

MAST30025: Linear Statistical Models

Solutions to Week 7 Lab

1. Recall the joint confidence region for the parameters of a full rank linear model:

$$(\mathbf{b} - \boldsymbol{\beta})^T X^T X (\mathbf{b} - \boldsymbol{\beta}) \leq ps^2 f_\alpha.$$

Use this to derive a test for the hypothesis $H_0 : \boldsymbol{\beta} = \boldsymbol{\beta}^*$. Show that this test is equivalent to the test for $H_0 : \boldsymbol{\beta} = \boldsymbol{\beta}^*$ obtained using the general linear hypothesis.

Solution: We do not reject H_0 if and only if $\boldsymbol{\beta}^*$ lies in the joint confidence region, i.e., if and only if

$$(\mathbf{b} - \boldsymbol{\beta}^*)^T X^T X (\mathbf{b} - \boldsymbol{\beta}^*) \leq ps^2 f_\alpha.$$

But the general linear hypothesis test does not reject H_0 if and only if

$$\begin{aligned} \frac{(\mathbf{b} - \boldsymbol{\beta}^*)^T X^T X (\mathbf{b} - \boldsymbol{\beta}^*)/p}{SS_{Res}/(n-p)} &\leq f_\alpha \\ (\mathbf{b} - \boldsymbol{\beta}^*)^T X^T X (\mathbf{b} - \boldsymbol{\beta}^*) &\leq p \frac{SS_{Res}}{n-p} f_\alpha \\ (\mathbf{b} - \boldsymbol{\beta}^*)^T X^T X (\mathbf{b} - \boldsymbol{\beta}^*) &\leq ps^2 f_\alpha. \end{aligned}$$

Therefore the two tests are equivalent.

2. Load the **beef** dataset from the website:

```
> beef <- read.csv('../data/beef.csv')
```

In the USA, the Cattlemen's Beef Board and the National Cattlemen's Beef Association promote the consumption of beef with an advertising campaign using the theme "Beef: it's what's for dinner". The campaign is paid for by the "Beef Checkoff", a law that requires all cattle producers to pay \$1 per head of cattle sold to support beef/veal promotion and research. In 1988 the Missoulian newspaper surveyed the cattle growers of Montana, and for each of Montana's 56 counties reported the percent of growers voting "yes" for the checkoff.

In this question we explain the size of the yes vote in terms of the characteristics of the farms in each county. Data on farms is taken from the U.S. Bureau of the Census, City and County Data Book, 1986. The variables given in the dataset are:

yes Percentage of farmers voting "yes" for the checkoff

big Percentage of farms with 500 acres or more

prin Percentage of operators whose principle income is farming

size Average size of farm (hundreds of acres)

val Average value of products sold (\$1000's)

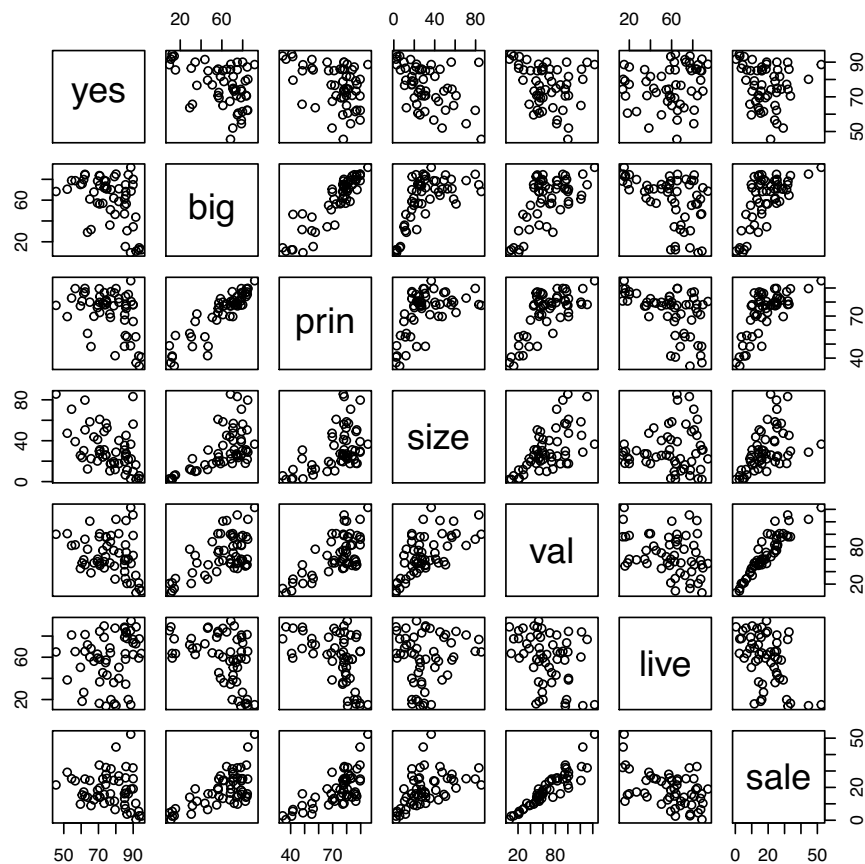
live Percentage of products sold from livestock and poultry

