

1 Initialization

```
> library(NCStats)
```

2 Salmon Sperm Example

2.1 Data Preparation

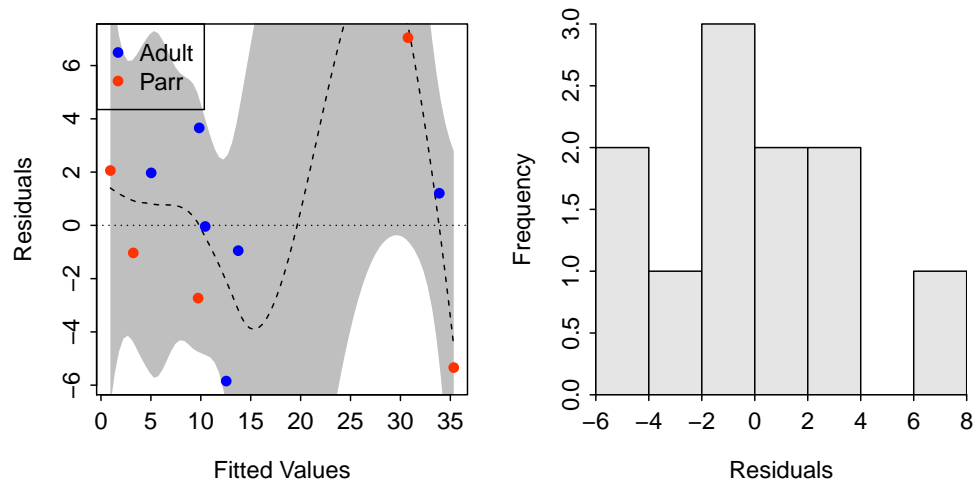
```
> ss <- read.csv("https://raw.githubusercontent.com/droglenc/NCData/master/SalmonSperm.csv")
```

```
> str(ss)
'data.frame': 11 obs. of 3 variables:
 $ step.len : num 2.94 3 3.02 3.17 3.18 3.2 3.27 3.31 3.72 3.84 ...
 $ fert.succ: num 3 2.2 7 7 13.5 10.4 6.7 12.8 37.8 30 ...
 $ mat      : Factor w/ 2 levels "Adult","Parr": 2 2 1 2 1 1 1 1 2 2 ...
> xlbl <- "Sperm Tail End Piece Length (um)"
> ylbl <- "Fertilization Success"
```

2.2 Fitting the Linear Model

```
> lm1 <- lm(fert.succ~step.len*mat,data=ss)
> residPlot(lm1,legend="topleft",main="")
```

Loading required namespace: *gplots*



```
> adTest(lm1$residuals)
Anderson-Darling normality test with lm1$residuals
A = 0.1784, p-value = 0.8932
> outlierTest(lm1)
```

```
No Studentized residuals with Bonferonni p < 0.05
Largest |rstudent|:
      rstudent unadjusted p-value Bonferonni p
12 2.905895      0.027125      0.29838
```

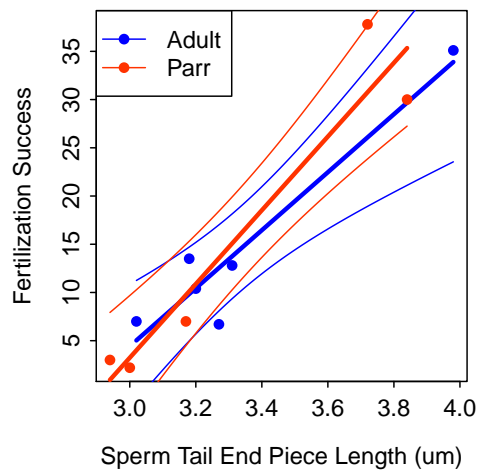
2.3 Model Exploration and Summarization

```
> summary(lm1)
Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    -85.769     20.266   -4.232  0.00388
step.len        30.066      6.066    4.956  0.00164
matParr        -25.661     27.273   -0.941  0.37809
step.len:matParr  8.155      8.148    1.001  0.35022

Residual standard error: 4.547 on 7 degrees of freedom
Multiple R-squared:  0.9139, Adjusted R-squared:  0.877
F-statistic: 24.78 on 3 and 7 DF,  p-value: 0.0004207

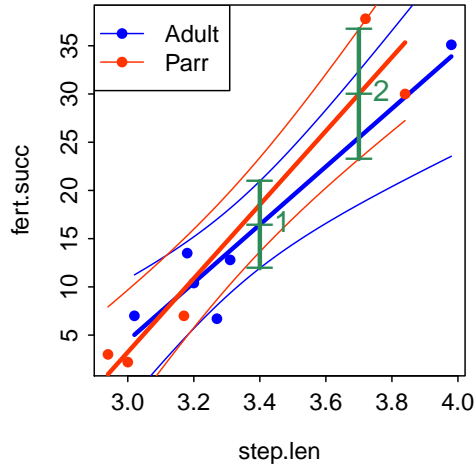
> confint(lm1)
              2.5 %    97.5 %
(Intercept)  -133.68997 -37.84811
step.len       15.72132  44.41036
matParr       -90.15097  38.82930
step.len:matParr -11.11233  27.42328

> fitPlot(lm1,interval="confidence",xlab=xlbl,ylab=ylbl,legend="topleft",main="")
```



```
> ( nd <- data.frame(step.len=c(3.4,3.7),mat=c("Adult","Parr")) )
  step.len  mat
1    3.4 Adult
2    3.7  Parr

> predictionPlot(lm1,nd,interval="confidence",legend="topleft",main="")
```



