R Handout - Logistic

Winter 2017, MTH207 Biometry

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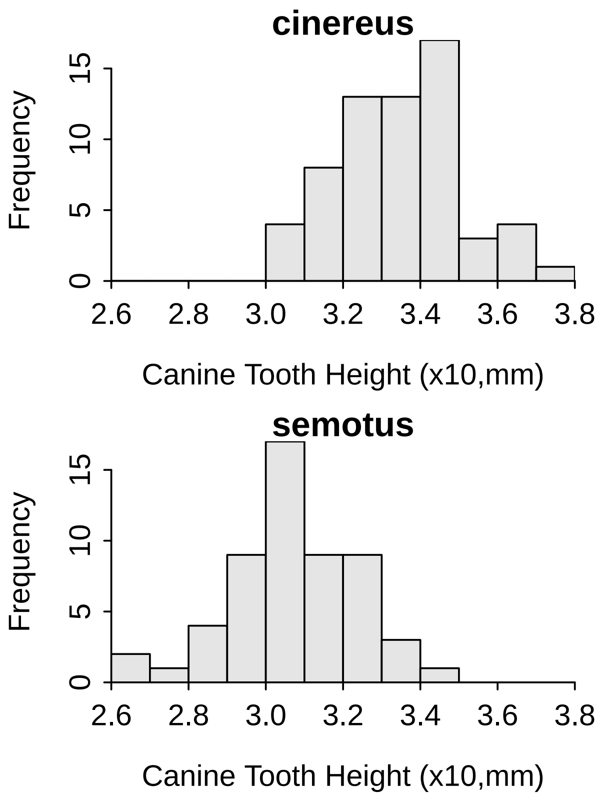
Initialization

```
> library(NCStats)
> library(plotrix)  #histStack()
> library(car)      #boot.case()
```

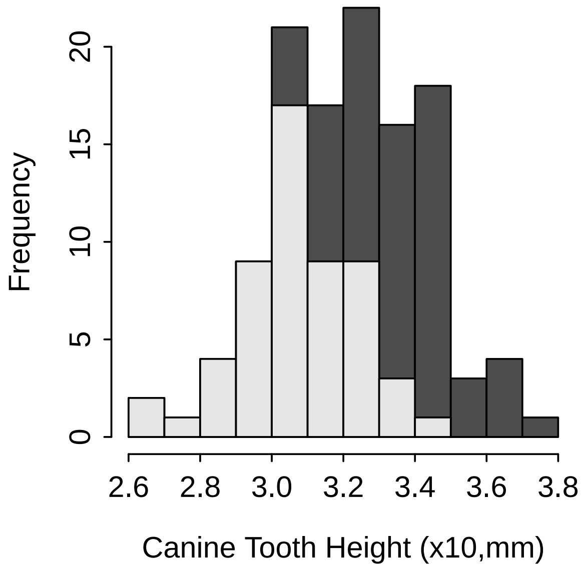
1 Bat Subspecies Example

1.1 Data Preparation and Examination

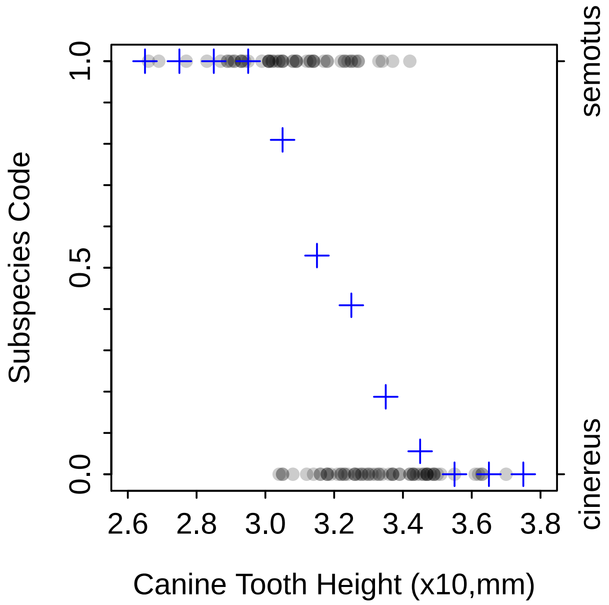
```
> bat <- read.csv("https://raw.githubusercontent.com/droglenc/NCData/master/Batmorph.csv")
> str(bat)

'data.frame': 118 obs. of  7 variables:
 $ subsp      : Factor w/ 2 levels "cinereus","semotus": 2 2 2 2 2 2 2 2 2 2 ...
 $ bodymass   : num  19.5 16.2 17 16.5 14.3 ...
 $ skulllength: num  1.6 1.55 1.56 1.56 1.53 ...
 $ canine     : num  0.326 0.308 0.291 0.287 0.301 0.305 0.277 0.313 0.289 0.293 ...
 $ coronoid   : num  0.303 0.282 0.292 0.303 0.279 0.284 0.286 0.281 0.278 0.28 ...
 $ wingspan   : num  0.358 0.358 0.359 0.353 0.351 0.361 0.351 0.363 0.34 0.365 ...
 $ hab        : Factor w/ 3 levels "A","B","C": 1 1 1 1 1 1 1 1 2 2 ...

> bat$canine10 <- bat$canine*10
> xlbl <- "Canine Tooth Height (x10,mm)"
> ylbl <- "Subspecies Code"
> hist(canine10~subsp,data=bat,breaks=seq(2.6,3.8,0.1),xlim=c(2.6,3.8),
       xlab=xlbl,nrow=2,ncol=1)
```



```
> histStack(canine10~subsp,data=bat,breaks=seq(2.6,3.8,0.1),xlim=c(2.6,3.8),
          col="gray.colors",xlab=xlbl,right=FALSE)
```