sale Percentage of farms with sales of \$100,000 or more

- (a) Use **pairs** to plot the data. Is there any evidence of non-linearity or heteroskedasticity?

Solution:

```
> pairs(beef)
```



There is some evidence of heteroskedasticity in `yes`, particularly vs `size` and `val`. We could consider taking logs of `size` and `val` and seeing if that improved the fit, though we won't for the moment.

- (b) Using the `add1` and `drop1` commands, use forward and backward selection to find parsimonious models for `yes`.

Solution: We use a 5% significance level. Forward selection:

```
> model0 <- lm(yes ~ 1, data = beef)
> add1(model0, scope = ~ . + big + prin + size + val + live + sale, test = "F")
Single term additions
```

Model:

`yes ~ 1`

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>		7689.2	277.64			
big	1	1482.29	6206.9	267.65	12.8960	0.0007112 ***
prin	1	1288.87	6400.3	269.37	10.8744	0.0017287 **
size	1	1925.80	5763.4	263.50	18.0439	8.572e-05 ***
val	1	538.85	7150.3	275.57	4.0694	0.0486484 *
live	1	226.19	7463.0	277.97	1.6366	0.2062603
sale	1	214.20	7475.0	278.06	1.5474	0.2188955

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> model1 <- lm(yes ~ size, data = beef)
> add1(model1, scope = ~ . + big + prin + val + live + sale, test = "F")
Single term additions
```

Model:

```
yes ~ size
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>		5763.4	263.50			
big	1	218.65	5544.7	263.33	2.0900	0.15415
prin	1	222.46	5540.9	263.30	2.1279	0.15054
val	1	35.20	5728.2	265.16	0.3256	0.57064
live	1	348.02	5415.3	262.01	3.4060	0.07055
sale	1	69.35	5694.0	264.82	0.6455	0.42533

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

None of the variables make a significant difference when added, so we end up with the model

$$yes = \beta_0 + \beta_1 size + \epsilon.$$

Backward selection:

```
> model0 <- lm(yes ~ ., data = beef)
```

```
> drop1(model0, scope = ~ ., test = "F")
```

Single term deletions

Model:

```
yes ~ big + prin + size + val + live + sale
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>		4540.7	260.15			
big	1	0.51	4541.2	258.15	0.0055	0.941407
prin	1	64.15	4604.9	258.93	0.6923	0.409434
size	1	750.11	5290.8	266.71	8.0946	0.006463 **
val	1	48.95	4589.7	258.75	0.5282	0.470810
live	1	461.28	5002.0	263.56	4.9778	0.030283 *
sale	1	411.63	4952.3	263.01	4.4420	0.040206 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> model1 <- lm(yes ~ prin + size + val + live + sale, data = beef)
```

```
> drop1(model1, scope = ~ ., test = "F")
```

Single term deletions

Model:

```
yes ~ prin + size + val + live + sale
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>		4541.2	258.15			
prin	1	201.55	4742.8	258.58	2.2191	0.142595
size	1	1079.23	5620.5	268.09	11.8826	0.001158 **
val	1	52.81	4594.0	256.80	0.5815	0.449322
live	1	492.67	5033.9	261.92	5.4244	0.023938 *
sale	1	436.69	4977.9	261.30	4.8080	0.033008 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
> model2 <- lm(yes ~ prin + size + live + sale, data = beef)
```

```
> drop1(model2, scope = ~ ., test = "F")
```

Single term deletions

Model:

```
yes ~ prin + size + live + sale
```

	Df	Sum of Sq	RSS	AIC	F value	Pr(>F)
<none>		4594.0	256.80			

```

prin    1    198.74 4792.8 257.17  2.2063 0.1436041
size    1   1566.35 6160.4 271.23 17.3886 0.0001183 ***
live    1    467.28 5061.3 260.23  5.1875 0.0269741 *
sale    1    804.56 5398.6 263.84  8.9317 0.0043034 **
---

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

> model3 <- lm(yes ~ size + live + sale, data = beef)
> drop1(model3, scope = ~ ., test = "F")

