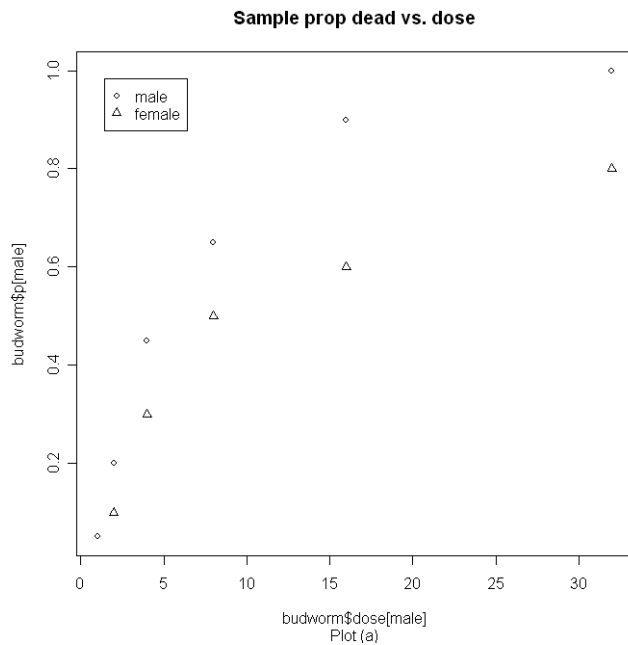


```

> budworm <- read.table(file="N:\\courses\\stat8620\\Fall 08\\budworm.dat",header=T)
> #budworm <- read.table(file="C:\\Documents and Settings\\dhall\\My Documents\\Dan's Work
Stuff\\courses\\STAT8620\\Fall 08\\budworm.dat",header=T)
> budworm[1:3,]
  sex dose y m
1  1   1  1 20
2  1   2  4 20
3  1   4  9 20
> budworm$p <- budworm$y/budworm$m
>
> male <- budworm$sex==1
> budworm$male <- as.numeric(male)
> plot(budworm$dose[male],budworm$p[male],
+ main="Sample prop dead vs. dose",pch=1, sub="Plot (a)")
> points(budworm$dose[!male],budworm$p[!male],pch=2)
> legend(locator(1),pch=c(1,2),legend=c("male", "female"))

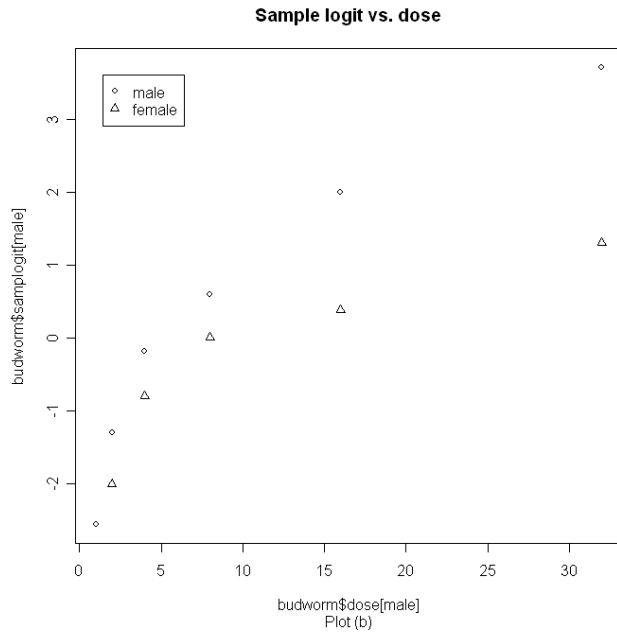
```



```

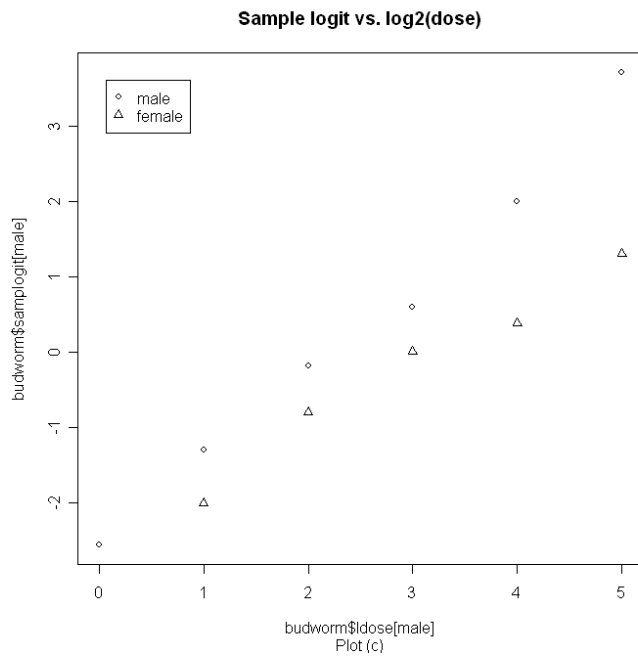
>
> budworm$samplogit <- log((budworm$y+0.5)/(budworm$m-budworm$y+0.5))
> budworm$ldose <- log2(budworm$dose)
>
> plot(budworm$dose[male],budworm$samplogit[male],
+ main="Sample logit vs. dose",pch=1, sub="Plot (b)")
> points(budworm$dose[!male],budworm$samplogit[!male],pch=2)
> legend(locator(1),pch=c(1,2),legend=c("male", "female"))

