

Supplementary information for ‘Stable isotopes combined with conventional dietary approaches reveal plasticity in central-place foraging status of little penguins (*Eudyptula minor*)’

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Supplementary information reporting the data analysis of this manuscript in a reproducible manner. Using RMarkdown in RStudio (RStudio Team 2015), we report here each step of the data analysis for each response variable analysed as follow:

- R Libraries
- File inspection
- Data exploration. Analysis run for all variables but reported by carbon only
- Full model $Response.Variable = BreedingStage + CalendarYear + Sex + BreedingSuccess + BreedingStage : Sex$
- Model selection
- Dredging (Barton 2013)
- Model validation
- Response variables, numbered from 6 to 14 to match sub-headings below:

- 6) Carbon delta 13
- 7) Nitrogen delta 15
- 8) Body mass
- 9) Anchovy
- 10) Barracouta
- 11) Pilchard
- 12) Squid
- 13) SIBER
- 14) Diversity

-
- 1) Reading datase

```
Sidata<- read.table(file="LP_SIA_adults_2003_11.txt", header=T, sep="\t",dec = ".")
```

- 2) Libraries

```
library(lattice)
library(stats)
library(MASS)
library(MuMIn)
```

3) Inspect the file

```
names(Sidata)
```

```
## [1] "ID"          "SEASON"      "D13C"        "D15N"        "SEX"
## [6] "LP_Weight"   "B_Stage"     "B_Succ"      "B_Succat"    "Bsuc2"
```

```
str(Sidata)
```

```
## 'data.frame': 717 obs. of 10 variables:
## $ ID : Factor w/ 715 levels "2003_2004_1",...: 1 67 78 106 2 18 38 42 54 57 ...
## $ SEASON : int 2003 2003 2003 2003 2003 2003 2003 2003 2003 2003 ...
## $ D13C : num -21.1 -19.1 -19.2 -19.1 -19.4 ...
## $ D15N : num 17.1 14.5 14.8 15.3 16.6 ...
## $ SEX : Factor w/ 2 levels "F","M": 1 1 1 1 1 1 1 1 1 1 ...
## $ LP_Weight: int 1120 1060 1080 1070 1040 1250 890 1040 1040 1070 ...
## $ B_Stage : Factor w/ 4 levels "1_prelaying",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ B_Succ : num 1.26 1.26 1.26 1.26 1.26 ...
## $ B_Succat : Factor w/ 3 levels "average","good",...: 2 2 2 2 2 2 2 2 2 2 ...
## $ Bsuc2 : Factor w/ 2 levels "1average","2good": 2 2 2 2 2 2 2 2 2 2 ...
```

4) Balanced sample size per breeding stage

```
table(Sidata$B_Stage)
```

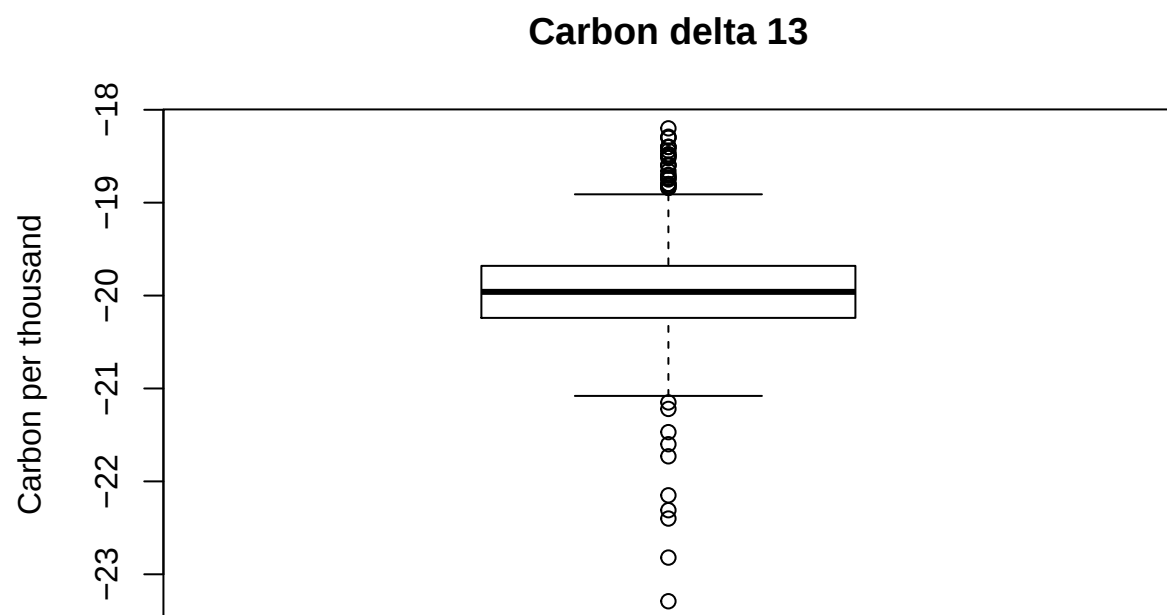
```
##
## 1_prelaying 2_incubation      3_guard 4_postguard
##          184          191          180          162
```

5) Data exploration

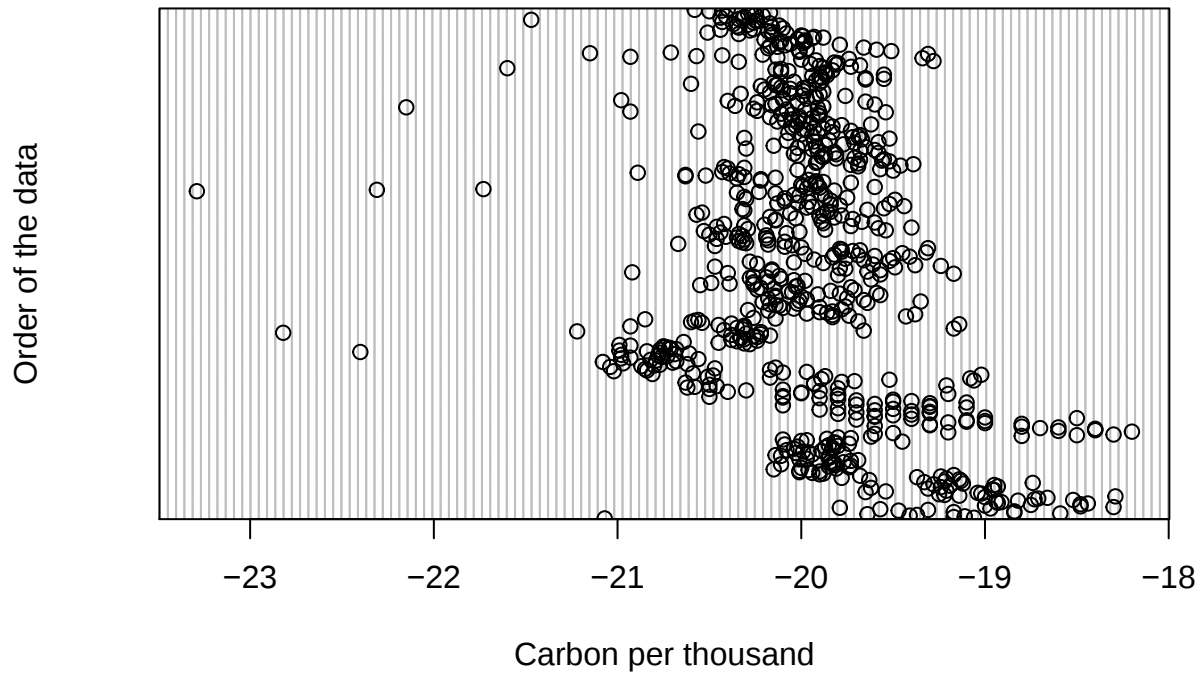
We tested for outliers, relationships (collinearity) and interactions, which guided us to what type of family distribution and analyses to select for the model. The data exploration was run for all response variable but only reported here for Carbon.

- 5a) Looking for Outliers

```
boxplot(Sidata$D13C,
        main = "Carbon delta 13",
        ylab = "Carbon per thousand")
dotchart(Sidata$D13C,
         main="Carbon delta 13",
         xlab = "Carbon per thousand",
         ylab = "Order of the data")
```



Carbon delta 13



- 5b) Relationships Y vs X

```
boxplot(D13C ~ SEX,
        data = Sidata,
        varwidth = TRUE,
        ylab = "Carbon delta 13",
        xlab = "sex",
        main = "")

boxplot(D13C ~ SEASON,
        data = Sidata,
        varwidth = TRUE,
        ylab = "Carbon delta 13",
        xlab = "year",
        main = "")

boxplot(D13C ~ LP_Weight,
        data = Sidata,
        varwidth = TRUE,
        ylab = "Carbon delta 13",
        xlab = "body mass",
        main = "")

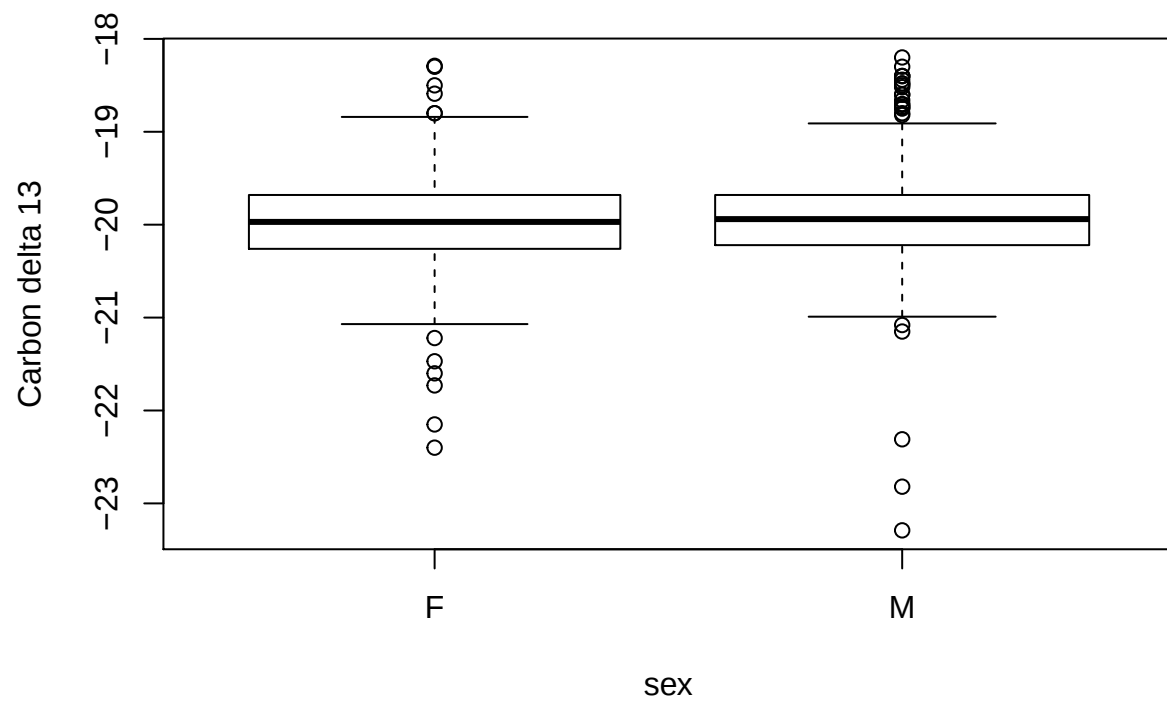
boxplot(D13C ~ B_Stage,
```