```

Single term deletions

Model:

```

yes ~ size + live + sale
      Df Sum of Sq    RSS    AIC F value    Pr(>F)
<none>                4792.8 257.17
size    1    2600.39 7393.2 279.45 28.2134 2.294e-06 ***
live    1     901.24 5694.0 264.82  9.7781  0.00289 **
sale    1     622.57 5415.3 262.01  6.7546  0.01214 *
---

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

All of the remaining variables make a significant difference when removed, so we end up with the model

$$yes = \beta_0 + \beta_1 size + \beta_2 sale + \beta_3 live + \epsilon.$$

- (c) Using the `step` command, starting from a model with just an intercept, use the AIC and stepwise selection to choose a model.

Solution:

```

> basemodel <- lm(yes ~ 1, data = beef)
> model <- step(basemodel, scope = ~ . + big + prin + size + val + live + sale)

```

Start: AIC=277.64

```
yes ~ 1
```

```

      Df Sum of Sq    RSS    AIC
+ size  1    1925.80 5763.4 263.50
+ big   1    1482.29 6206.9 267.65
+ prin  1    1288.87 6400.3 269.37
+ val   1     538.85 7150.3 275.57
<none>                7689.2 277.64
+ live  1     226.19 7463.0 277.97
+ sale  1     214.20 7475.0 278.06

```

Step: AIC=263.5

```
yes ~ size
```

```

      Df Sum of Sq    RSS    AIC
+ live  1     348.02 5415.3 262.01
+ prin  1     222.46 5540.9 263.30
+ big   1     218.65 5544.7 263.33
<none>                5763.4 263.50
+ sale  1      69.35 5694.0 264.82
+ val   1      35.20 5728.2 265.16
- size  1    1925.80 7689.2 277.64

```

Step: AIC=262.01

```
yes ~ size + live
```

```

      Df Sum of Sq    RSS    AIC

```

```

+ sale 1      622.57 4792.8 257.17
+ val  1      332.68 5082.7 260.46
<none>                5415.3 262.01
- live 1      348.02 5763.4 263.50
+ prin 1       16.75 5398.6 263.84
+ big  1       15.35 5400.0 263.85
- size 1     2047.63 7463.0 277.97

```

Step: AIC=257.17
yes ~ size + live + sale

```

      Df Sum of Sq    RSS    AIC
+ prin 1      198.74 4594.0 256.80
<none>                4792.8 257.17
+ big  1       92.28 4700.5 258.08
+ val  1       50.00 4742.8 258.58
- sale 1      622.57 5415.3 262.01
- live 1      901.24 5694.0 264.82
- size 1     2600.39 7393.2 279.45

```

Step: AIC=256.8
yes ~ size + live + sale + prin

```

      Df Sum of Sq    RSS    AIC
<none>                4594.0 256.80
- prin 1      198.74 4792.8 257.17
+ val  1       52.81 4541.2 258.15
+ big  1        4.37 4589.7 258.75
- live 1      467.28 5061.3 260.23
- sale 1      804.56 5398.6 263.84
- size 1     1566.35 6160.4 271.23

```

In this case our model is even larger:

$$yes = \beta_0 + \beta_1 size + \beta_2 sale + \beta_3 live + \beta_4 prin + \epsilon.$$

- (d) Show that the model found in 2c can be improved by adding the interaction term **size*sale**. (Important here is how you judge “improved”).

Use stepwise selection again to see if adding **size*sale** can let you remove any other variables from the model.

Solution:

```

> model1 <- lm(yes ~ size + live + sale + prin + size*sale, data = beef)
> model2 <- step(model1, scope = ~ .)

```

Start: AIC=251.08
yes ~ size + live + sale + prin + size * sale

```

      Df Sum of Sq    RSS    AIC
- prin 1         8.54 4010.7 249.20
<none>                4002.1 251.08
- live 1      535.79 4537.9 256.11
- size:sale 1     591.90 4594.0 256.80

```

Step: AIC=249.2
yes ~ size + live + sale + size:sale

```

      Df Sum of Sq    RSS    AIC
<none>                4010.7 249.20
+ prin 1         8.54 4002.1 251.08

```