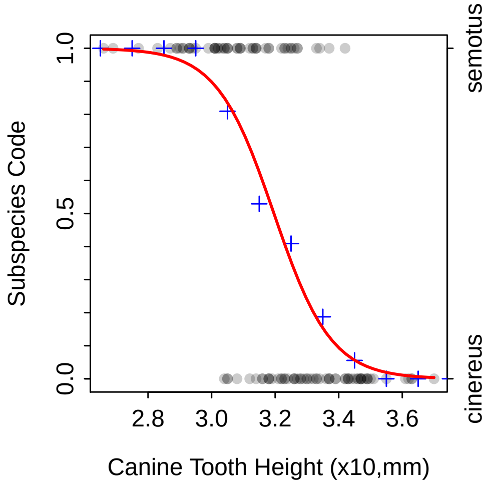


```
> plotBinResp(subsp~canine10,data=bat,breaks=seq(2.6,3.8,0.1),xlim=c(2.6,3.8),
            xlab=xlbl,ylab=ylbl)
```



1.2 Model Fitting and Examination

```
> glm1 <- glm(subsp~canine10,data=bat,family=binomial)
> fitPlot(glm1,breaks=seq(2.6,3.8,0.1),xlab=xlbl,ylab=ylbl,main="")
```



```
> summary(glm1)

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   35.516      6.428   5.525 3.29e-08
canine10     -11.112      2.005  -5.543 2.97e-08

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 163.040  on 117  degrees of freedom
Residual deviance:  97.178  on 116  degrees of freedom
AIC: 101.18

Number of Fisher Scoring iterations: 5
> confint(glm1)
Waiting for profiling to be done...
                2.5 %   97.5 %
(Intercept)  24.21685 49.66132
canine10    -15.52430 -7.58941
```

1.3 Interpretation of Slope

```
> x1 <- c(3,4)                      # purposely pick two canine10 values 1 unit apart
> ( p1 <- predict(glm1,data.frame(canine10=x1)) )
        1         2
 2.179940 -8.931994
> p1[[2]]-p1[[1]]
[1] -11.11193
> exp(-11.112)                      # back-transformed 'slope' from summary() above
```

```
[1] 1.493206e-05
> ( bp1 <- exp(p1) )
           1            2
8.8457728416 0.0001320944
> bp1[[2]]/bp1[[1]]
[1] 1.493306e-05
```

1.4 Predicting Probabilities

```
> ( p2 <- predict(glm1,data.frame(canine10=c(3,3.4))) )
        1         2
 2.179940 -2.264834
> exp(p2)/(1+exp(p2))
         1          2
0.89843357 0.09407761
> predict(glm1,data.frame(canine10=c(3,3.4)),type="response")
         1          2
0.89843357 0.09407761
```

1.5 X for a Certain Proportion

```
> ( cfs <- coef(glm1) )
(Intercept)    canine10
   35.51574   -11.11193
> p <- 0.5    # canine tooth height where subspecies ratio is 50/50
> ( x <- (log(p/(1-p))-cfs[[1]])/cfs[[2]] )
[1] 3.19618
> predict(glm1,data.frame(canine10=x),type="response")    # test the answer
  1
0.5
> p <- 0.9    # length where 90% are semotus, 10% are cinereus
> (log(p/(1-p))-cfs[[1]])/cfs[[2]]
[1] 2.998444
```