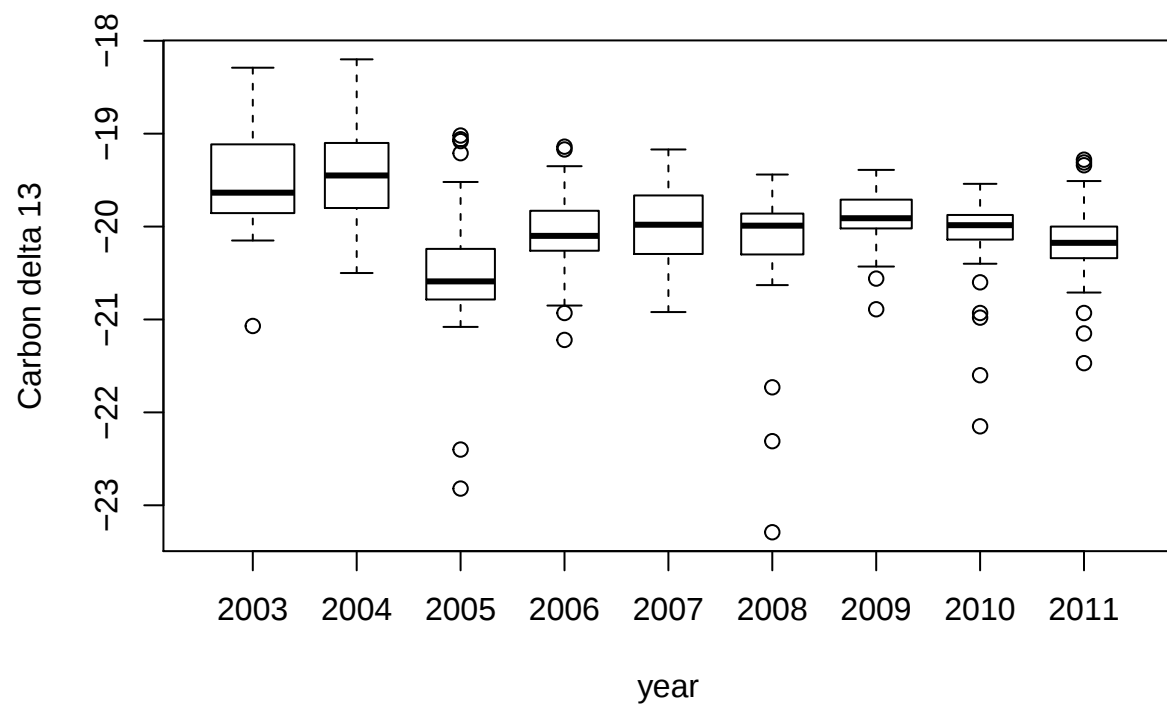
```

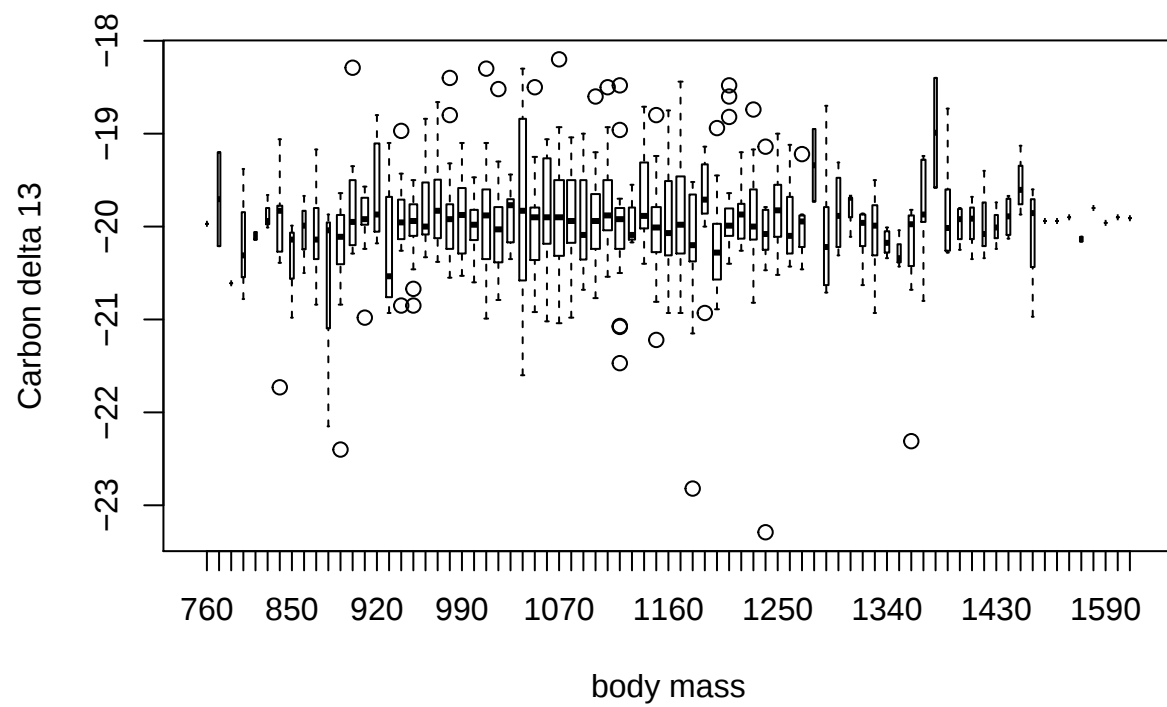
data = Sidata,
varwidth = TRUE,
ylab = "Carbon delta 13",
xlab = "breeding stage",
main = "")

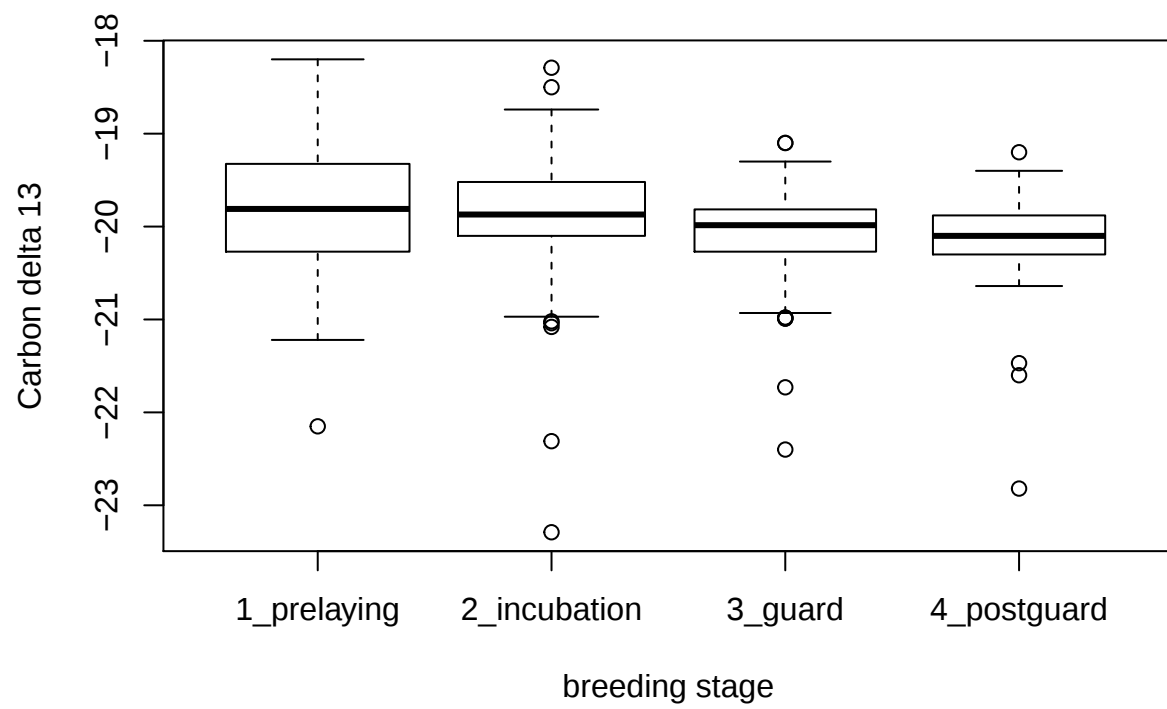
boxplot(D13C ~ B_Succat,
data = Sidata,
varwidth = TRUE,
ylab = "Carbon delta 13",
xlab = "breeding success",
main = "")

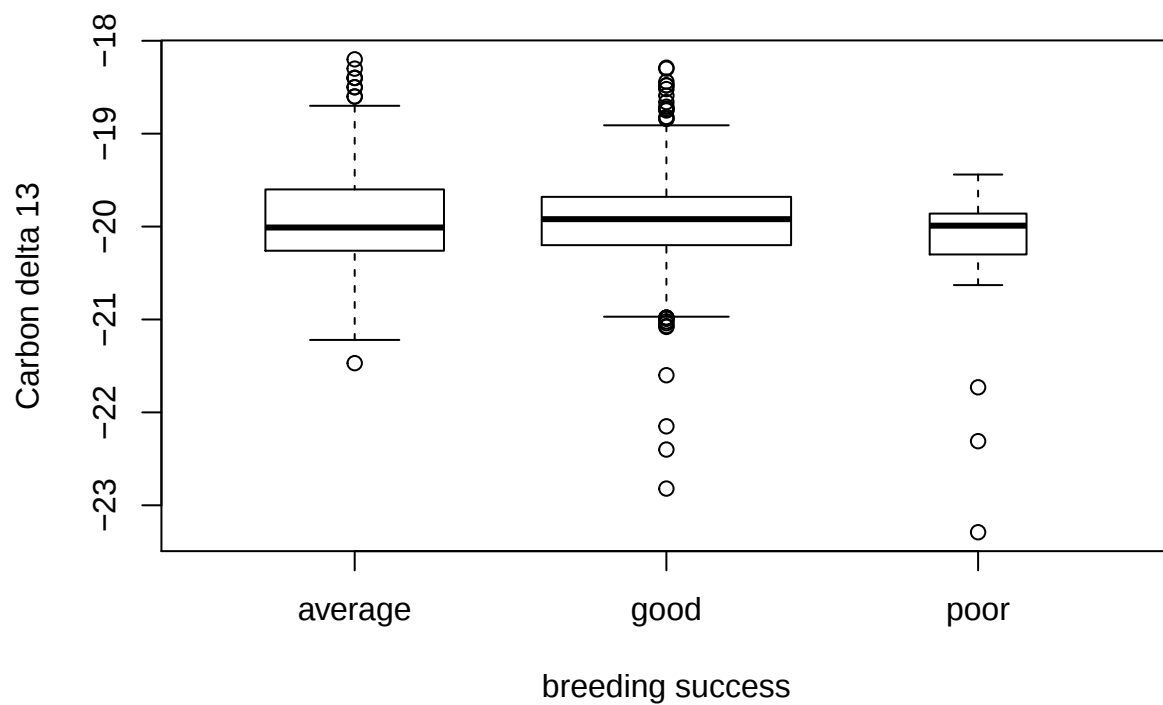
```











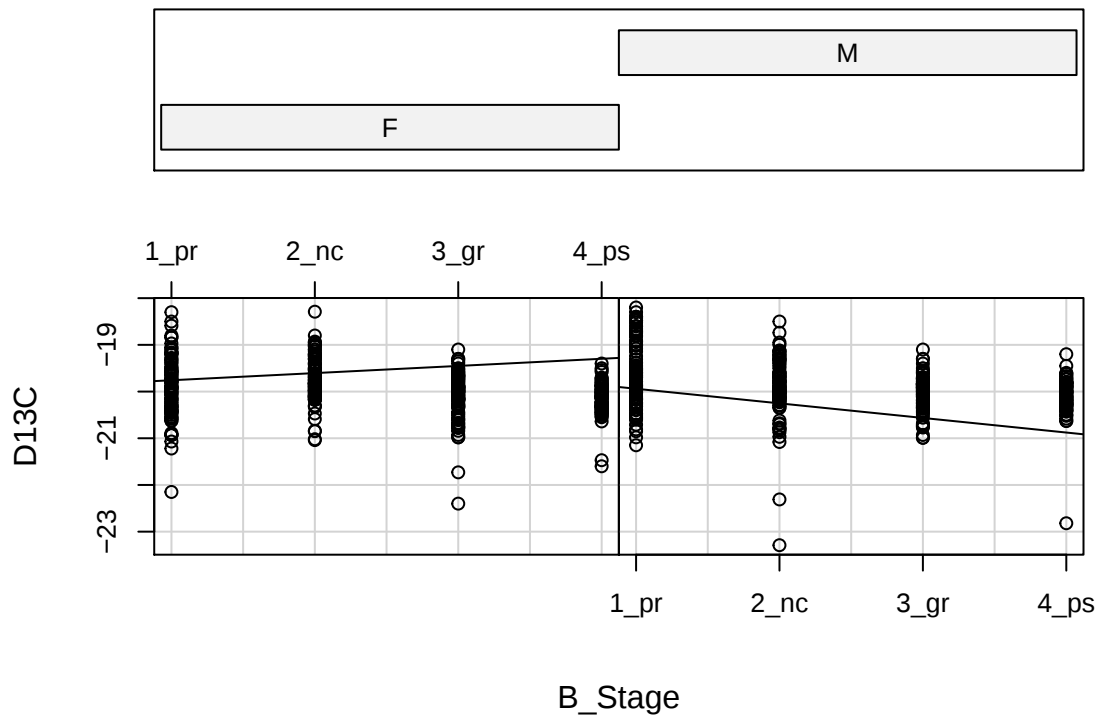
- 5c) Interaction

```
coplot(D13C ~ B_Stage | factor(SEX),
  data = Sidata,
  panel = function(x, y, ...) {
    tmp <- lm(y ~ x, na.action = na.omit)
    abline(tmp)
    points(x, y) })
```

```
## Warning in abline(tmp): only using the first two of 4 regression
## coefficients
```

```
## Warning in abline(tmp): only using the first two of 4 regression
## coefficients
```

Given : factor(SEX)



- 5c) Zero inflation - proportion

```
100 * sum(Sidata$D13C == 0) / nrow(Sidata)
```

```
## [1] 0
```

- 6) Carbon analysis

- 6a) Full model

```
C2<-glm(D13C~SEX + B_Stage +SEASON +Bsuc2+SEX:B_Stage, data=Sidata)
```