```
- live      1      563.60 4574.3 254.56
- size:sale 1      782.10 4792.8 257.17
```

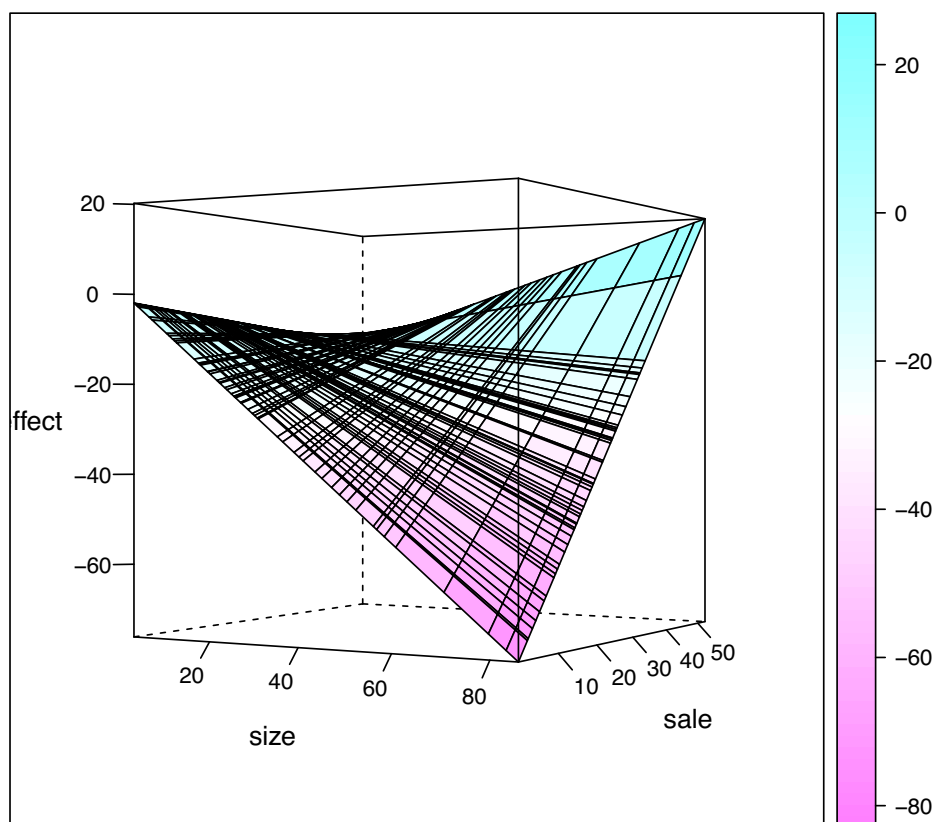
The model `yes ~ size + live + sale + prin` has AIC 256.80 and the model `yes ~ size + live + sale + prin + size*sale` has AIC 251.08, indicating a better fit. Removing `prin` improves the AIC further. Note that R does not consider removing `size` or `sale` while `size:sale` is still in the model. Current model is

$$yes = \beta_0 + \beta_1 size + \beta_2 sale + \beta_3 live + \beta_{12} size \times sale + \epsilon.$$

- (e) Suppose that β_1 , β_2 and β_{12} are the coefficients of $x_1 = \text{size}$, $x_2 = \text{sale}$ and $\text{size} \times \text{sale}$, in the model from 2d. Plot $\beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_1 \times x_2$ as a function of (x_1, x_2) , to see the combined effect of these variables on the yes vote. You may need the `wireframe` function from the `lattice` library, and also `expand.grid`.

Solution:

```
> library(lattice)
> df <- expand.grid(size=beef$size, sale=beef$sale)
> f <- function(x, y) sum( model2$coefficients[c(2, 4, 5)] * c(x, y, x*y) )
> df$effect <- mapply(f, df$size, df$sale)
> wireframe(effect ~ size + sale, data = df, drape = T,
+   scales = list(arrows=F), screen = list(z = 30, x = -90, y = -60))
```



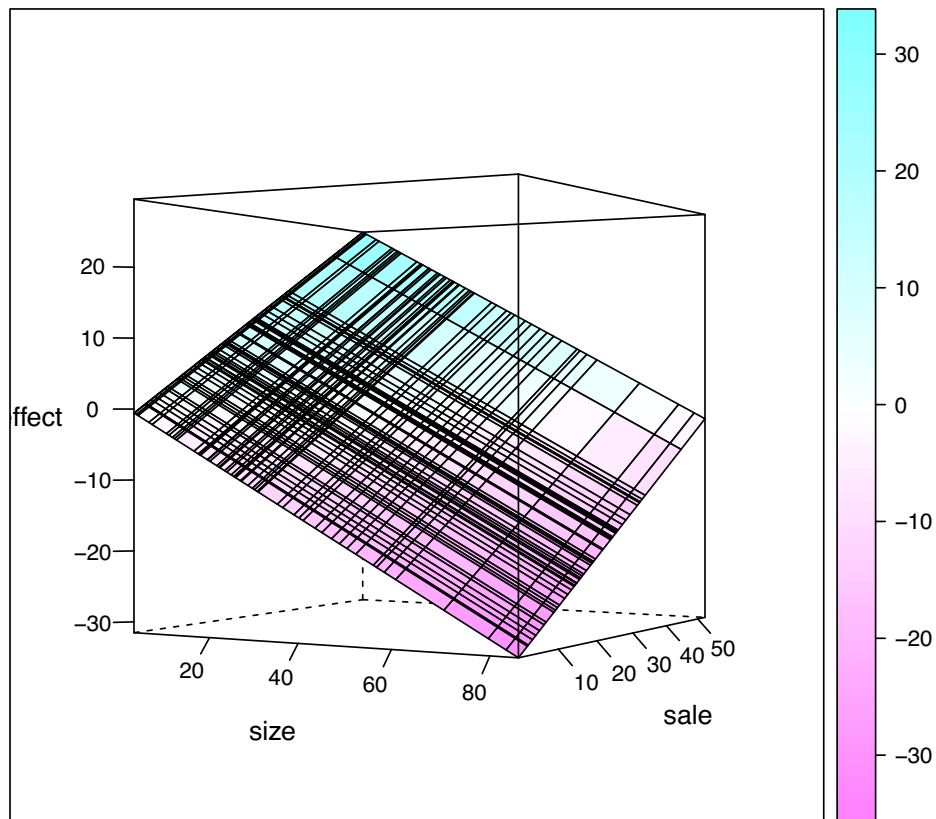
We see that `sale` has a big effect on `yes` when `size` is large, but when `size` is small `sale` isn't so important.

- (f) Repeat the above question using the model with no `size*sale` interaction term from 2c.

Solution:

```
> f <- function(x, y) sum( model$coefficients[c(2, 4)] * c(x, y) )
> df$effect <- mapply(f, df$size, df$sale)
```

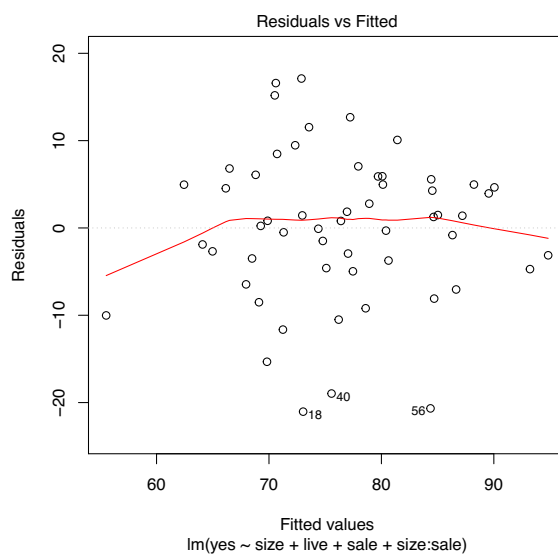
```
> wireframe(effect ~ size + sale, data = df, drape = T,
+   scales = list(arrows=F), screen = list(z = 30, x = -90, y = -60))
```



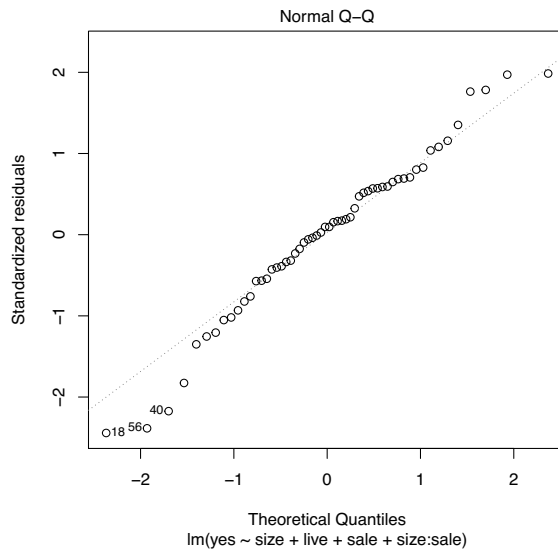
- (g) Use the diagnostic plots provided by R to assess the model from 2d. Refer back to 2a; do you need to transform the data and start again?

Solution:

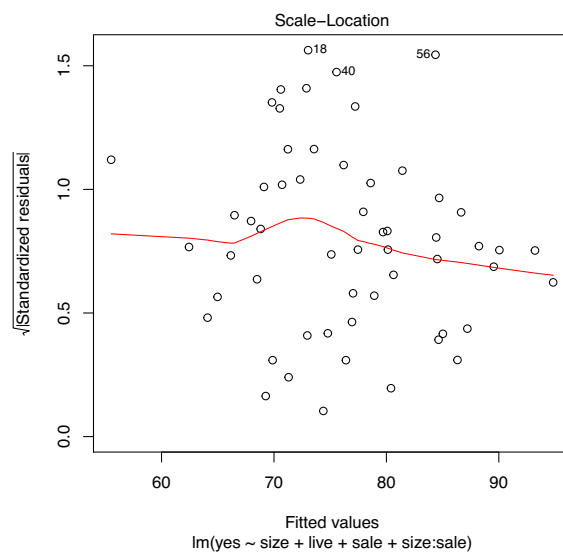
```
> plot(model2, which = 1)
```



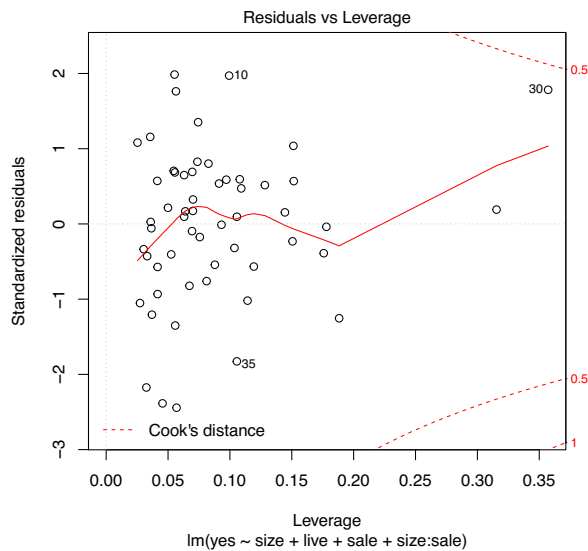
```
> plot(model2, which = 2)
```



```
> plot(model2, which = 3)
```



```
> plot(model2, which = 5)
```

There is perhaps some evidence of heteroskedasticity in the plot of the square root of the absolute standardised residuals against fitted values, but not enough to be a problem, so no need to consider transforming the data.

- (h) Which are the most important variables when it comes to predicting the yes vote? In deciding this, take into account the average size of the variables as well as the size of the fitted coefficients.

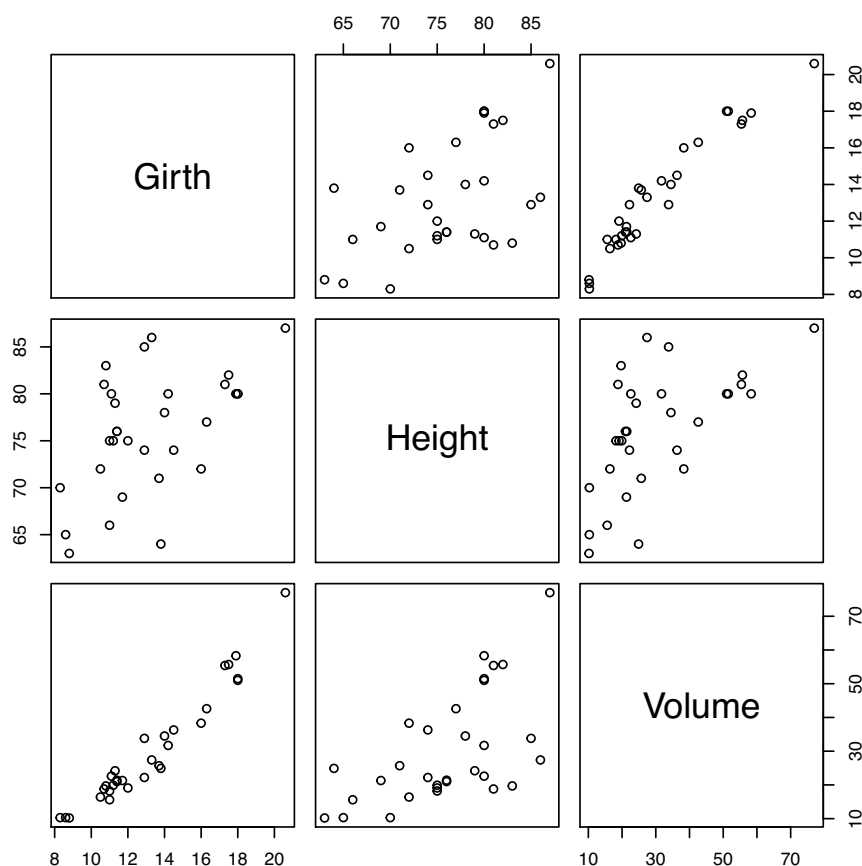
Solution: Significance is not the same as importance. The average contribution of each variable to the overall mean can be calculated as follows

