```
> library(NCStats)
> ff <- read.table("http://www.ncfaculty.net/dogle/R/Data_Master/R/FlyingFox1.txt",header=TRUE)
> str(ff)
  'data.frame':   223 obs. of 3 variables:
   $ forearm.len: num 152 154 157 157 158 ...
   $ body.mass : num 779 788 839 761 763 ...
   $ sex   : Factor w/ 3 levels "female","male",..: 2 2 2 2 2 2 2 2 2 2 ...
> ff$sex <- factor(ff$sex,levels=c("young","male","female"))
> table(ff$sex)

   young   male female
      79   75   69

> lm1 <- lm(body.mass~forearm.len*sex,data=ff)

> transChooser(lm1,show.stats=TRUE)
```
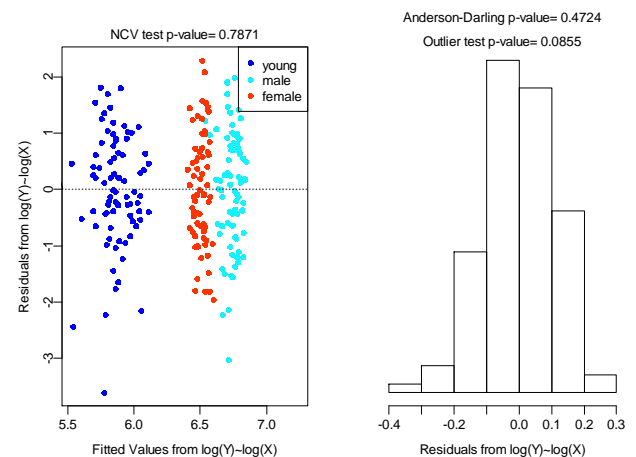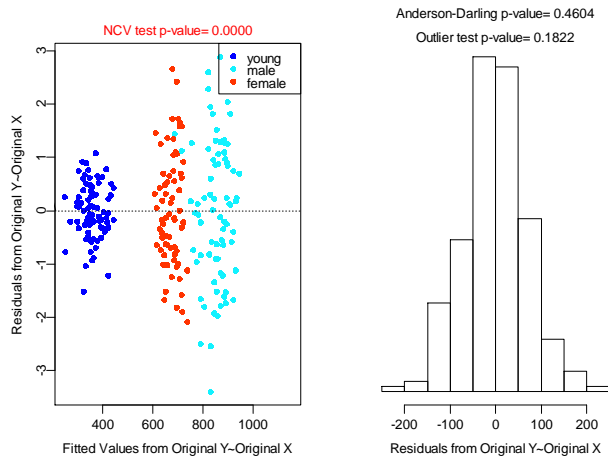


```
> anova(lm1)
  Response: body.mass
                   Df Sum Sq Mean Sq   F value   Pr(>F)
  forearm.len   1 9051340 9051340 1792.2167 < 2e-16 ***
  sex   2 987212 493606   97.7368 < 2e-16 ***
  forearm.len:sex   2   30210   15105   2.9908 0.05232 .
  Residuals   217 1095928   5050

> compSlopes(lm1)
  Multiple Slope Comparisons
      comparison   diff   lwr   upr   raw.p   adj.p
  1   male-young   5.67494   0.80082 10.54905 0.02270 0.06178
  2 female-young -0.08093 -4.76632 4.60445 0.97287 0.97287
  3 female-male -5.75587 -11.27945 -0.23228 0.04119 0.06178

  Slope Information
    level slopes   lwr   upr   raw.p   adj.p
  3 female 7.2419 3.4534 11.030 0.00021 0.00021
  1 young 7.3229 4.5661 10.080 0.00000 0.00000
  2   male 12.9978 8.9782 17.017 0.00000 0.00000

> compIntercepts(lm1)
  Tukey HSD on adjusted means assuming parallel lines.
      comparison   diff   lwr   upr p.adj
  1   male-young 274.22 247.00 301.44   0
  2 female-young 117.43   89.61 145.25   0
  3 female-male -156.79 -184.95 -128.63   0

  Mean adjusted values at a covariate value of 154.9
   young   male female
  490.56 764.78 607.99
```
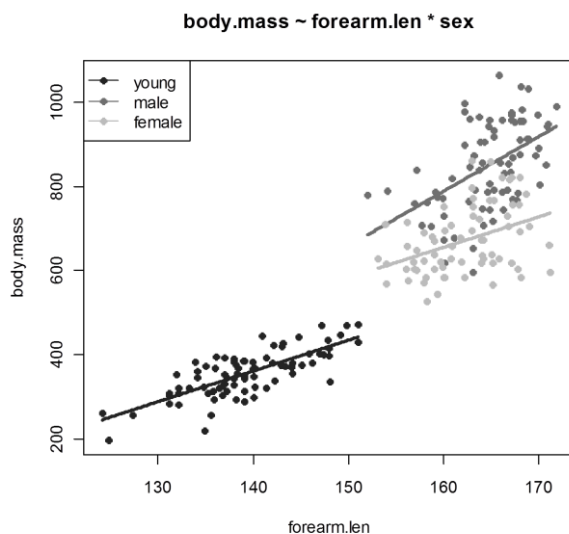
```
> fitPlot(lm1,legend="topleft",col="gray")
```

**body.mass ~ forearm.len * sex**



```
> predict(lm1,data.frame(forearm.len=c(155,155,155),sex=c("young","male","female")))
        1        2        3
 471.0677 723.9145 619.1563
```

```
> ff$log.bm <- log(ff$body.mass)
> ff$log.fl <- log(ff$forearm.len)
```

```
> lm2 <- lm(log.bm~log.fl*sex,data=ff)
```

```
> anova(lm2)
 Response: log.bm
             Df  Sum Sq Mean Sq   F value  Pr(>F)
 log.fl       1 31.4080 31.4080 2588.8126 < 2e-16 ***
 sex          2  1.8891  0.9445   77.8534 < 2e-16 ***
 log.fl:sex   2  0.0606  0.0303    2.4973 0.08467 .