- 6b) Summary

```
library(xtable)
t1<-xtable(summary(C2))
print(t1,type="latex")
```

% latex table generated in R 3.1.1 by xtable 1.7-3 package % Wed Oct 28 10:16:15 2015

- 6c) Best fit models with Akaike weights >90% using Dredge function

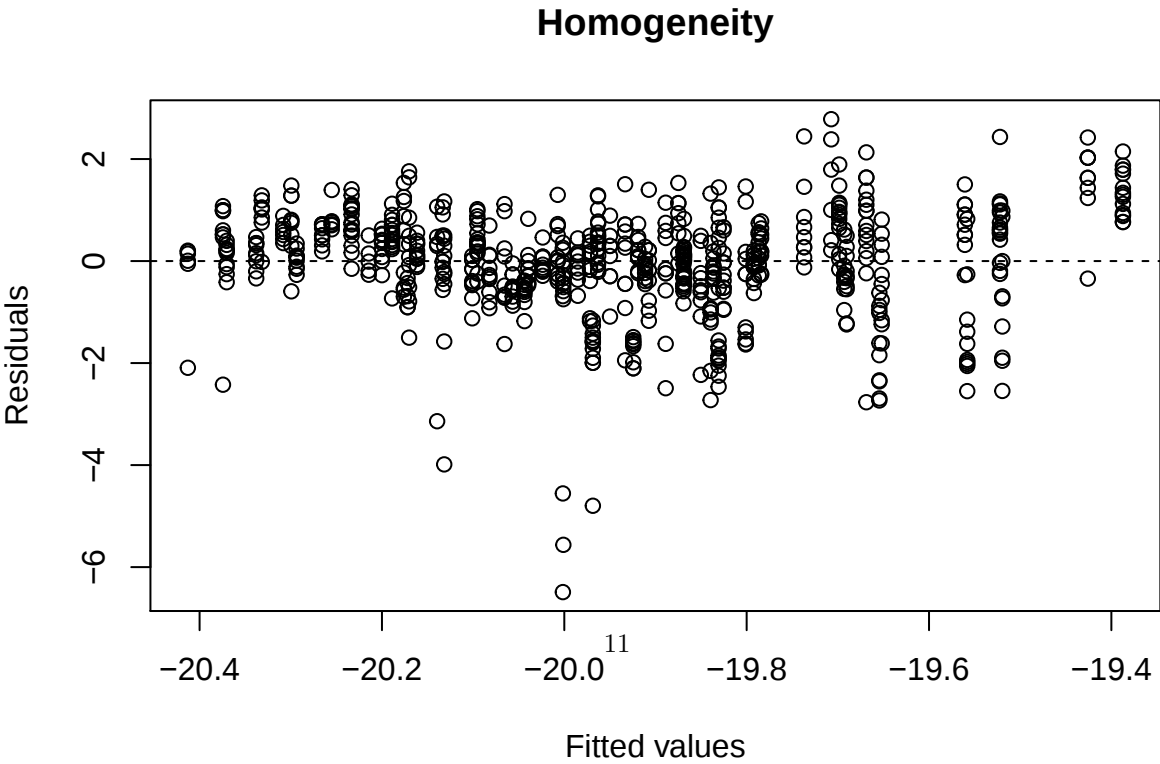
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	112.8362	14.5704	7.74	0.0000
SEXM	0.2814	0.0752	3.74	0.0002
B_Stage2_incubation	0.1466	0.0742	1.97	0.0488
B_Stage3_guard	-0.1677	0.0752	-2.23	0.0261
B_Stage4_postguard	-0.2427	0.0793	-3.06	0.0023
SEASON	-0.0661	0.0073	-9.11	0.0000
Bsuc22good	-0.0276	0.0394	-0.70	0.4834
SEXM:B_Stage2_incubation	-0.4577	0.1054	-4.34	0.0000
SEXM:B_Stage3_guard	-0.2371	0.1069	-2.22	0.0270
SEXM:B_Stage4_postguard	-0.2388	0.1101	-2.17	0.0303

```
knitr::kable(head(dredge(C2), 4))
```

	(Intercept)	B_Stage	Bsuc2	SEASON	SEX	B_Stage:SEX	df	logLik	AICc	delta	weight
30	111.2632	+	NA	-0.0653640	+	+	10	-529.7622	1079.836	0.000000	0.68437
32	112.8362	+	+	-0.0661394	+	+	11	-529.5130	1081.400	1.564429	0.31302
6	112.0477	+	NA	-0.0656846	NA	NA	6	-539.9912	1092.101	12.264678	0.00148
14	111.7829	+	NA	-0.0655642	+	NA	7	-539.2614	1092.681	12.844693	0.00117

- 6d) Homogeneity

```
E1 <- rstandard(C2)
F1 <- fitted(C2)
par(mfrow = c(1, 1))
plot(x = F1,
     y = E1,
     xlab = "Fitted values",
     ylab = "Residuals",
     main = "Homogeneity")
abline(h = 0, v = 0, lty = 2)
```



```

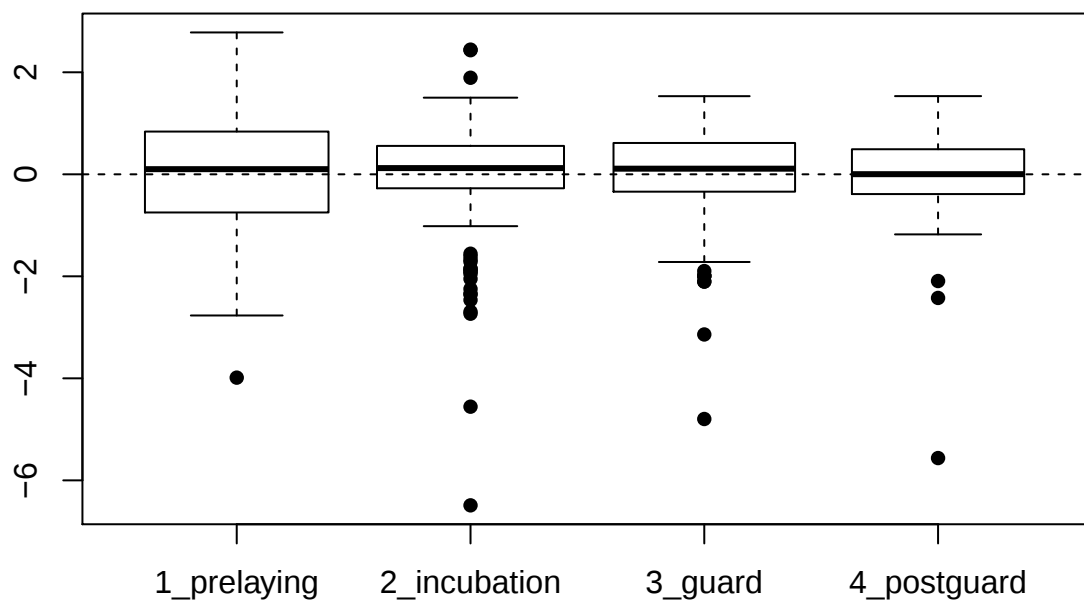
boxplot(E1 ~ Sidata$B_Stage, pch =16, varwidth = TRUE)
abline(h = 0, lty = 2)

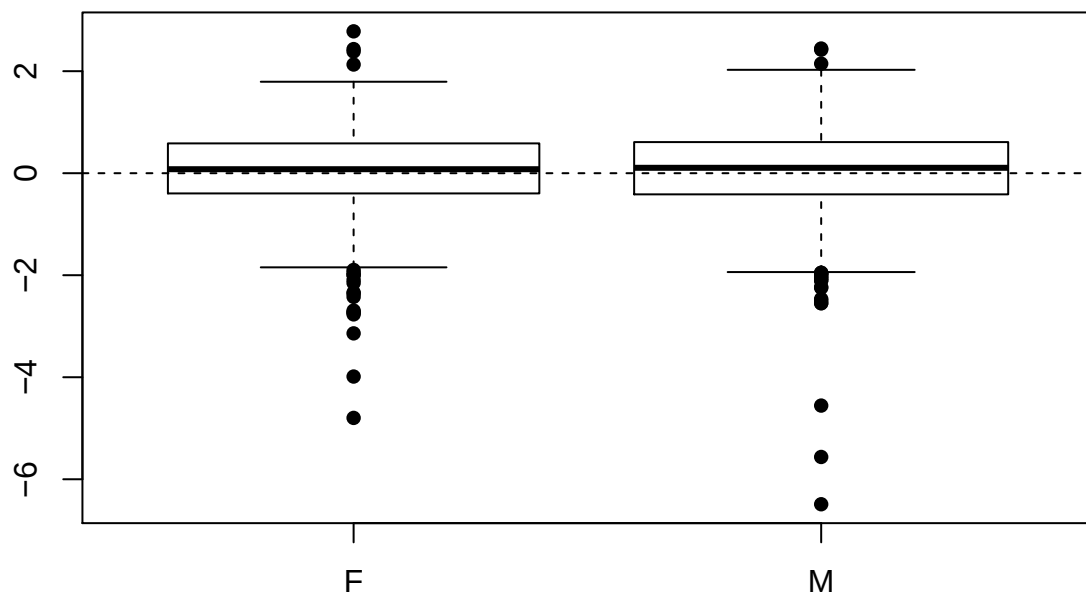
boxplot(E1 ~ factor(Sidata$SEX), pch =16, varwidth = TRUE)
abline(h = 0, lty = 2)

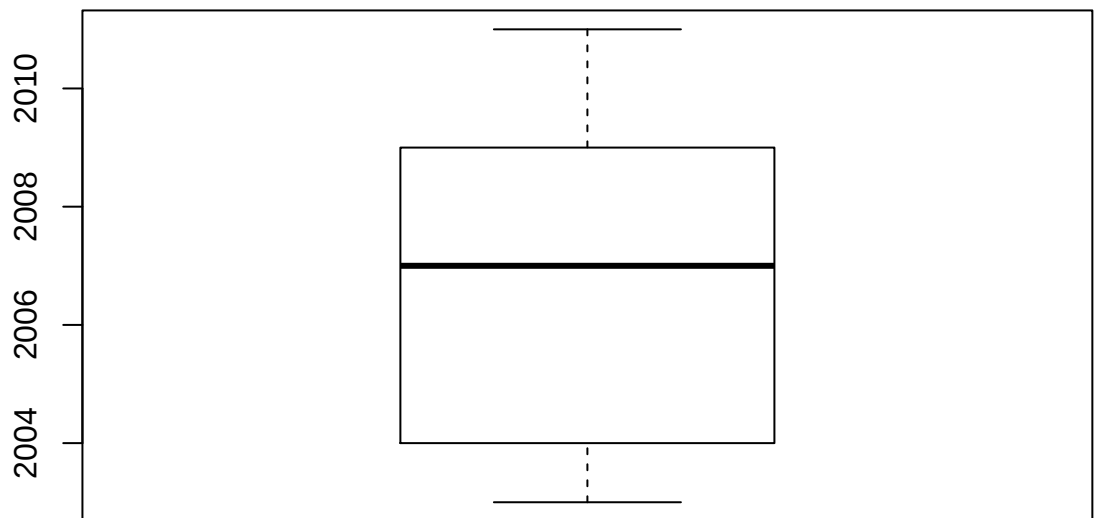
boxplot(y = E1,
        x = Sidata$SEASON,
        pch =16)
abline(h = 0, lty = 2)

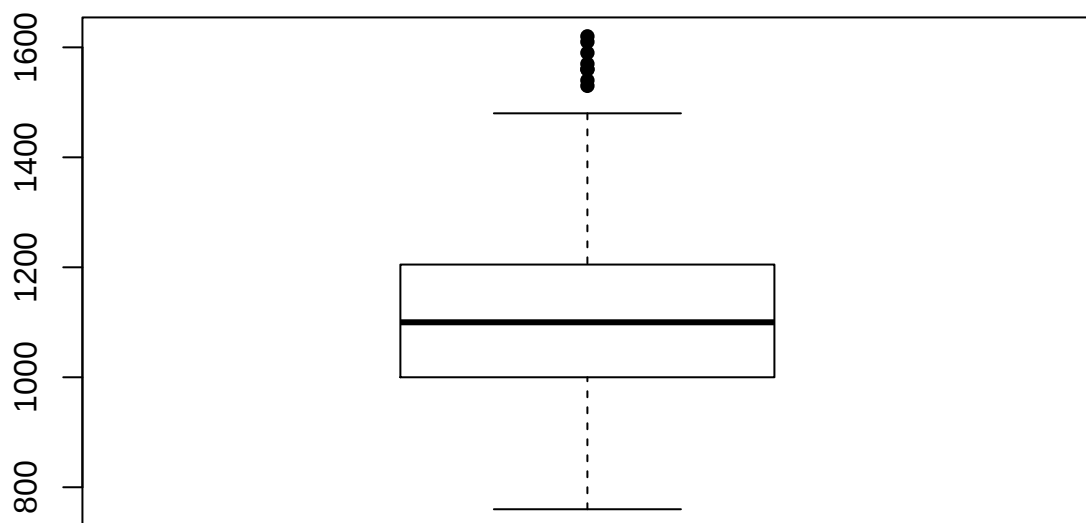
boxplot(y = E1,
        x = Sidata$LP_Weight,
        pch =16)
abline(h = 0, lty = 2)