	obs	step.len	mat	fit	lwr	upr
1	1	3.4	Adult	16.45483	11.94067	20.96899
2	2	3.7	Parr	29.98900	23.25902	36.71899

2.4 ANOVA Demonstration

```
> lm1 <- lm(fert.succ~step.len*mat,data=ss)
> anova(lm1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
step.len	1	1510.23	1510.23	73.0316	5.966e-05
mat	1	6.11	6.11	0.2953	0.6037
step.len:mat	1	20.72	20.72	1.0017	0.3502
Residuals	7	144.75	20.68		
Total	10	1681.81			

```
> lm2 <- lm(fert.succ~step.len+mat,data=ss)
> anova(lm2)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
step.len	1	1510.23	1510.23	73.0157	2.709e-05
mat	1	6.11	6.11	0.2952	0.6017
Residuals	8	165.47	20.68		
Total	10	1681.81			

```
> lm3 <- lm(fert.succ~step.len,data=ss)
> anova(lm3)
```

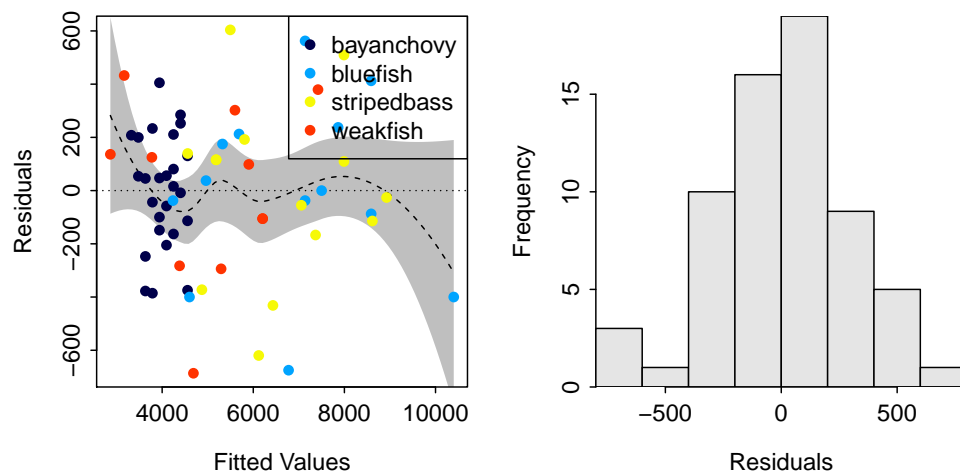
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
step.len	1	1510.23	1510.23	79.219	9.35e-06
Residuals	9	171.58	19.06		
Total	10	1681.81			

3 Fish Energy Density Example

```
> FED <- read.csv("https://raw.githubusercontent.com/droglenc/NCData/master/FishEnergyDensity.csv")
> str(FED)

'data.frame': 64 obs. of 3 variables:
 $ species: Factor w/ 4 levels "bayanchovy","bluefish",...: 2 2 2 2 2 2 2 2 2 2 ...
 $ dw      : int  39 34 34 32 31 30 30 29 26 25 ...
 $ ed      : int 10000 9000 8500 8100 7500 7100 7700 6100 5900 5500 ...
```

```
> lm1 <- lm(ed~dw*species,data=FED)
> residPlot(lm1,main="")
```