```



>

```
> plot(budworm$dose[male],budworm$samplogit[male],
+ main="Sample logit vs. log2(dose)",pch=1, sub="Plot (c)")
> points(budworm$dose[!male],budworm$samplogit[!male],pch=2)
> legend(locator(1),pch=c(1,2),legend=c("male","female"))
```



>

>

```
> m1 <- glm(p~ldose*male,data=budworm,weights=rep(20,12),
+ family=binomial(link="logit"))
> dead.alive <- cbind(budworm$y,rep(20,12)-budworm$y)
> m1alt <- glm(dead.alive~ldose*male,data=budworm,
```

```

+ family=binomial(link="logit"))
>
> bud2 <- rbind(budworm,budworm)
> bud2$dead <- c(rep(1,12),rep(0,12))
> bud2$freq <- c(budworm$y,20-budworm$y)
> dead.alt <- rep(bud2$dead,times=bud2$freq)
> ldose.alt <- rep(bud2$ldose,times=bud2$freq)
> male.alt <- rep(bud2$male,times=bud2$freq)
> budworm2 <- data.frame(cbind(dead.alt,ldose.alt,male.alt))
> budworm2[1:6,]
  dead.alt ldose.alt male.alt
1      1      0      1
2      1      1      1
3      1      1      1
4      1      1      1
5      1      1      1
6      1      2      1
> budworm2[121:126,]
  dead.alt ldose.alt male.alt
121      0      0      1
122      0      0      1
123      0      0      1
124      0      0      1
125      0      0      1
126      0      0      1
> m1alt2 <- glm(dead.alt~ldose.alt*male.alt,data=budworm2,
+ family=binomial(link="logit"))
>
> m1

```

Call: glm(formula = p ~ ldose \* male, family = binomial(link = "logit"), data = budworm, weights = rep(20, 12))

Coefficients:  
(Intercept) ldose male ldose:male  
-2.9935 0.9060 0.1750 0.3529

Degrees of Freedom: 11 Total (i.e. Null); 8 Residual  
Null Deviance: 124.9  
Residual Deviance: 4.994 AIC: 43.1  
> m1alt

Call: glm(formula = dead.alive ~ ldose \* male, family = binomial(link = "logit"), data = budworm)

Coefficients:  
(Intercept) ldose male ldose:male  
-2.9935 0.9060 0.1750 0.3529

Degrees of Freedom: 11 Total (i.e. Null); 8 Residual  
Null Deviance: 124.9  
Residual Deviance: 4.994 AIC: 43.1  
> m1alt2

