
1 101.51 36.5 1.1 40.15
2 79.54 33.0 1.0 33.00
3 20.62 22.0 0.3 6.60
4 53.07 26.0 0.5 13.00
5 43.02 24.0 0.5 12.00
6 31.88 24.0 0.4 9.60
> dim(dat)
[1] 35 4
```

Look at data

> summary(dat) TNA HT CAL HTCAL Min. : 11.18 :16.00 :0.3000 Min. : 5.115 Min. Min. 1st Qu.: 21.55 1st Qu.:18.25 1st Qu.:0.4000 1st Qu.: 7.585 Median : 43.02 Median :24.00 Median :0.5000 Median:10.810 Mean : 70.35 Mean :28.39 Mean :0.5491 Mean :17.096 3rd Qu.:128.75 3rd Qu.:38.00 3rd Qu.:0.6550 3rd Qu.:25.720 Max. :186.00 Max. :51.00 Max. :1,1000 Max. :40.150

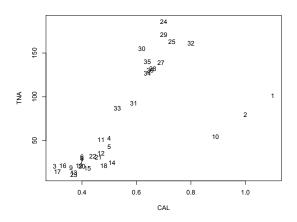
Look at data

> pairs(dat)



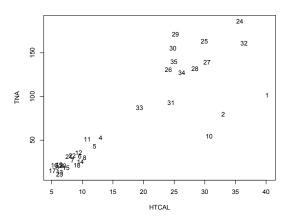
Scatterplot

- > plot(dat\$CAL, dat\$TNA, type="n", xlab="CAL", ylab="TNA")
- > text(dat\$CAL, dat\$TNA)



Scatterplot

- > plot(dat\$HTCAL, dat\$TNA, type="n", xlab="HTCAL", ylab="TNA")
- > text(dat\$HTCAL, dat\$TNA)



Data Checking

```
Look at cases 1, 2 and 10

> dat[c(1,2,10),]

TNA HT CAL HTCAL

1 101.51 36.5 1.10 40.150

2 79.54 33.0 1.00 33.000

10 54.30 34.5 0.89 30.705
```

- It was found they are recording errors
- We will remove them for subsequent analyses

$$>dat2=dat[-c(1,2,10),]$$

Model Fitting

Consider the model:

$$TNA = \beta_0 + \beta_1 CAL + \beta_2 HT + \beta_3 HTCAL + \epsilon$$

```
> fit2 <- lm(TNA~CAL+HT+HTCAL, data=dat2)</pre>
```

> summary(fit2)

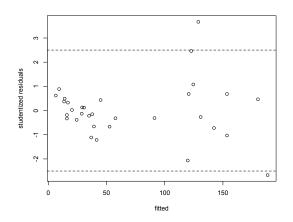
Residuals:

Mın	1Ų	Median	34	Max
-27.387	-6.534	-2.072	6.424	42.147

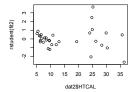
Coefficients:

Residual standard error: 14.94 on 28 degrees of freedom Multiple R-squared: 0.9423, Adjusted R-squared: 0.9361 F-statistic: 152.5 on 3 and 28 DF, p-value: < 2.2e-16

```
> plot(fitted(fit2), rstudent(fit2), xlab="fitted",
  ylab="studentized residuals")
> abline(h=c(-2.5,2.5),lty=2)
```

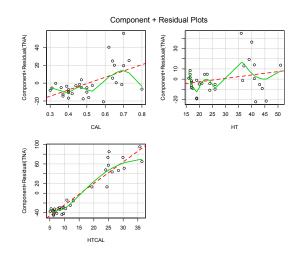


Studentized Residuals vs. Each Predictor



Partial Residuals vs. Each Predictor

- > library(car)
- > crPlots(fit2)

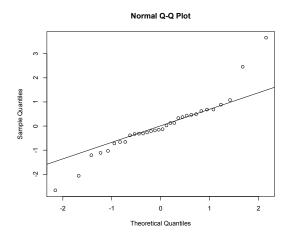


Summary of Residual Plots

- (Studentized) Residuals vs. Fitted Values Purpose: check whether $E(\epsilon) = 0$
 - ▶ Random pattern (no pattern), the above assumption is correct. Next, check non-constant variance, outliers...
 - Non-random pattern, need to check which term is nonlinear.
- (Studentized) Residuals vs. Each Predictor $x_j, j = 1, ..., p$ Purpose: check if E(y) is linear in x_j
 - Random pattern (no pattern), y is linear in x_i
 - Non-random pattern, y is not linear in x_i
- OR Partial residuals vs. Each Predictor $x_j, j = 1, ..., p$ Purpose: check if E(y) is linear in x_j
 - Linear pattern, y is linear in x_i
 - ▶ Non-linear pattern, y is not linear in x_j

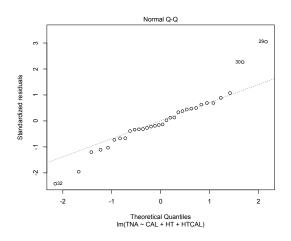
QQ Plot

- > qqnorm(rstudent(fit2))
- > qqline(rstudent(fit2))



QQ Plot

> plot(fit2, which=2)



Normality Test

Shapiro-Wilk Normality Test:
 H₀: the (studentized) residuals follow a normal distribution
 H_a: the (studentized) residuals do not follow a normal distribution

In R,