```
> mean(beef$size)*model2$coefficients[2]
      size
-27.85712
> mean(beef$live)*model2$coefficients[3]
      live
10.38959
> mean(beef$sale)*model2$coefficients[4]
      sale
-3.22588
> mean(beef$size*beef$sale)*model2$coefficients[5]
size:sale
16.12498
```

So `size` has the most influence, followed by `sale` because of the interaction term.

3. Load and examine the dataset `trees` using

```
> data(trees)
> ?trees
> pairs(trees)
```



We will model the volume of a black cherry tree as a function of its girth and height.

- (a) By calculating $R(\gamma_1|\gamma_2)$ and SS_{Res} from the data \mathbf{y} and design matrix X , use an F test to determine if including the variable **Height** significantly improves the model fitted using only **Girth** (and an intercept).

Repeat the test using the `lm` and `anova` commands, to see if you get the same numbers.

Solution: By “hand”:

```
> y <- trees$Volume
> n <- length(y)
> X <- cbind(1, trees$Girth, trees$Height)
> b <- solve(t(X) %*% X, t(X) %*% y)
> (SS_res <- sum((y - X %*% b)^2))
[1] 421.9214

> SS_reg <- sum((X %*% b)^2)
> X2 <- X[,-3]
> b2 <- solve(t(X2) %*% X2, t(X2) %*% y)
> SS_reg2 <- sum((X2 %*% b2)^2)
> (R_glg2 <- SS_reg - SS_reg2)
[1] 102.3812

> (Fstat <- (R_glg2/1)/(SS_res/(n - 3)))
[1] 6.79433

> pf(Fstat, 1, n - 3, lower.tail = F)
[1] 0.01449097
```

Using `lm` and `anova`:

```
> model1 <- lm(Volume ~ Girth, data = trees)
> model2 <- lm(Volume ~ Girth + Height, data = trees)
> anova(model1, model2)
```

Analysis of Variance Table

Model 1: Volume ~ Girth

Model 2: Volume ~ Girth + Height

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	29	524.30				
2	28	421.92	1	102.38	6.7943	0.01449 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

- (b) Add variables `Girth` squared and `Girth` squared times `Height` to the model, then use stepwise selection to simplify the model. (You can use `step` for this step.)

Comment on the form of your final model.

Solution:

```
> trees$GirthSq <- trees$Girth^2
> model <- lm(Volume ~ Girth + Height + GirthSq + GirthSq*Height, data = trees)
> model <- step(model, scope = ~ .)
```

Start: AIC=64.36

Volume ~ Girth + Height + GirthSq + GirthSq * Height

	Df	Sum of Sq	RSS	AIC
- Girth	1	0.2288	179.27	62.402
- Height:GirthSq	1	6.9694	186.01	63.547
<none>			179.04	64.363

Step: AIC=62.4

Volume ~ Height + GirthSq + Height:GirthSq

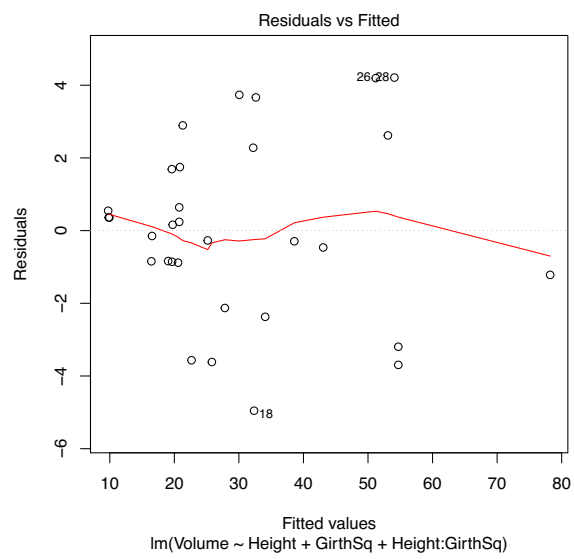
	Df	Sum of Sq	RSS	AIC
<none>			179.27	62.402
+ Girth	1	0.229	179.04	64.363
- Height:GirthSq	1	40.164	219.44	66.669

Note that R will not attempt to drop `GirthSq` and `Height` while `GirthSq*Height` is still in the model.

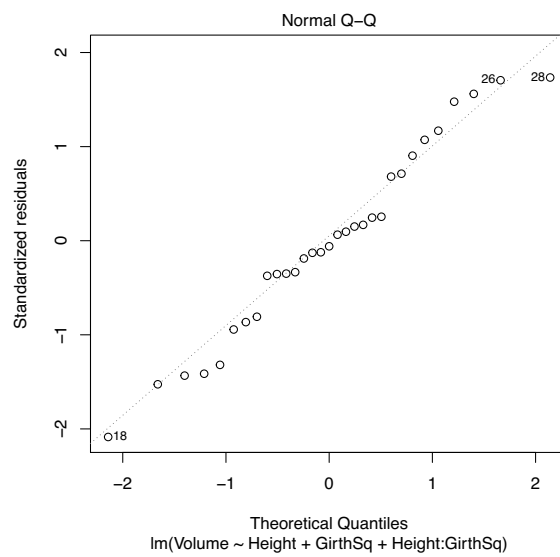
- (c) Use diagnostic plots to check the fit of your final model.

Solution:

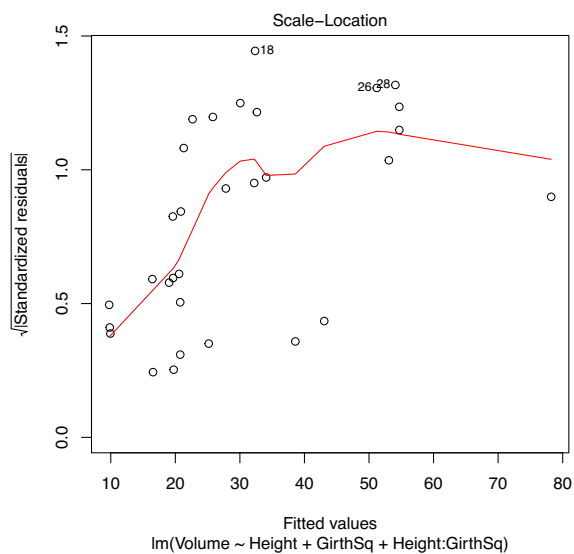
```
> plot(model, which = 1)
```



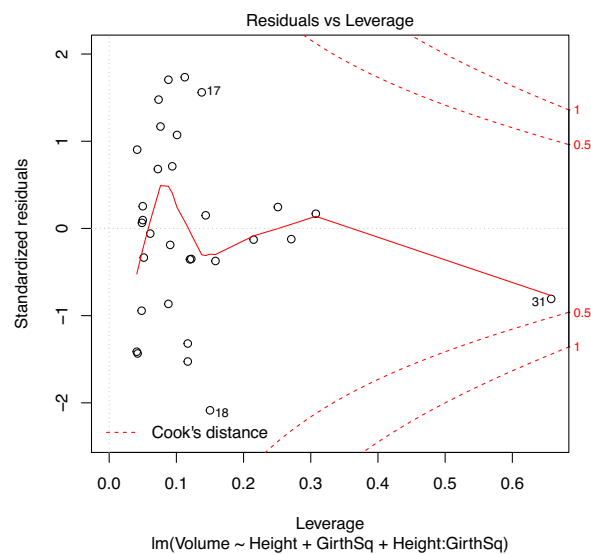
```
> plot(model, which = 2)
```



```
> plot(model, which = 3)
```



```
> plot(model, which = 5)
```



From the third plot we see that the residuals get larger as the fitted values increase. Perhaps, rather than including the girth squared term, we should take logs. The only way to be sure is to try and see if the residuals look better. If you do this you will see that the diagnostic plots are much the same for the transformed model as for the previous one, making it hard to choose between them. (Note that because we have transformed the response, we can't meaningfully compare the AIC scores for the two models.)