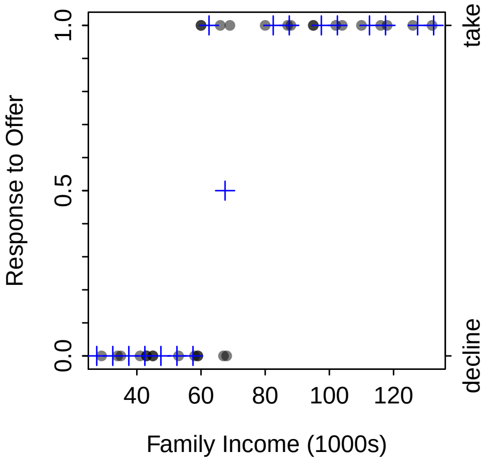
2 Bootstrapping

```
> bc1 <- bootCase(glm1)      # bootstrapping, be patient!
> head(bc1)

     (Intercept)  canine10
[1,]    35.81998 -11.21662
[2,]    36.46938 -11.37874
[3,]    40.50277 -12.61516
[4,]    26.56209  -8.20114
[5,]    40.00093 -12.50260
[6,]    35.67100 -11.02964

> confint(bc1)

              95% LCI  95% UCI
(Intercept)  26.24424 50.73736
canine10    -15.88791 -8.20068

> predProb <- function(x,alpha,beta1) exp(alpha+beta1*x)/(1+exp(alpha+beta1*x))
> predProb(3,coef(glm1)[[1]],coef(glm1)[[2]])

[1] 0.8984336

> p3 <- predProb(3,bc1[,1],bc1[,2])
> head(p3)

[1] 0.8975332 0.9115875 0.9344588 0.8763892 0.9236589 0.9296982

> quantile(p3,c(0.025,0.975))

     2.5%     97.5%
0.8118832 0.9636279

> predX <- function(p,alpha,beta1) (log(p/(1-p))-alpha)/beta1
> x50 <- predX(0.5,bc1[,1],bc1[,2])
> head(x50)

[1] 3.193473 3.205047 3.210642 3.238829 3.199409 3.234102

> quantile(x50,c(0.025,0.975))

    2.5%    97.5%
3.149542 3.241326
```

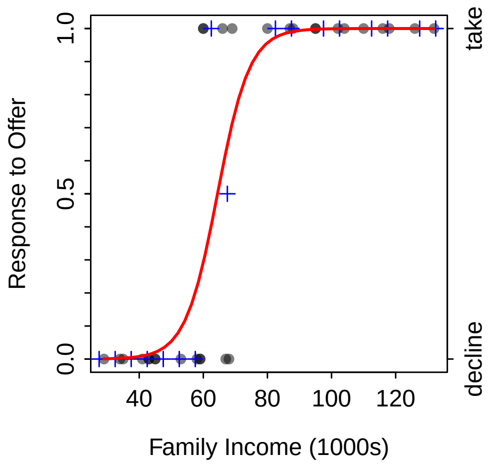
3 Solar Panel Offer Data

```
> sp <- read.csv("https://raw.githubusercontent.com/droglenc/NCData/master/SolarOffer.csv")
> str(sp)
'data.frame': 30 obs. of  5 variables:
 $ income   : int  80 60 35 45 29 43 34 104 102 59 ...
 $ age      : int  30 34 25 27 23 28 24 43 46 36 ...
 $ takeoffer: Factor w/ 2 levels "decline","take": 2 2 1 1 1 1 1 2 2 1 ...
 $ mortgage : int  2000 2100 1500 1800 1900 1600 1500 2400 2700 2600 ...
 $ famsize  : int  4 3 2 4 2 3 1 5 3 2 ...
> xlbl <- "Family Income (1000s)"
> ylbl <- "Response to Offer"
```

```
> plotBinResp(takeoffer~income,data=sp,xlab=xlbl,ylab=ylbl,breaks=seq(25,135,5))
```



```
> glm2 <- glm(takeoffer~income,data=sp,family=binomial)
> summary(glm2)

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -12.84503    6.16398  -2.084   0.0372
income        0.19934    0.09774   2.039   0.0414

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 41.455  on 29  degrees of freedom
Residual deviance: 13.035  on 28  degrees of freedom
AIC: 17.035

Number of Fisher Scoring iterations: 8
> fitPlot(glm2,xlab=xlbl,ylab=ylbl,breaks=seq(25,135,5),main="")
```



```
> p <- 0.25
> (log(p/(1-p))-coef(glm2)[1])/coef(glm2)[2]

(Intercept)
   58.92646

> predict(glm2,data.frame(income=80),type="response")

        1
0.9569831
```