Call: glm(formula = dead.alt ~ Idose.alt \* male.alt, family = binomial(link = "logit"), data = budworm2)

Coefficients:  
(Intercept) Idose.alt male.alt Idose.alt:male.alt  
-2.9935 0.9060 0.1750 0.3529

Degrees of Freedom: 239 Total (i.e. Null); 236 Residual  
Null Deviance: 331.4  
Residual Deviance: 211.5 AIC: 219.5  
> logLik(m1)  
'log Lik.' -17.55206 (df=4)  
> logLik(m1alt)  
'log Lik.' -17.55206 (df=4)  
> logLik(m1alt2)  
'log Lik.' -105.7388 (df=4)  
> logLik(m1)-sum(log(choose(budworm\$m,budworm\$y)))  
'log Lik.' -105.7388 (df=4)  
>  
> summary(m1,corr=F)

Call:  
glm(formula = p ~ Idose \* male, family = binomial(link = "logit"),  
data = budworm, weights = rep(20, 12))

Deviance Residuals:  
Min 1Q Median 3Q Max  
-1.39849 -0.32094 -0.07592 0.38220 1.10375

Coefficients:  
Estimate Std. Error z value Pr(>|z|)  
(Intercept) -2.9935 0.5527 -5.416 6.09e-08 \*\*\*  
Idose 0.9060 0.1671 5.422 5.89e-08 \*\*\*  
male 0.1750 0.7783 0.225 0.822  
Idose:male 0.3529 0.2700 1.307 0.191  
---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 124.8756 on 11 degrees of freedom  
Residual deviance: 4.9937 on 8 degrees of freedom  
AIC: 43.104

Number of Fisher Scoring iterations: 4

```
>
> #saturated model:
> m2 <- glm(p~factor(ldose)*factor(male),data=budworm,weights=rep(20,12),
+ family=binomial(link="logit"))
>
> summary(m2,corr=F)
```

Call:

```
glm(formula = p ~ factor(ldose) * factor(male), family = binomial(link = "logit"),
    data = budworm, weights = rep(20, 12))
```

Deviance Residuals:

```
[1] 0 0 0 0 0 0 0 0 0 0 0 0
```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	-25.752	52998.328	-4.86e-04	1	
factor(ldose)1	23.555	52998.328	4.44e-04	1	
factor(ldose)2	24.904	52998.328	4.70e-04	1	
factor(ldose)3	25.752	52998.328	4.86e-04	1	
factor(ldose)4	26.157	52998.328	4.94e-04	1	
factor(ldose)5	27.138	52998.328	0.001	1	
factor(male)1	22.807	52998.328	4.30e-04	1	
factor(ldose)1:factor(male)1	-21.996	52998.328	-4.15e-04	1	1
factor(ldose)2:factor(male)1	-22.161	52998.328	-4.18e-04	1	1
factor(ldose)3:factor(male)1	-22.188	52998.328	-4.19e-04	1	1
factor(ldose)4:factor(male)1	-21.016	52998.328	-3.97e-04	1	1
factor(ldose)5:factor(male)1	1.558	74951.009	2.08e-05	1	1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1.2488e+02 on 11 degrees of freedom  
Residual deviance: 5.2388e-10 on 0 degrees of freedom  
AIC: 54.11

Number of Fisher Scoring iterations: 22

```
>
> #deviance of model m1 is GOF statistic:
> summary(m1)
```

Call:

```
glm(formula = p ~ ldose * male, family = binomial(link = "logit"),
    data = budworm, weights = rep(20, 12))
```

Deviance Residuals:

```
Min    1Q  Median    3Q    Max
-1.39849 -0.32094 -0.07592  0.38220  1.10375
```

Coefficients:

```
Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.9935    0.5527 -5.416 6.09e-08 ***
ldose      0.9060    0.1671  5.422 5.89e-08 ***
male       0.1750    0.7783  0.225  0.822
ldose:male 0.3529    0.2700  1.307  0.191
```

