Logistic Regression

R Handout

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Initialization

```
> library(NCStats)
> library(plotrix)  #histStack()
> library(car)      #bootCase()
> setwd("C:/aaaWork/Web/GitHub/NCMTH207/modules/LogisticRegression")
```

Bat Morphology Example

Background

Researchers measured (among other things) the canine tooth height (cm) from two subspecies of Hoary bats (*Lasiurus cinereus cinereus* and *Lasiurus cinereus semotus*) found in Hawaii. Their primary question was to determine if canine tooth height differed between the subspecies and, more importantly to them, could the canine tooth height be used to predict the subspecies of bat.

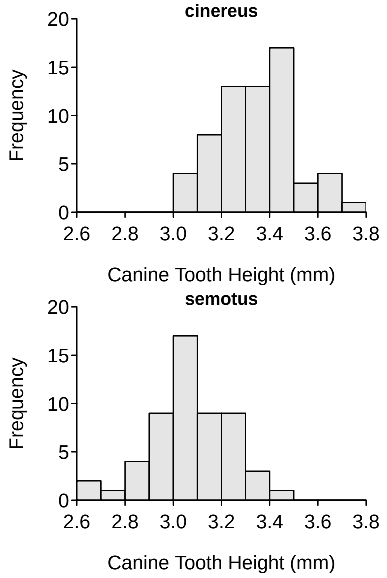
```
> bat <- read.csv("Batmorph.csv")[,c("subsp","canine")]  # for class demo purposes only
> str(bat)
```

```
'data.frame':   118 obs. of  2 variables:
 $ subsp : Factor w/ 2 levels "cinereus","semotus": 2 2 2 2 2 2 2 2 2 2 ...
 $ canine: num  0.326 0.308 0.291 0.287 0.301 0.305 0.277 0.313 0.289 0.293 ...
```

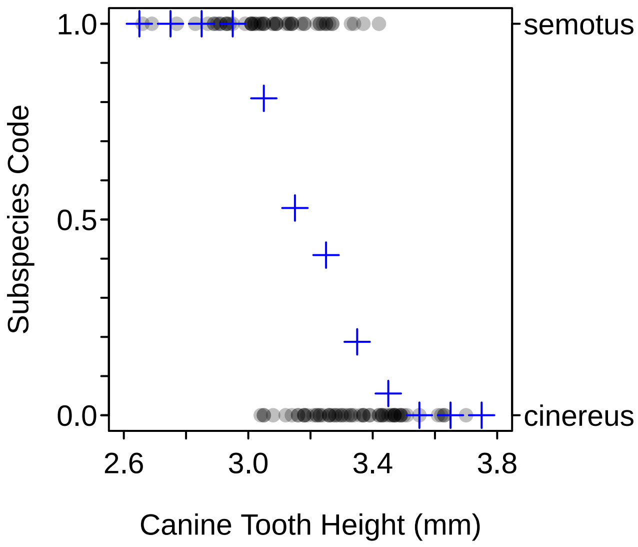
```
> bat$canine <- bat$canine*10  # convert cm to mm
> xlbl <- "Canine Tooth Height (mm)"
> ylbl <- "Subspecies Code"
```

Explorations

```
> hist(canine~subsp,data=bat,w=0.1,xlim=c(2.6,3.8),ymax=20,xlab=xlbl,nrow=2,ncol=1)
```

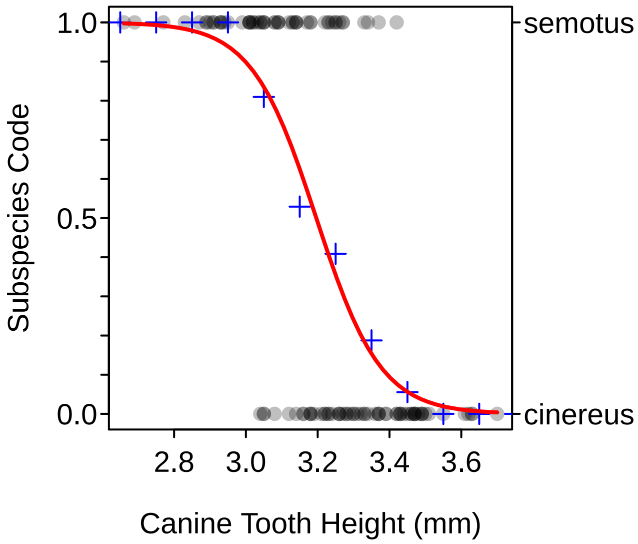


```
> plotBinResp(subsp~canine,data=bat,breaks=seq(2.6,3.8,0.1),xlim=c(2.6,3.8),
              xlab=xlbl,ylab=ylbl)
```