```
> shapiro.test(rstudent(fit2))
Shapiro-Wilk normality test

data: rstudent(fit2)
W = 0.9158, p-value = 0.01604
```

• Since p-value= 0.01604 < 0.05, Reject H_0 .

Leverage

```
> hatvalues(fit2)
0.22584297 0.08295463 0.08516022 0.08810006 0.05319807 0.13408625 0.10333210 0.0644
                                          15
                   13
                               14
                                                      16
                                                                 17
                                                                            18
0.07980348 0.08588250 0.16550782 0.06615480 0.15089373 0.19603094 0.10656738 0.0882
        20
                   21
                              22
                                          23
                                                     24
                                                                 25
                                                                            26
0.07027305 0.10956585 0.06083412 0.08588250 0.29579006 0.14472101 0.08140189 0.1089
        28
                   29
                              30
                                          31
                                                     32
                                                                 33
                                                                            34
0.09263875 0.14538859 0.09234465 0.15984114 0.42486893 0.19216122 0.08390370 0.0752
> 2*4/32
[1] 0.25
> which(hatvalues(fit2)>0.25)
[1] 24 32
```

Cook's Distance

```
> cooks.distance(fit2)
1.823248e-02 2.352843e-03 1.049554e-02 1.144257e-03 2.461355e-04 1.710854e-02 4.118
          11
                       12
                                     13
                                                  14
                                                               15
                                                                             16
3.347968e-03 5.203396e-04 8.172448e-04 7.150411e-02 2.693299e-03 3.515950e-02 2.404
          18
                       19
                                     20
                                                  21
                                                               22
                                                                             23
3.667164e-02 2.709213e-03 1.248025e-05 5.240002e-04 2.532045e-04 2.634907e-03 2.349
          25
                       26
                                    27
                                                  28
                                                               29
                                                                             30
2.016396e-02 1.060849e-02 3.242375e-02 1.351241e-02 3.959810e-01 1.303862e-01 1.816
          32
                       33
                                    34
                                                  35
1.078827e+00 5.904776e-03 1.664538e-03 2.351611e-02
> qf(0.5,4,32-4)
[1] 0.8598354
```

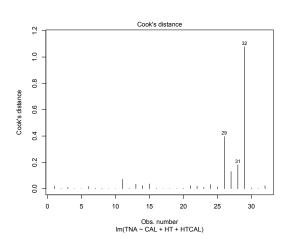
CZ

[1] 32

> which(cooks.distance(fit2)>0.86)

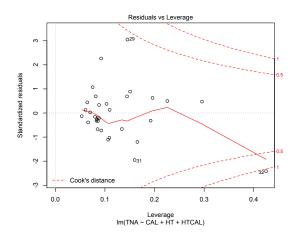
Cook's Distance

> plot(fit2, which=4)



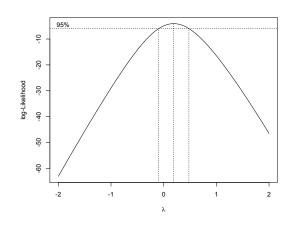
Residual, Leverage & Cook's D

> plot(fit2, which=5)



Box Cox Transformation

- > library(MASS)
- > boxcox(fit2)



Transformed Model

Consider the model:

$$log(TNA) = \beta_0 + \beta_1 CAL + \beta_2 HT + \beta_3 HTCAL + \epsilon$$

Residuals:

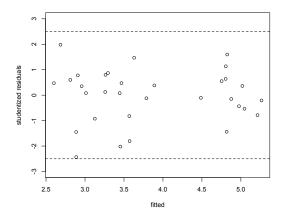
```
Min 1Q Median 3Q Max -0.47292 -0.11734 0.02279 0.12950 0.38300
```

Coefficients:

Residual standard error: 0.2204 on 28 degrees of freedom Multiple R-squared: 0.9471, Adjusted R-squared: 0.9414 F-statistic: 167.1 on 3 and 28 DF, p-value: < 2.2e-16

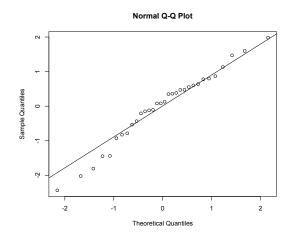
Residual vs fitted

```
> plot(fitted(fit3), rstudent(fit3), xlab="fitted",
ylab="studentized residuals")
> abline(h=c(-2.5, 2.5), lty=2)
```



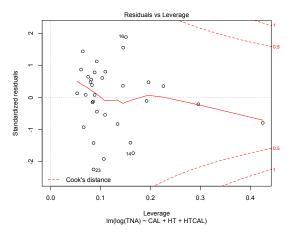
QQ Plot

- > qqnorm(rstudent(fit3))
- > qqline(rstudent(fit3))



Residual, Leverage & Cook's D

```
> plot(fit3, which=5)
> qf(0.5,4,32-4)
[1] 0.8598354
> 2*4/32
[1] 0.25
```



Conclusion

The final fitted regression model is:

$$log(\widehat{TNA}) = -0.447 + 6.022CAL + 0.105HT - 0.108HTCAL$$

Based on the final model, we can:

- Interpretation
- Estimation
- Prediction