```



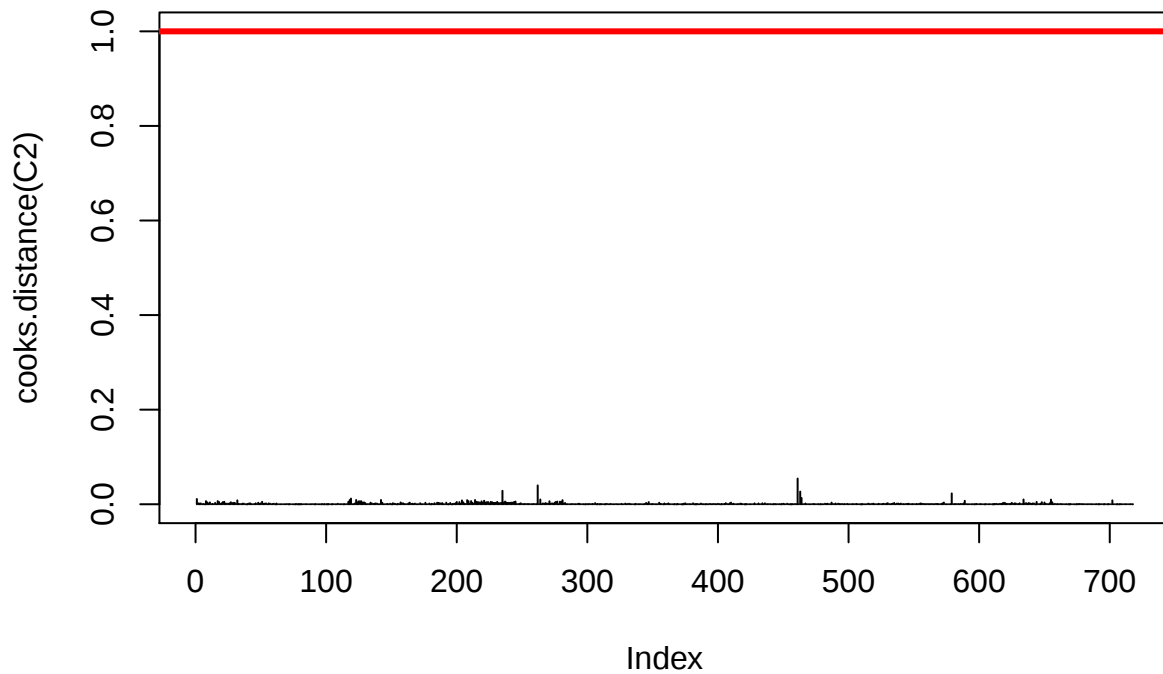






- 6f) Model outliers - Cook's distance

```
plot(cooks.distance(C2), type = "h", ylim = c(0, 1))  
abline(h = 1, col = 2, lwd = 3)
```



7) Nitrogen analysis

- 7a) Full model

```
N2<-glm(D15N~SEX + B_Stage +Bsuc2+SEASON +SEX:B_Stage, data=Sidata)
```

- 7b) Summary

```
library(xtable)
t2<-xtable(summary(N2))
print(t2,type="latex")
```

% latex table generated in R 3.1.1 by xtable 1.7-3 package % Wed Oct 28 10:16:15 2015

- 7c) Best fit models with Akaike weights >90% using Dredge function

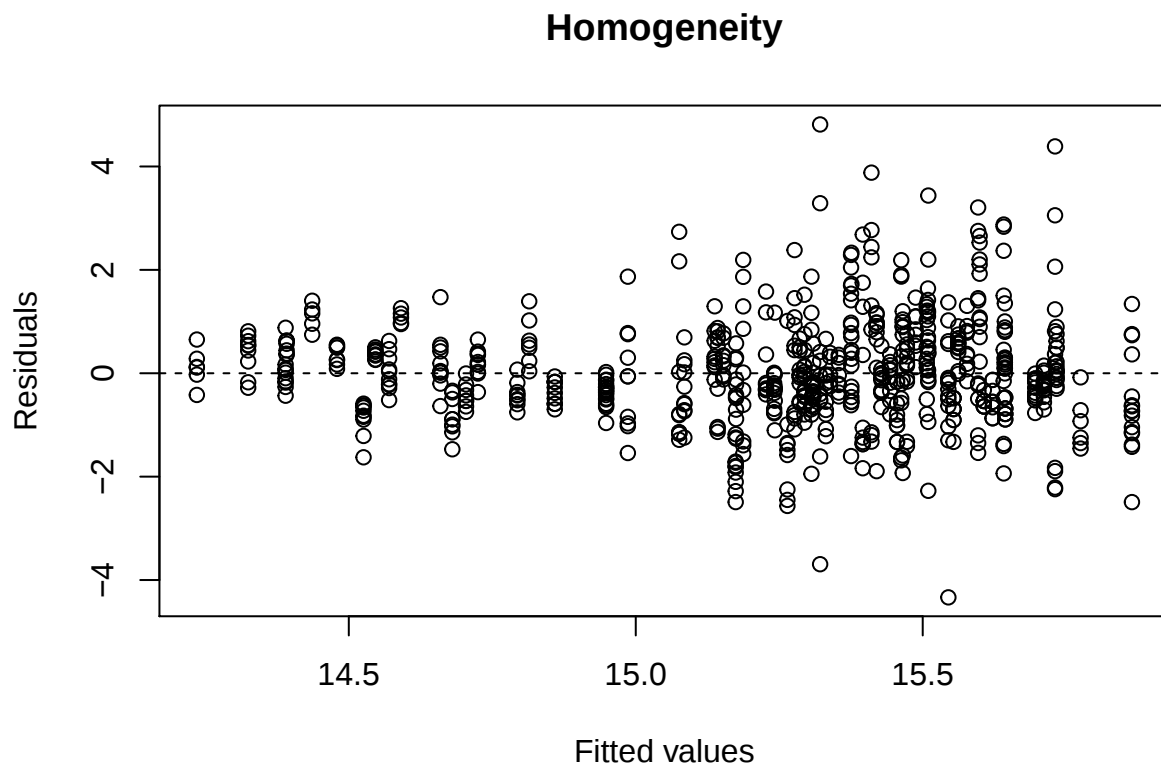
```
knitr::kable(head(dredge(N2), 4))
```

	(Intercept)	B_Stage	Bsuc2	SEASON	SEX	B_Stage:SEX	df	logLik	AICc	delta	weight
6	151.7954	+	NA	-0.0679462	NA	NA	6	-980.0295	1972.177	0.000000	0.409176
14	152.1832	+	NA	-0.0681225	+	NA	7	-979.5710	1973.300	1.122793	0.233399
30	151.3244	+	NA	-0.0676317	+	+	10	-976.6398	1973.591	1.414045	0.201768
8	150.4371	+	+	-0.0672764	NA	NA	7	-979.9761	1974.110	1.933016	0.155654

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	150.0457	27.1813	5.52	0.0000
SEXM	-0.3199	0.1403	-2.28	0.0229
B_Stage2_incubation	-0.1314	0.1385	-0.95	0.3432
B_Stage3_guard	-0.1686	0.1403	-1.20	0.2299
B_Stage4_postguard	-1.0709	0.1480	-7.24	0.0000
Bsuc22good	0.0225	0.0735	0.31	0.7600
SEASON	-0.0670	0.0135	-4.95	0.0000
SEXM:B_Stage2_incubation	0.2298	0.1966	1.17	0.2429
SEXM:B_Stage3_guard	0.3351	0.1995	1.68	0.0934
SEXM:B_Stage4_postguard	0.4746	0.2053	2.31	0.0211

- 7d) Homogeneity

```
E2 <- rstandard(N2)
F2 <- fitted(N2)
par(mfrow = c(1, 1))
plot(x = F2,
     y = E2,
     xlab = "Fitted values",
     ylab = "Residuals",
     main = "Homogeneity")
abline(h = 0, v = 0, lty = 2)
```