 Residuals  217  2.6327  0.0121
```

```
> compSlopes(lm2)
 Multiple Slope Comparisons
      comparison     diff     lwr      upr   raw.p   adj.p
 1    male-young -0.43715 -1.6134  0.73908 0.46465 0.46465
 2 female-young -1.26771 -2.3880 -0.14740 0.02675 0.08025
 3  female-male -0.83056 -2.2220  0.56091 0.24070 0.36105

 Slope Information
    level slopes    lwr    upr   raw.p   adj.p
 3 female 1.7103 0.75957 2.6610 0.00048 0.00048
 2   male 2.5409 1.52483 3.5569 0.00000 0.00000
 1  young 2.9780 2.38538 3.5706 0.00000 0.00000
```
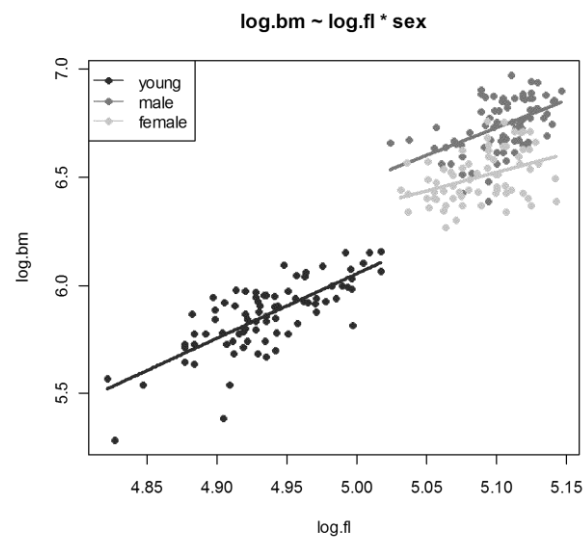
```
> compIntercepts(lm2)
 Tukey HSD on adjusted means assuming parallel lines.
      comparison     diff      lwr      upr p.adj
 1    male-young  0.43712  0.39502  0.47921     0
 2 female-young  0.24246  0.19944  0.28548     0
 3  female-male -0.19465 -0.23821 -0.15110     0

 Mean adjusted values at a covariate value of 5.039
  young   male female
 6.1314 6.5685 6.3739
```

```
> fitPlot(lm2,legend="topleft",col="gray")
```

log.bm ~ log.fl * sex


```
> predict(lm2,data.frame(log.fl=c(5.04,5.04,5.04),sex=c("young","male","female")))
       1        2        3
6.172781 6.575204 6.419336
```

```
> library(NCStats)
> d <- readData("C:/aaaWork/Consulting/Kennedy (Tony) -- 50maturity/NewData.csv")
> str(d)
'data.frame':   735 obs. of  6 variables:
 $ Year    : int  2011 2011 2011 2011 2011 2011 2011 2011 2011 2011 ...
 $ Maturity: int  0 0 0 0 0 0 0 0 0 0 ...
 $ Sex     : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
 $ TL      : int  405 397 395 322 295 305 278 314 351 300 ...
 $ Weight  : int  592 524 554 294 208 232 188 240 394 240 ...
 $ Age     : int  4 3 4 2 2 2 2 2 3 2 ...
> d$Maturity <- factor(d$Maturity)

> glm1 <- glm(Maturity~TL,data=d,family=binomial)

> fitPlot(glm1,main="",xlab="Total Length (mm)",ylab="Maturity Code")
```
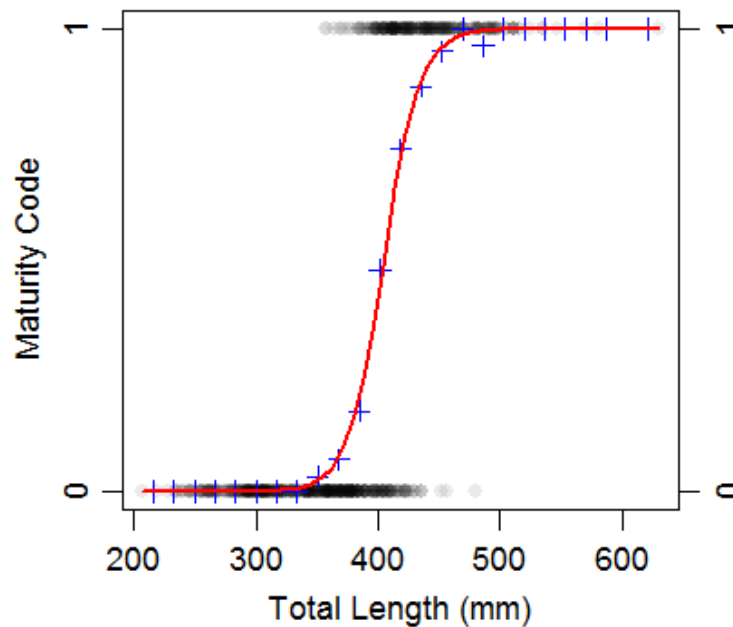


```
> summary(glm1)
Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -27.619919   2.314125  -11.94   <2e-16 ***
TL            0.068230   0.005738   11.89   <2e-16 ***

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 948.93  on 734  degrees of freedom
Residual deviance: 355.00  on 733  degrees of freedom
AIC: 359
```