Model Fitting and Examination

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



```
> summary(glm1)
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)   35.516      6.428   5.525 3.29e-08
canine       -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
canine      -15.52430 -7.58941
```

Lecture Support – Interpretation of Slope

```
> x1 <- c(3,4)                # purposely picked two canine values 1 unit apart
> ( p1 <- predict(glm1,data.frame(canine=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
```

Predicting Probabilities

```
> ( p2 <- predict(glm1,data.frame(canine=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(canine=c(3,3.4)),type="response")
```

```
         1          2
0.89843357 0.09407761
```

X for a Certain Proportion

```
> ( cfs <- coef(glm1) )
```

```
(Intercept)      canine
   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(canine=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
```

Bootstrapping

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

```
     (Intercept)     canine
[1,]    28.71481  -9.102347
[2,]    27.36832  -8.535495
[3,]    33.83273 -10.601386
[4,]    24.07838  -7.542993
[5,]    35.59767 -11.107211
[6,]    33.54310 -10.332912
```

```
> confint(bc1)
```

```
              95% LCI   95% UCI
(Intercept)  26.67080 51.425584
canine      -16.12459 -8.310609
```

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

```
(Intercept)
  0.8984336
```

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

```
[1] 0.8034141 0.8534397 0.8837646 0.8099054 0.9068728 0.9271936
```

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

```
     2.5%     97.5%
0.8132979 0.9671475
```

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

```
[1] 3.154660 3.206413 3.191350 3.192151 3.204915 3.246238
```

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

```
    2.5%    97.5% 
3.149765 3.241546 
```

Solar Panel Offer Data

Background

Households were asked if they would accept an offer to put solar panels on the roof of their house if they would receive a 50% subsidy from the state. Demographic variables for each household such as income, size, monthly mortgage payment, and age of the head of household were also recorded. The researchers had three primary questions:

- At what income will 25% of households accept?
- What is the probability of acceptance for a household with an income of $80000?
- How much does odds of acceptance change for each $1000 increase in household income?

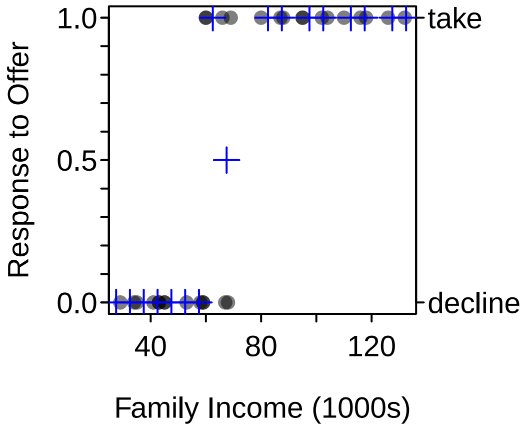
```
> sp <- read.csv("SolarOffer.csv")
> str(sp)
```

```
'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"
```

Analysis

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



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

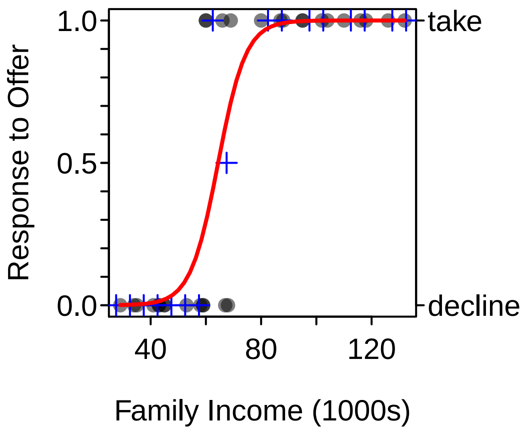
```
Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -12.84503    6.16398  -2.084   0.0372
income        0.19934    0.09774   2.039   0.0414

(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]]
```

```
[1] 58.92646
```

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

```
        1
0.9569831
```