- 7e) Independence - plot residuals versus covariates

```

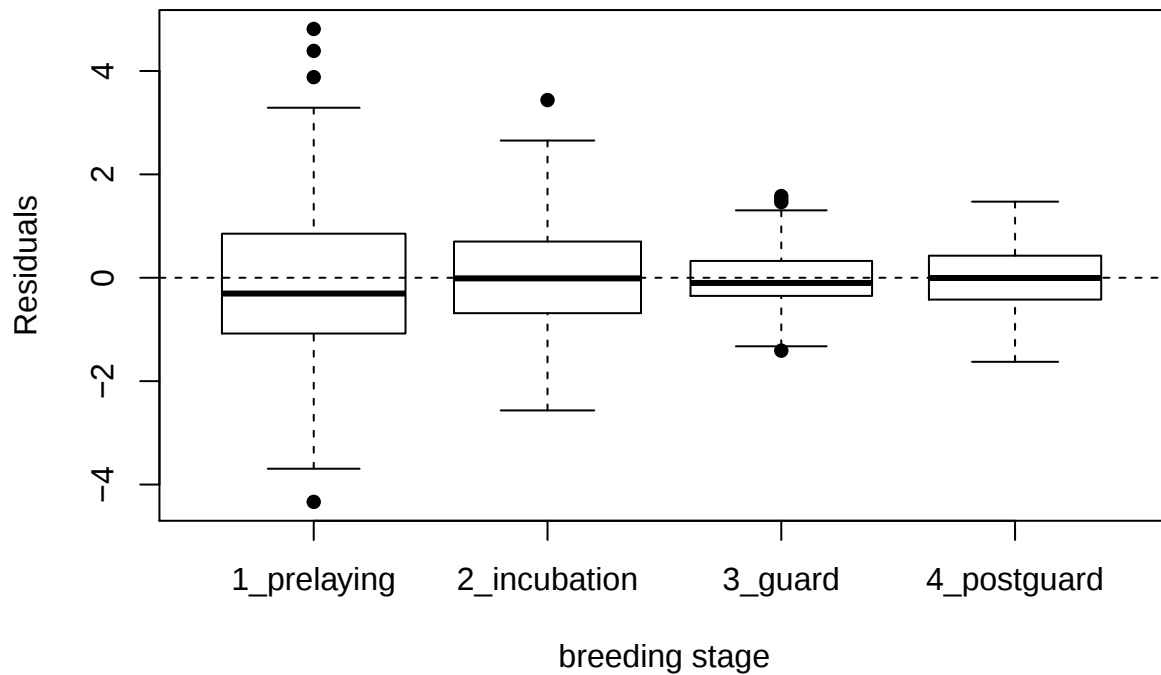
boxplot(E2 ~ Sidata$B_Stage, xlab = "breeding stage",
        ylab = "Residuals", pch = 16, varwidth = TRUE)
abline(h = 0, lty = 2)

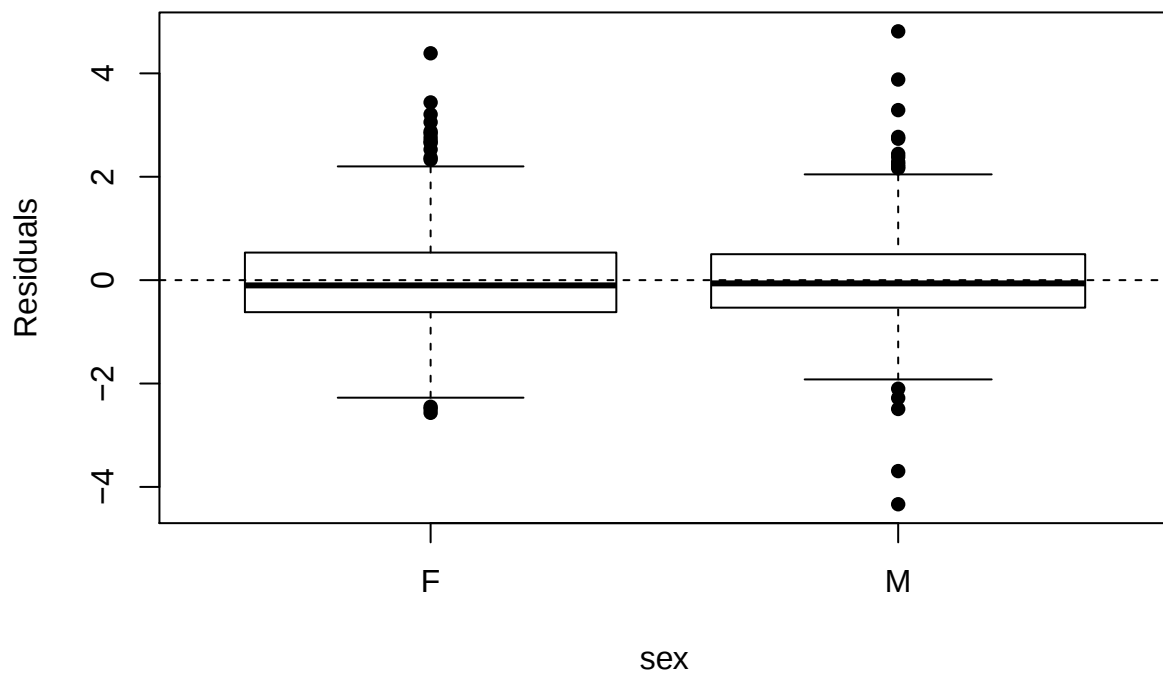
boxplot(E2 ~ factor(Sidata$SEX), xlab = "sex",
        ylab = "Residuals", pch = 16, varwidth = TRUE)
abline(h = 0, lty = 2)

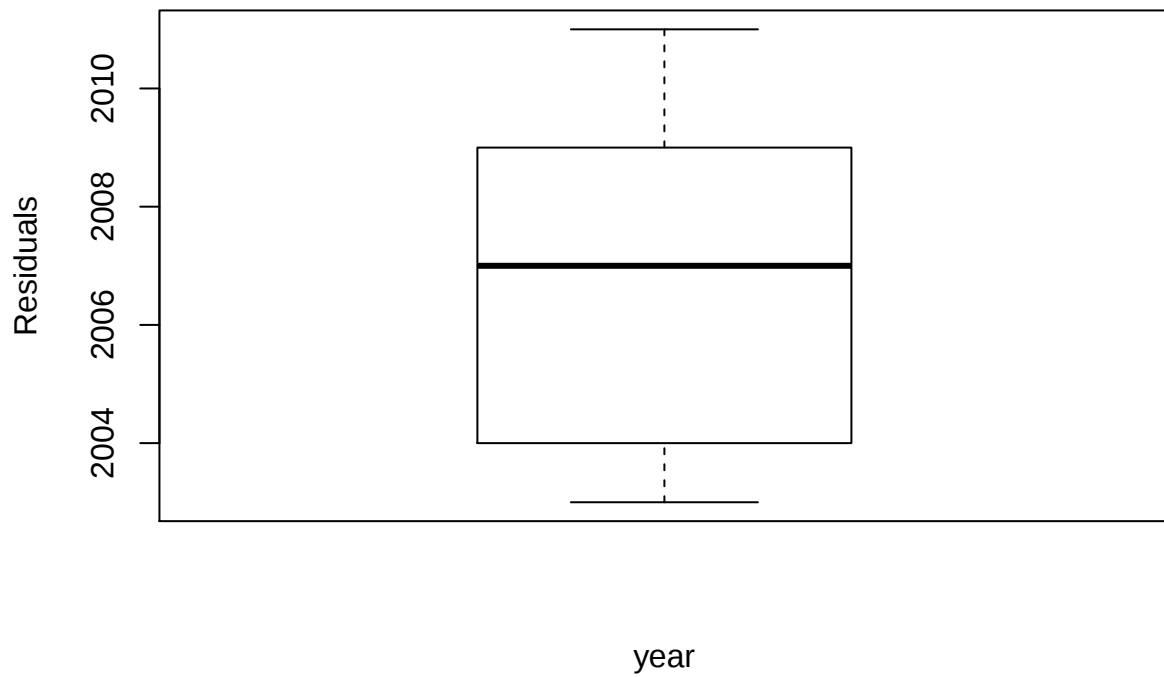
boxplot(y = E2,
        x = Sidata$SEASON, xlab = "year",
        ylab = "Residuals",
        pch = 16)
abline(h = 0, lty = 2)

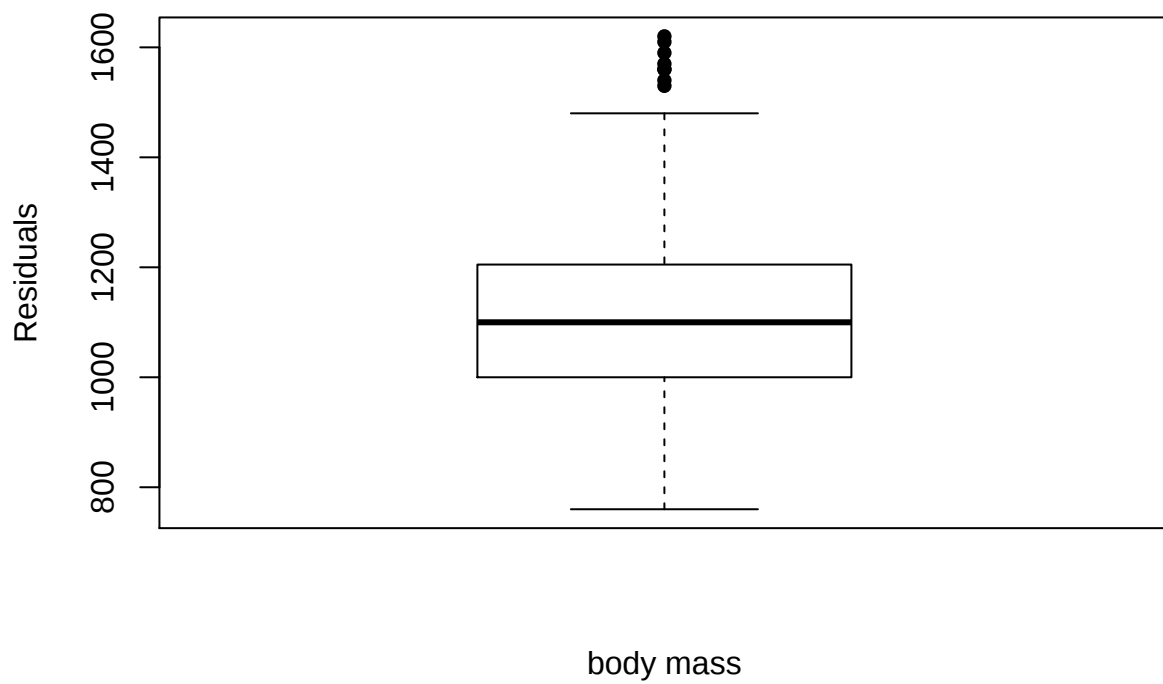
boxplot(y = E2,
        x = Sidata$LP_Weight, xlab = "body mass",
        ylab = "Residuals",
        pch = 16)
abline(h = 0, lty = 2)

```



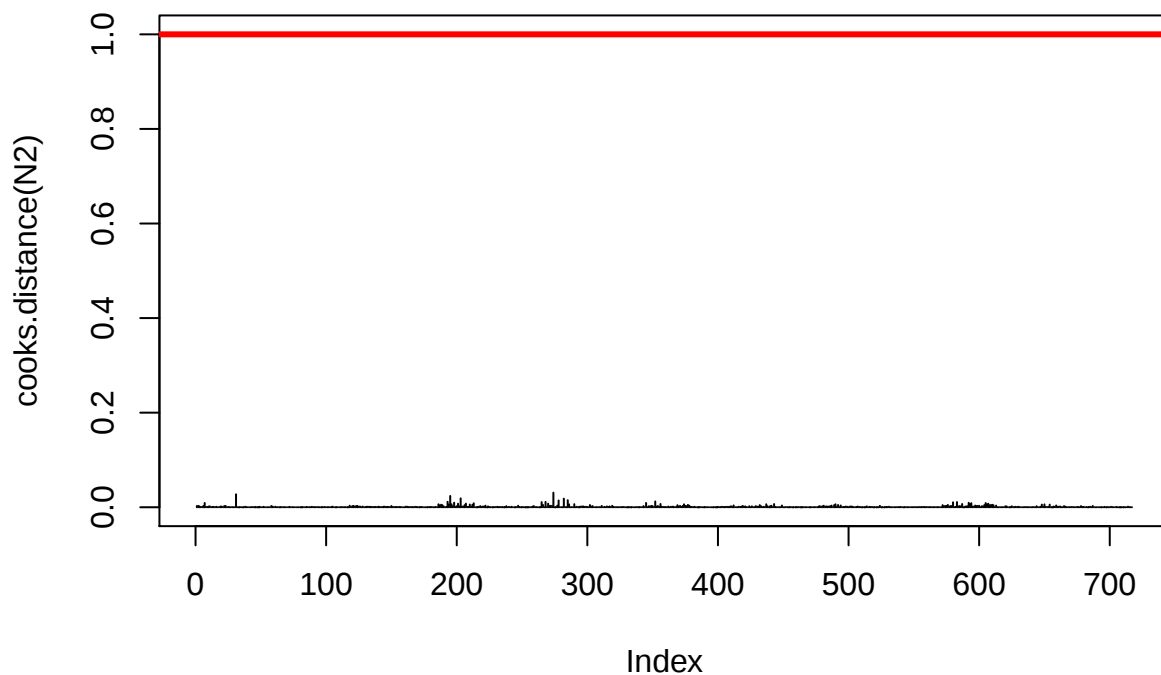






- 7f) Model outliers - Cook's distance

```
plot(cooks.distance(N2), type = "h", ylim = c(0, 1))  
abline(h = 1, col = 2, lwd = 3)
```



8) Body mass analysis

```
xdata<-read.table(file="LP_SIA_adults_2003_11.txt", header=T, sep="\t")
```

- 8a) Full model

```
W1<-glm(LP_Weight~SEX + B_Stage + SEX*B_Stage + SEASON+Bsuc2, data=xdata)
```

- 8b) Summary

```
library(xtable)
t3<-xtable(summary(W1))
print(t3,type="latex")
```

% latex table generated in R 3.1.1 by xtable 1.7-3 package % Wed Oct 28 10:16:16 2015

- 8c) Best fit models with Akaike weights >90% using Dredge function

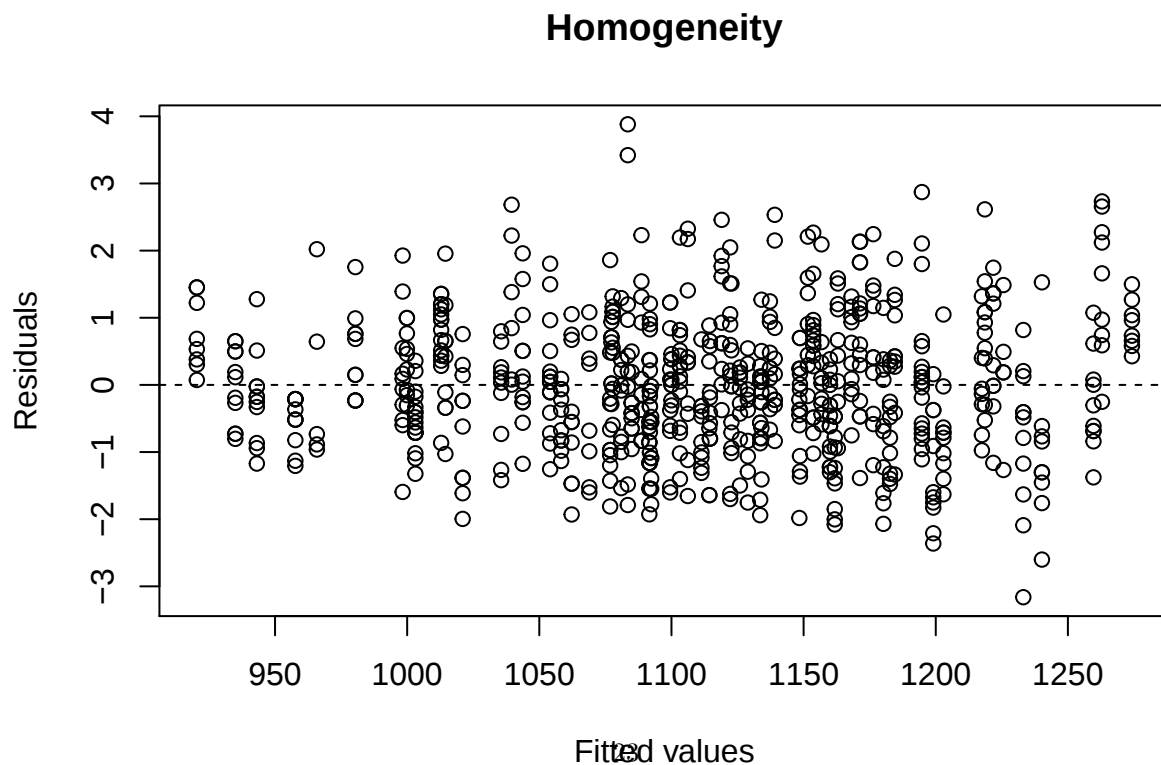
```
knitr::kable(head(dredge(W1), 4))
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-21713.6618	3761.0705	-5.77	0.0000
SEXM	49.1208	19.4082	2.53	0.0116
B_Stage2_incubation	-41.2355	19.1595	-2.15	0.0317
B_Stage3_guard	-119.1094	19.4114	-6.14	0.0000
B_Stage4_postguard	29.3936	20.5523	1.43	0.1531
SEASON	11.3539	1.8737	6.06	0.0000
Bsuc22good	25.9197	10.1721	2.55	0.0110
SEXM:B_Stage2_incubation	91.6757	27.1984	3.37	0.0008
SEXM:B_Stage3_guard	107.7498	27.6011	3.90	0.0001
SEXM:B_Stage4_postguard	62.1543	28.4594	2.18	0.0293

	(Intercept)	B_Stage	Bsuc2	SEASON	SEX	B_Stage:SEX	df	logLik	AICc	delta	weight
32	-21713.66	+	+	11.35389	+	+	11	-4504.911	9032.197	0.000000	0.90183
30	-20243.90	+	NA	10.62937	+	+	10	-4508.188	9036.689	4.491877	0.095439
16	-21697.70	+	+	11.32946	+	NA	8	-4513.894	9043.992	11.794621	0.002477
14	-20201.98	+	NA	10.59202	+	NA	7	-4517.219	9048.596	16.399397	0.000247

- 8d) Homogeneity