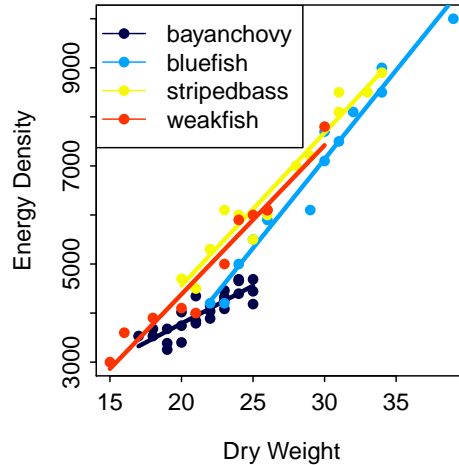
```
> adTest(lm1$residuals)

Anderson-Darling normality test with lm1$residuals
A = 0.353, p-value = 0.4549

> outlierTest(lm1)

No Studentized residuals with Bonferonni p < 0.05
Largest |rstudent|:
      rstudent unadjusted p-value Bonferonni p
20 -2.492888      0.015711      NA
```

```
> fitPlot(lm1,xlab="Dry Weight",ylab="Energy Density",legend="topleft",main="")
```



```
> anova(lm1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
dw	1	170693154	170693154	1858.966	< 2.2e-16
species	3	10592036	3530679	38.452	1.258e-13
dw:species	3	4105617	1368539	14.904	3.002e-07
Residuals	56	5142008	91822		
Total	63	190532816			

```
> compSlopes(lm1)
```

Multiple Slope Comparisons

	comparison	diff	lwr	upr	raw.p	adj.p
1	bluefish-bayanchovy	208.30952	145.62788	270.99117	0.00000	0.00000
2	stripedbass-bayanchovy	157.62055	94.29774	220.94336	0.00001	0.00003
3	weakfish-bayanchovy	149.60379	83.20906	215.99852	0.00003	0.00006
4	stripedbass-bluefish	-50.68898	-101.08569	-0.29227	0.04873	0.05848
5	weakfish-bluefish	-58.70573	-112.91192	-4.49955	0.03430	0.05145
6	weakfish-stripedbass	-8.01676	-62.96310	46.92958	0.77116	0.77116

Slope Information

	level	slopes	lwr	upr	raw.p	adj.p
1	bayanchovy	154.1905	102.2341	206.1469	0	0
4	weakfish	303.7943	262.4567	345.1318	0	0
3	stripedbass	311.8110	275.6128	348.0092	0	0
2	bluefish	362.5000	327.4355	397.5645	0	0

```
> FED1 <- Subset(FED,species!="bayanchovy")
> lm2 <- lm(ed~dw*species,data=FED1)
> anova(lm2)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
dw	1	104962559	104962559	838.6208	< 2.2e-16
species	2	2583571	1291785	10.3210	0.0003476
dw:species	2	556352	278176	2.2225	0.1247887
Residuals	32	4005150	125161		
Total	37	112107632			

```
> compIntercepts(lm2)
```

Warning:
Model contains an interaction term which will be removed (i.e., assume parallel lines) for testing intercepts.

```
Tukey HSD on adjusted means assuming parallel lines.
      comparison      diff      lwr      upr      p.adj
1 stripedbass-bluefish 631.3980 291.1082 971.6878 0.0001843341
2 weakfish-bluefish    506.4749 144.5318 868.4180 0.0044160914
3 weakfish-stripedbass -124.9231 -480.8922 231.0461 0.6693967026
```

Mean adjusted values at a covariate value of 26.10526

```
bluefish stripedbass weakfish
5828.663   6460.061   6335.138
```

```
> compIntercepts(lm2,common.cov=0)
```

Warning:

Model contains an interaction term which will be removed (i.e., assume parallel lines) for testing intercepts.

```
Tukey HSD on adjusted means assuming parallel lines.
```

```
      comparison      diff      lwr      upr      p.adj
1 stripedbass-bluefish 631.3980 291.1082 971.6878 0.0001843341
2 weakfish-bluefish    506.4749 144.5318 868.4180 0.0044160914
3 weakfish-stripedbass -124.9231 -480.8922 231.0461 0.6693967026
```

Mean adjusted values at a covariate value of 0

```
bluefish stripedbass weakfish
-2752.451  -2121.053  -2245.976
```

```
> compIntercepts(lm2,common.cov=20)
```

Warning:

Model contains an interaction term which will be removed (i.e., assume parallel lines) for testing intercepts.

```
Tukey HSD on adjusted means assuming parallel lines.
```

```
      comparison      diff      lwr      upr      p.adj
1 stripedbass-bluefish 631.3980 291.1082 971.6878 0.0001843341
2 weakfish-bluefish    506.4749 144.5318 868.4180 0.0044160914
3 weakfish-stripedbass -124.9231 -480.8922 231.0461 0.6693967026
```

Mean adjusted values at a covariate value of 20

```
bluefish stripedbass weakfish
3821.790   4453.188   4328.265
```

```
> fitPlot(lm2,xlab="Dry Weight",ylab="Energy Density",legend="topleft",main="")
```

