

Logistic Regression Handout

1 Initialization

```
> library(NCStats)
```

2 Bat Subspecies Example

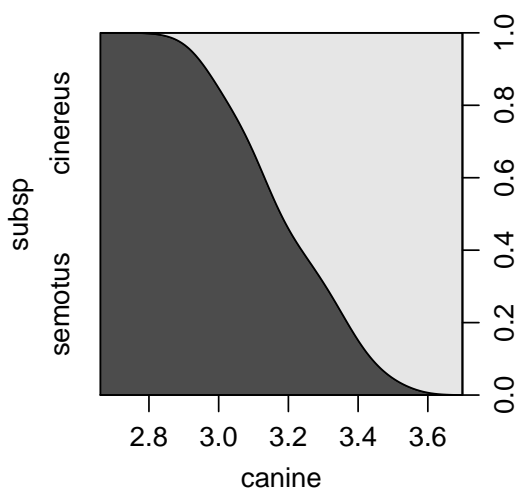
You must change the directory to where the following file is located. In addition, I changed the canine measurements to mm (from cm) for ease of explanation later on.

```
> bat <- read.table("BatMorph.txt",head=TRUE)
> 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 ...

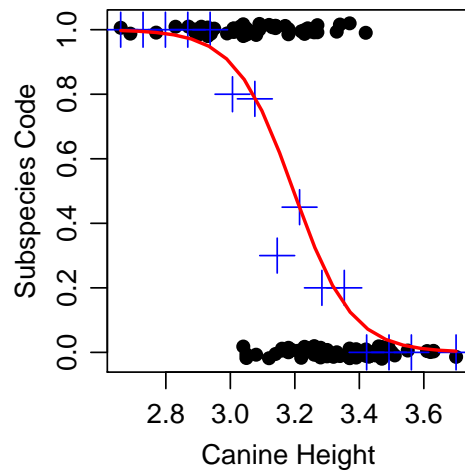
> bat$canine <- bat$canine*10

> cdplot(subsp~canine,data=bat,ylevels=2:1)
```



```
> glm1 <- glm(subsp~canine,data=bat,family=binomial)
> logregPlot(glm1,p.ints=15,xlab="Canine Height",ylab="Subspecies Code")
```

glm, subsp ~ canine, binomial, bat



```
> coef(glm1)

(Intercept)      canine 
 35.51574    -11.11193 

> confint(glm1)

                2.5 %   97.5 % 
(Intercept)  24.21685 49.66132 
canine      -15.52430 -7.58941 

> predict(glm1,data.frame(canine=c(3,4)))

      1      2 
2.179940 -8.931994 

> -8.931994-2.179940

[1] -11.11193 

> exp(coef(glm1))

(Intercept)      canine 
2.656377e+15 1.493306e-05 

> exp(predict(glm1,data.frame(canine=c(3,4))))

      1      2 
8.8457728416 0.0001320944 

> 0.0001320944/8.8457728416

[1] 1.493305e-05
```

```

> summary(glm1)

Call:
glm(formula = subsp ~ canine, family = binomial, data = bat)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.9483  -0.6384  -0.1377   0.5923   2.2658

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

> predict(glm1,data.frame(canine=c(3,3.4)))

      1      2
2.179940 -2.264834

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

      1      2
0.8984336 0.0940776

```