```
E3 <- rstandard(W1)
F3 <- fitted(W1)
par(mfrow = c(1, 1))
plot(x = F3,
     y = E3,
     xlab = "Fitted values",
     ylab = "Residuals",
     main = "Homogeneity")
abline(h = 0, v = 0, lty = 2)
```



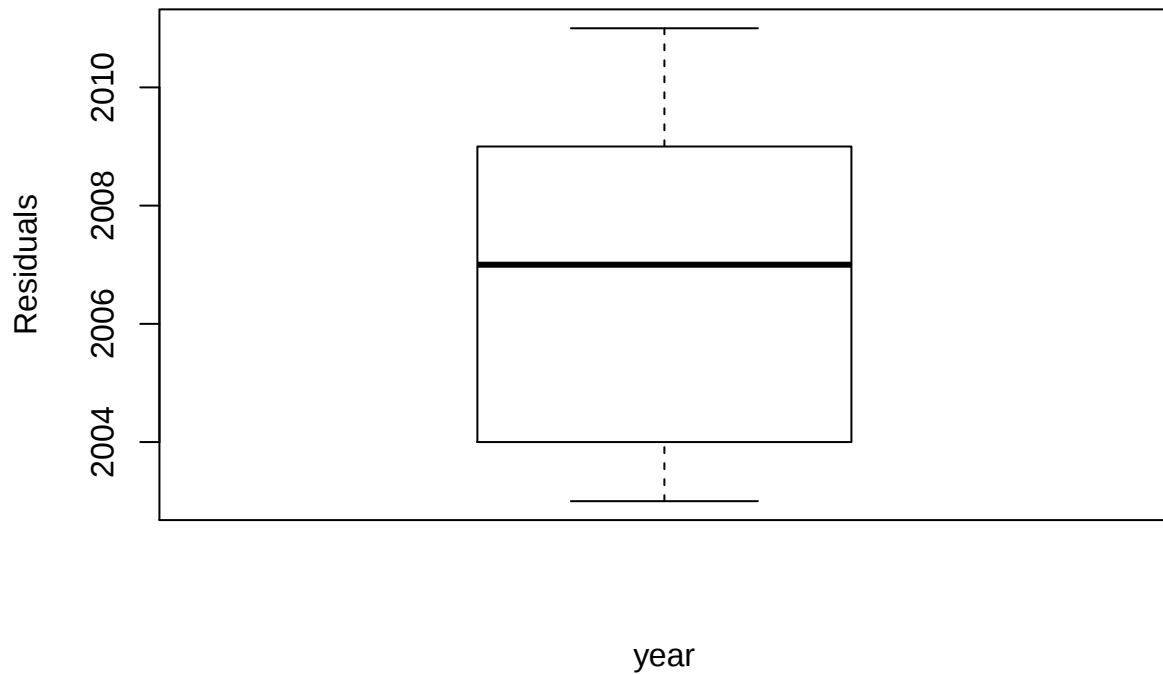
- 8e) Independence - plot residuals versus covariates

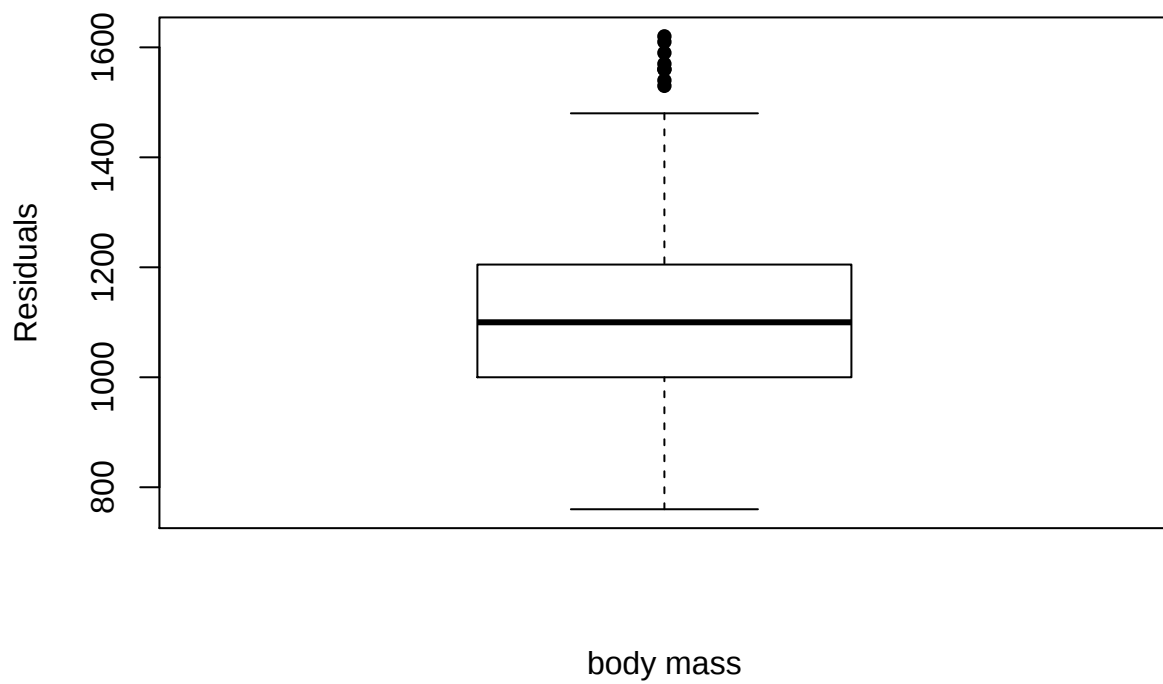
```

    pch =16)
abline(h = 0, lty = 2)

boxplot(y = E3,
        x = xdata$LP_Weight, xlab = "body mass",
        ylab = "Residuals",
        pch =16)
abline(h = 0, lty = 2)

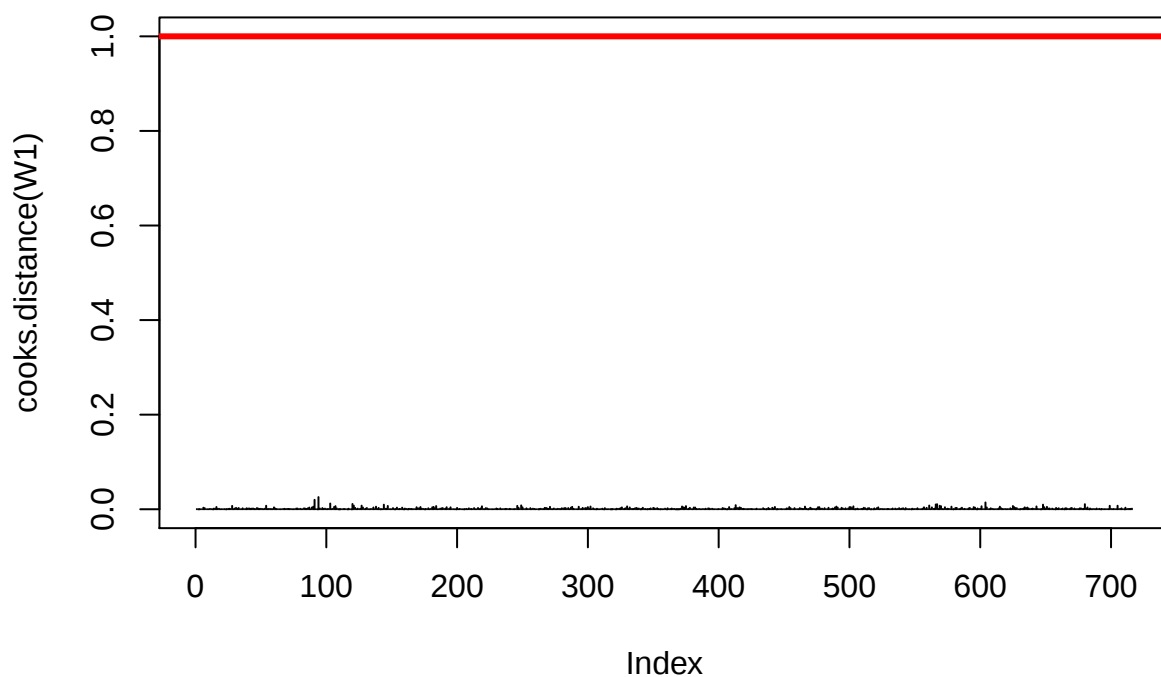
```





- 8f) Model outliers - Cook's distance

```
plot(cooks.distance(W1), type = "h", ylim = c(0, 1))  
abline(h = 1, col = 2, lwd = 3)
```



9) Anchovy

- 9a) Reading conventional diet data and checking for balanced or missing data

```
Diet01<- read.table(file="Diet1985-2012 occurrence.txt", header=T, sep="\t",dec = ".")
table(Diet01$YEAR,Diet01$BSTAGE)
```

```
##
##      1 Pre-laying 2 Incubation 3 Guard 4 Post-Guard
## 1985           5           0       7           9
## 1986          76           0       0          78
## 1987          74           0      36          37
## 1995           0           4       2           0
## 1996           5          10      16          35
## 1998           0          14      16          31
## 2000           0          10      20          38
## 2001          12          11      42          30
## 2002          10          10      38          50
## 2003          20          12      18          30
## 2004           0          10      17          23
## 2005           8          16      10          26
## 2006           0           9       8           8
## 2007           8           9      10          10
## 2008          20          20      10           9
## 2009          10           4      21           8
```

```
## 2010      0      0      10      10
## 2011      5      0       9       9
## 2012     10      0      10      10
```

- 9b) Grouping breeding stage

```
table(Diet01$YEAR,Diet01$BSTAGEG)
```

```
##
##      1 Pre-chick 2 Guard 3 Post-Guard
## 1985      5      7      9
## 1986     76      0     78
## 1987     74     36     37
## 1995      4      2      0
## 1996     15     16     35
## 1998     14     16     31
## 2000     10     20     38
## 2001     23     42     30
## 2002     20     38     50
## 2003     32     18     30
## 2004     10     17     23
## 2005     24     10     26
## 2006      9      8      8
## 2007     17     10     10
## 2008     40     10      9
## 2009     14     21      8
## 2010      0     10     10
## 2011      5      9      9
## 2012     10     10     10
```

- 9c) Removing years with missing data for one or more breeding stage

```
Diet02<-Diet01[Diet01$YEAR!=1995 & Diet01$YEAR!=1986 & Diet01$YEAR!=2010,]
```

- 9c) Conventional diet data structure

```
names(Diet02)
```

```
## [1] "YEAR"      "BAND"      "SEX"      "ANCHOVY"   "SARDINE"
## [6] "REDCOD"    "PLUNKNOWN" "BARRACOUTA" "BLUEWAREHOU" "SQUID"
## [11] "KRILL"     "BSTAGE"    "BSTAGEG"   "BSUCCESS"
```

```
str(Diet02)
```

```
## 'data.frame': 973 obs. of 14 variables:
## $ YEAR : int 1985 1985 1985 1985 1985 1985 1985 1985 1985 1985 ...
## $ BAND : Factor w/ 866 levels "719F8DB","00688E9A",...: 866 219 231 232 241 233 234 235 236 2...
## $ SEX : Factor w/ 2 levels "F","M": 1 2 2 1 1 2 1 1 1 1 ...
## $ ANCHOVY : int 0 0 0 0 0 0 0 0 0 0 ...
## $ SARDINE : int 0 0 0 0 0 0 1 0 0 0 ...
## $ REDCOD : int 0 0 0 0 0 1 0 0 0 0 ...
```

```
## $ PLUNKOWN : int 0 0 0 0 0 0 0 0 0 0 ...
## $ BARRACOUTA : int 0 1 1 1 0 0 0 0 0 0 ...
## $ BLUEWAREHOU: int 1 1 1 1 0 1 1 0 0 1 ...
## $ SQUID : int 1 1 1 0 0 1 1 1 1 1 ...
## $ KRILL : int 0 0 0 1 0 0 0 0 1 1 ...
## $ BSTAGE : Factor w/ 4 levels "1 Pre-laying",...: 1 1 1 1 1 3 3 3 3 3 ...
## $ BSTAGEG : Factor w/ 3 levels "1 Pre-chick",...: 1 1 1 1 1 2 2 2 2 2 ...
## $ BSUCCESS : Factor w/ 3 levels "average","high",...: 3 3 3 3 3 3 3 3 3 3 ...
```

- 9c) Full model

```
A1 <- glm(ANCHOVY ~ SEX+BSTAGEG+YEAR+BSUCCESS+BSTAGEG:SEX,
          data = Diet02,
          family = binomial(link = "logit"))
```

- 9d) Summary

```
library(xtable)
t4<-xtable(summary(A1))
print(t4,type="latex")
```

% latex table generated in R 3.1.1 by xtable 1.7-3 package % Wed Oct 28 10:16:16 2015

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-206.7039	28.5629	-7.24	0.0000
SEXM	0.1336	0.3103	0.43	0.6668
BSTAGEG2 Guard	1.0244	0.3053	3.35	0.0008
BSTAGEG3 Post-Guard	1.1437	0.2943	3.89	0.0001
YEAR	0.1025	0.0143	7.18	0.0000
BSUCCESShigh	-0.0392	0.1926	-0.20	0.8389
BSUCCESSlow	-0.1249	0.1975	-0.63	0.5271
SEXM:BSTAGEG2 Guard	0.1439	0.4027	0.36	0.7208
SEXM:BSTAGEG3 Post-Guard	0.3470	0.3830	0.91	0.3649

- 9f) Best fit models with Akaike weights >90% using Dredge function

```
knitr::kable(head(dredge(A1), 5))
```

	(Intercept)	BSTAGEG	BSUCCESS	SEX	YEAR	BSTAGEG:SEX	df	logLik	AICc	delta
14	-209.4013	+	NA	+	0.1037135	NA	5	-542.6866	1095.435	0.000000
10	-206.6189	+	NA	NA	0.1024264	NA	4	-545.2730	1098.587	3.152106
30	-209.7202	+	NA	+	0.1039340	+	7	-542.2478	1098.612	3.176469
16	-206.3496	+	+	+	0.1022223	NA	7	-542.4810	1099.078	3.642757
12	-202.7386	+	+	NA	0.1005214	NA	6	-545.0203	1102.128	6.692425

10) Barracouta

- 10a) Full model

```
B1 <- glm(BARRACOUTA ~ SEX+BSTAGEG+YEAR+BSUCCESS+BSTAGEG:SEX,
          data = Diet02,
          family = binomial(link = "logit"))
```

- 10b) Summary

```
library(xtable)
t5<-xtable(summary(B1))
print(t5,type="latex")
```

% latex table generated in R 3.1.1 by xtable 1.7-3 package % Wed Oct 28 10:16:16 2015

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-99.2224	27.7039	-3.58	0.0003
SEX	-0.4605	0.4576	-1.01	0.3143
BSTAGEG2 Guard	2.5681	0.3712	6.92	0.0000
BSTAGEG3 Post-Guard	3.0568	0.3701	8.26	0.0000
YEAR	0.0473	0.0138	3.42	0.0006
BSUCCESShigh	2.4477	0.2449	9.99	0.0000
BSUCCESSlow	2.2262	0.2459	9.05	0.0000
SEX:BSTAGEG2 Guard	0.7705	0.5282	1.46	0.1446
SEX:BSTAGEG3 Post-Guard	0.9534	0.5212	1.83	0.0673

- 10c) Best fit models with Akaike weights >90% using Dredge function

```
knitr::kable(head(dredge(B1)))
```

	(Intercept)	BSTAGEG	BSUCCESS	SEX	YEAR	BSTAGEG:SEX	df	logLik	AICc	delt
16	-98.562427	+	+	+	0.0467498	NA	7	-439.5296	893.1753	0.000000
32	-99.222399	+	+	+	0.0472849	+	9	-437.8598	893.9066	0.731321
12	-96.595768	+	+	NA	0.0458618	NA	6	-441.0244	894.1357	0.960441
8	-4.980505	+	+	+	NA	NA	6	-445.3321	902.7512	9.575972
4	-4.805060	+	+	NA	NA	NA	5	-446.6468	903.3556	10.180314
24	-4.586448	+	+	+	NA	+	8	-443.7841	903.7176	10.542367

11) Pilchard

- 11a) Full model

```
SA1 <- glm(SARDINE ~ SEX+BSTAGEG+YEAR+BSUCCESS+BSTAGEG:SEX,
           data = Diet02,
           family = binomial(link = "logit"))
```

- 11b) Summary

```
library(xtable)
t6<-xtable(summary(SA1))
print(t6,type="latex")
```

% latex table generated in R 3.1.1 by xtable 1.7-3 package % Wed Oct 28 10:16:16 2015

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-182.2478	42.5667	-4.28	0.0000
SEXM	-0.2197	0.3498	-0.63	0.5299
BSTAGEG2 Guard	0.1787	0.3534	0.51	0.6132
BSTAGEG3 Post-Guard	-0.1835	0.3577	-0.51	0.6080
YEAR	0.0899	0.0213	4.23	0.0000
BSUCCESShigh	0.8975	0.2731	3.29	0.0010
BSUCCESSlow	-0.3160	0.3280	-0.96	0.3353
SEXM:BSTAGEG2 Guard	0.3274	0.4799	0.68	0.4951
SEXM:BSTAGEG3 Post-Guard	-0.0295	0.4931	-0.06	0.9524

- 11c) Best fit models with Akaike weights >90% using Dredge function

```
knitr::kable(head(dredge(SA1),4))
```

	(Intercept)	BSTAGEG	BSUCCESS	SEX	YEAR	BSTAGEG:SEX	df	logLik	AICc	delta
12	-182.1485	+	+	NA	0.0898332	NA	6	-342.0054	696.0978	0.000000
11	-188.0567	NA	+	NA	0.0928059	NA	4	-344.6958	697.4329	1.335139
16	-181.0898	+	+	+	0.0893368	NA	7	-341.8477	697.8114	1.713578
15	-187.1100	NA	+	+	0.0923638	NA	5	-344.5154	699.0928	2.994945

12) Squid

- 12a) Full model

```
S1 <- glm(SQUID ~ SEX+BSTAGEG+YEAR+BSUCCESS+BSTAGEG:SEX,
  data = Diet02,
  family = binomial(link = "logit"))
```

- 12b) Summary

```
library(xtable)
t7<-xtable(summary(S1))
print(t7,type="latex")
```

% latex table generated in R 3.1.1 by xtable 1.7-3 package % Wed Oct 28 10:16:17 2015

- 12c) Best fit models with Akaike weights >90% using Dredge function

```
knitr::kable(head(dredge(S1),6))
```

	(Intercept)	BSTAGEG	BSUCCESS	SEX	YEAR	BSTAGEG:SEX	df	logLik	AICc	delta
12	51.621007	+	+	NA	-0.0268159	NA	6	-574.1180	1160.323	0.000000
16	51.592232	+	+	+	-0.0268038	NA	7	-574.1166	1162.349	2.026229
4	-2.007730	+	+	NA	NA	NA	5	-576.7107	1163.483	3.160432
32	51.940409	+	+	+	-0.0270034	+	9	-572.8297	1163.846	3.523346
8	-2.015888	+	+	+	NA	NA	6	-576.7060	1165.499	5.175966
24	-2.060183	+	+	+	NA	+	8	-575.4508	1167.051	6.727996

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	51.9404	23.7392	2.19	0.0287
SEXM	0.1010	0.2453	0.41	0.6807
BSTAGEG2 Guard	0.6894	0.2688	2.56	0.0103
BSTAGEG3 Post-Guard	0.7868	0.2590	3.04	0.0024
YEAR	-0.0270	0.0119	-2.27	0.0229
BSUCCESShigh	1.7817	0.2089	8.53	0.0000
BSUCCESSlow	2.4954	0.2135	11.69	0.0000
SEXM:BSTAGEG2 Guard	-0.4410	0.3605	-1.22	0.2212
SEXM:BSTAGEG3 Post-Guard	0.1047	0.3424	0.31	0.7597

13) SIBER analysis

```
siber<-read.table(file="LP_SIBER_adults_2003_11.txt", header=T, sep="\t")
str(siber)
```

```
## 'data.frame': 7200 obs. of 5 variables:
## $ SEASON : int 2003 2003 2003 2003 2003 2003 2003 2003 2003 2003 ...
## $ B_Stage: Factor w/ 4 levels "1_prelaying",...: 1 1 1 1 1 1 1 1 1 1 ...
## $ SEX : Factor w/ 2 levels "F","M": 1 1 1 1 1 1 1 1 1 1 ...
## $ SEAB : num 1.95 1.95 2.05 1.93 1.93 1.6 1.97 1.97 1.45 1.44 ...
## $ Bsucc : Factor w/ 2 levels "average","good": 2 2 2 2 2 2 2 2 2 2 ...
```

- 13a) Full model - negative binomial

```
SI2<-glm.nb(SEAB~SEX + B_Stage + Bsucc+SEX:B_Stage + SEASON, data=siber)
```

- 13b) Summary % latex table generated in R 3.1.1 by xtable 1.7-3 package % Wed Oct 28 10:16:18 2015

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-46.0764	7.3958	-6.23	0.0000
SEXM	-0.1305	0.0297	-4.40	0.0000
B_Stage2_incubation	-0.6244	0.0344	-18.17	0.0000
B_Stage3_guard	-0.8377	0.0369	-22.69	0.0000
B_Stage4_postguard	-0.8274	0.0368	-22.49	0.0000
Bsuccgood	-0.0136	0.0191	-0.71	0.4759
SEASON	0.0235	0.0037	6.37	0.0000
SEXM:B_Stage2_incubation	0.0762	0.0496	1.54	0.1248
SEXM:B_Stage3_guard	0.0311	0.0537	0.58	0.5629
SEXM:B_Stage4_postguard	0.0729	0.0531	1.37	0.1700

- 13c) Best fit models with Akaike weights >90% using Dredge function

```
knitr::kable(head(dredge(SI2)))
```

	(Intercept)	B_Stage	Bsucc	SEASON	SEX	B_Stage:SEX	df	logLik	AICc	delta	weig
14	-46.56367	+	NA	0.0236858	+	NA	7	-9367.817	18749.65	0.000000	0.54505
16	-46.09354	+	+	0.0234553	+	NA	8	-9367.563	18751.15	1.496184	0.25795
30	-46.54651	+	NA	0.0236858	+	+	10	-9366.214	18752.46	2.810021	0.13373
32	-46.07638	+	+	0.0234553	+	+	11	-9365.960	18753.96	4.307861	0.06324
6	-46.60966	+	NA	0.0236858	NA	NA	6	-9380.173	18772.36	22.709347	0.00000
8	-46.13954	+	+	0.0234554	NA	NA	7	-9379.919	18773.85	24.204969	0.00000

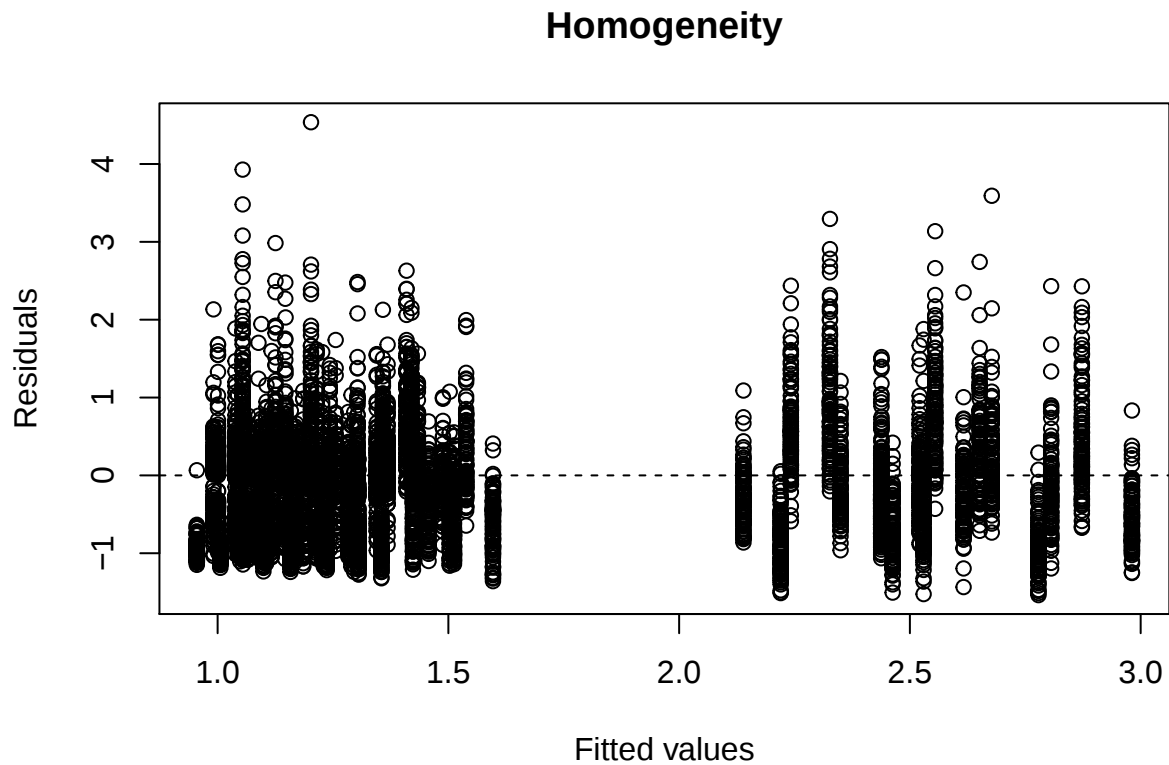
- 13d) Homogeneity

```
F5 <- rstandard(SI2)
```

```

xlab = "Fitted values",
ylab = "Residuals",
main = "Homogeneity")
abline(h = 0, v = 0, lty = 2)

```

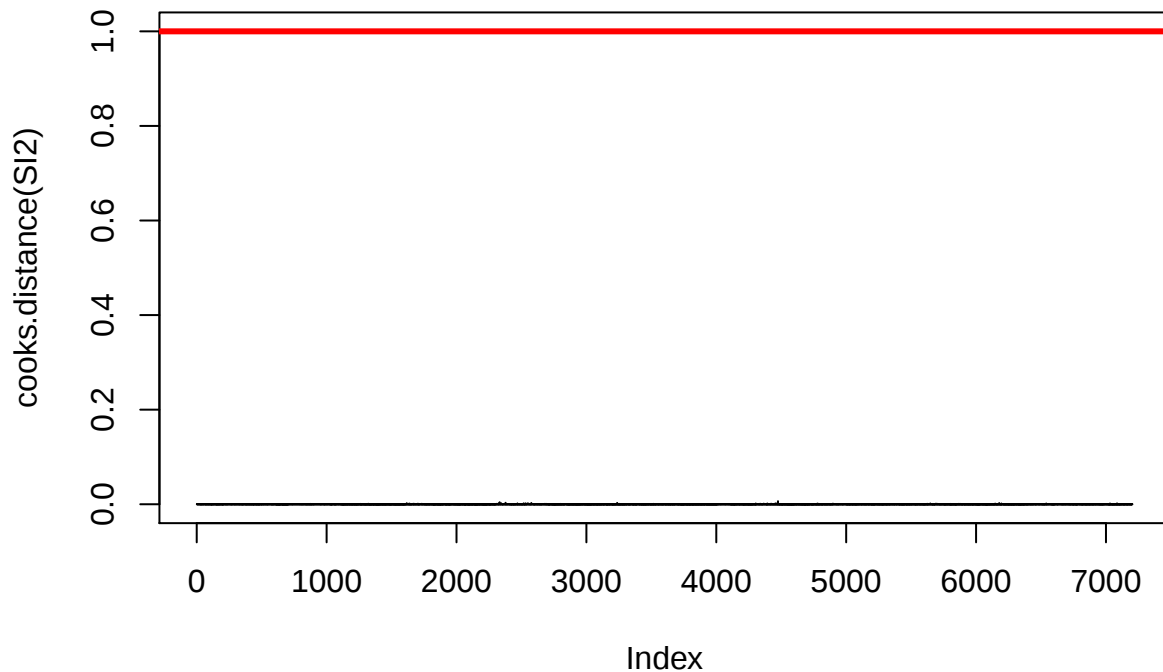


- 13e) Model outliers - Cook's distance

```

plot(cooks.distance(SI2), type = "h", ylim = c(0, 1))
abline(h = 1, col = 2, lwd = 3)

```



14) Diversity analysis

```
Div1<-read.table(file="LP_H_intraannual_adults_sex.txt", header=T, sep="\t")
str(Div1)
```

```
## 'data.frame': 355 obs. of 5 variables:
## $ SEASON : int 2003 2003 2003 2003 2003 2003 2003 2003 2003 2003 2003 ...
## $ B_Stage: Factor w/ 4 levels "1 Pre-laying",...: 1 1 1 1 1 1 1 1 2 2 2 ...
## $ SEX : Factor w/ 2 levels "F","M": 2 2 2 2 1 1 1 2 1 1 ...
## $ H : num 0.32508 0.00691 0.00691 0.00691 0.01382 ...
## $ Bsucc : Factor w/ 2 levels "1average","2good": 2 2 2 2 2 2 2 2 2 2 ...
```

- 14a) Full model - linear model

```
D1=lm(H~SEX + B_Stage + Bsucc+ SEX*B_Stage + SEASON, data=Div1)
```

- 14b) Summary % latex table generated in R 3.1.1 by xtable 1.7-3 package % Wed Oct 28 10:16:23 2015
- 14c) Best fit models with Akaike weights >90% using Dredge function

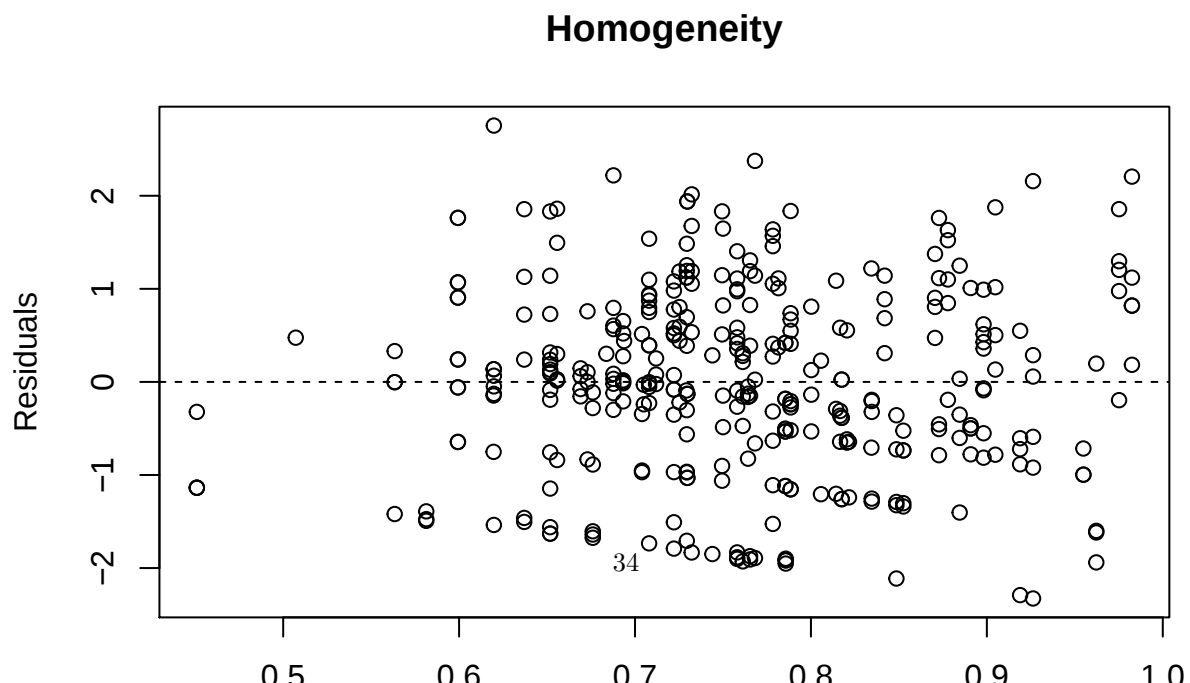
```
knitr::kable(head(dredge(D1),10))
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-55.7275	15.4343	-3.61	0.0004
SEXM	-0.1304	0.1245	-1.05	0.2955
B_Stage2 Incubation	0.0877	0.1281	0.68	0.4939
B_Stage3 Guard	0.0384	0.1129	0.34	0.7336
B_Stage4 Post-Guard	0.1408	0.1119	1.26	0.2092
Bsucc2good	-0.0078	0.0446	-0.18	0.8606
SEASON	0.0281	0.0077	3.66	0.0003
SEXM:B_Stage2 Incubation	0.0984	0.1616	0.61	0.5431
SEXM:B_Stage3 Guard	0.2401	0.1451	1.65	0.0989
SEXM:B_Stage4 Post-Guard	0.0601	0.1425	0.42	0.6736

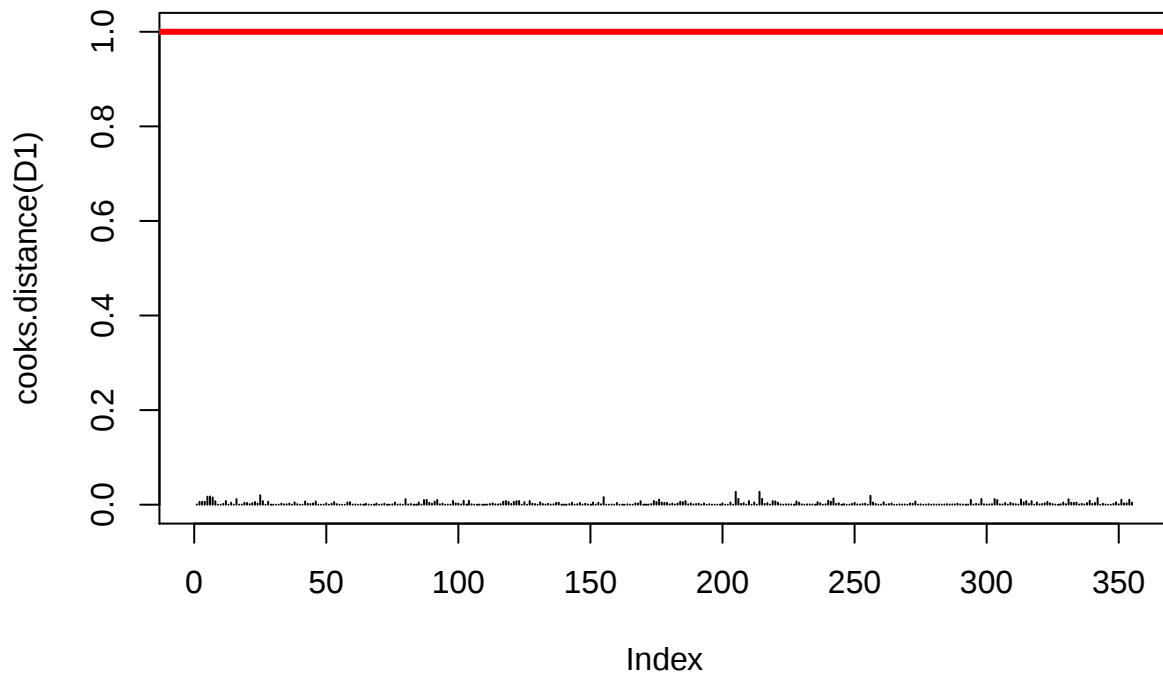
	(Intercept)	B_Stage	Bsucc	SEASON	SEX	B_Stage:SEX	df	logLik	AICc	delta	weight
6	-54.98278	+	NA	0.0277011	NA	NA	6	-175.1979	362.6373	0.000000	0.348925
5	-49.22888	NA	NA	0.0249106	NA	NA	3	-179.1425	364.3534	1.716162	0.147935
14	-54.90012	+	NA	0.0276638	+	NA	7	-175.1587	364.6401	2.002838	0.128180
8	-54.84216	+	+	0.0276335	NA	NA	7	-175.1803	364.6833	2.046065	0.125439
13	-49.11327	NA	NA	0.0248592	+	NA	4	-178.9933	366.1009	3.463639	0.061746
7	-49.22609	NA	+	0.0249093	NA	NA	4	-179.1425	366.3993	3.762049	0.053188
30	-55.86096	+	NA	0.0281802	+	+	10	-172.9526	366.5447	3.907429	0.049459
16	-54.76749	+	+	0.0275999	+	NA	8	-175.1426	366.7014	4.064081	0.045732
15	-49.11667	NA	+	0.0248608	+	NA	5	-178.9933	368.1585	5.521239	0.022070
32	-55.72755	+	+	0.0281162	+	+	11	-172.9367	368.6431	6.005783	0.017321

- 14d) Homogeneity

```
E6 <- rstandard(D1)
F6 <- fitted(D1)
par(mfrow = c(1, 1))
plot(x = F6,
     y = E6,
     xlab = "Fitted values",
     ylab = "Residuals",
     main = "Homogeneity")
abline(h = 0, v = 0, lty = 2)
```



```
plot(cooks.distance(D1), type = "h", ylim = c(0, 1))  
abline(h = 1, col = "red", lwd = 3)
```



References

Barton, K. (2013). “MuMIn: Multi-model inference.” R package version 1.9.13., from <http://CRAN.R-project.org/package=MuMIn>.

RStudio Team (2015). RStudio: Integrated Development for R. RStudio, Inc., Boston, MA URL <http://www.rstudio.com/>.