---

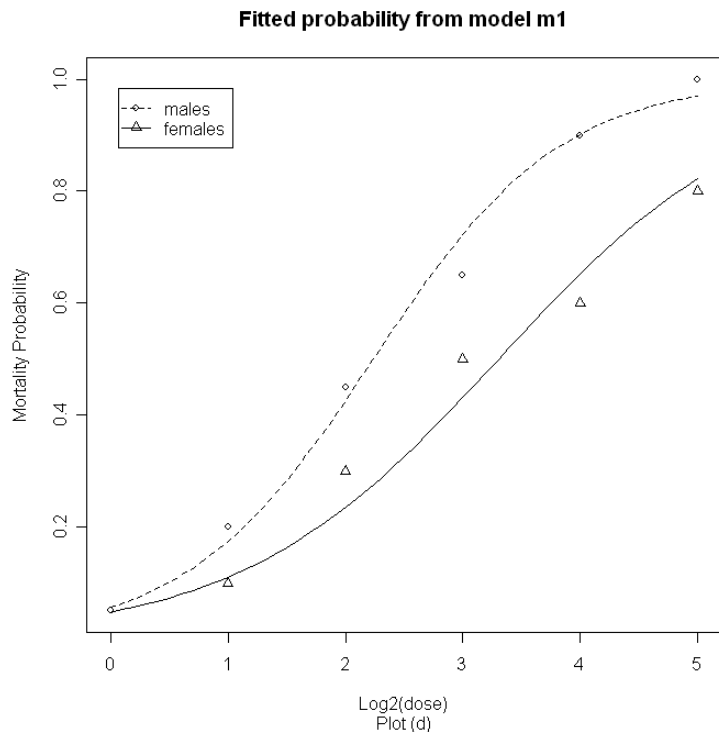
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 124.8756 on 11 degrees of freedom
Residual deviance: 4.9937 on 8 degrees of freedom
AIC: 43.104
```

Number of Fisher Scoring iterations: 4

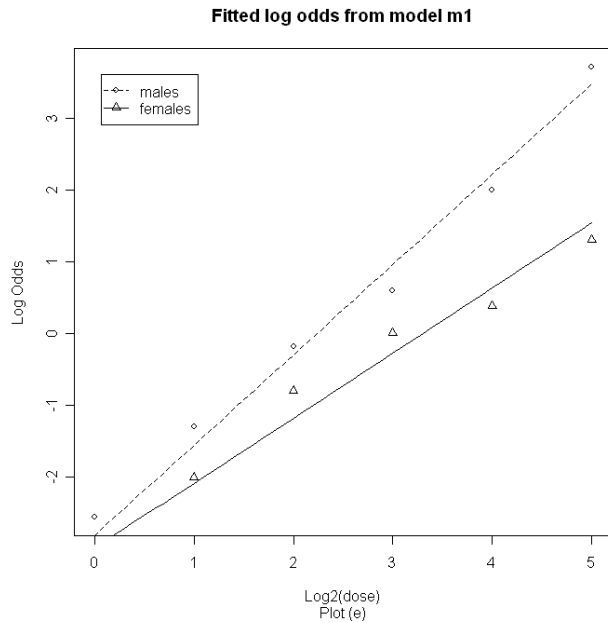
```
> deviance(m1)
[1] 4.993727
> 2*(logLik(m2)-logLik(m1))
[1] 4.993727
attr(,"df")
[1] 12
attr(,"class")
[1] "logLik"
> #Pearson X^2 statistic:
> sum(resid(m1,type="pearson")^2)
[1] 3.504694
>
> # The value commented out below reproduces the loglikelihood result given
> # for model m2 in budworm.sas
> #logLik(m2)-sum(log( choose(budworm$m,budworm$y) ))
>
> ldose0 <- seq(from=0,to=5,by=.1)
> expit <- function(x) {1/(1+exp(-x)) }
> plot(budworm$ldose[male],budworm$p[male],xlab="Log2(dose)",
+ ylab="Mortality Probability", sub="Plot (d)",
+ main="Fitted probability from model m1",pch=1)
> points(budworm$ldose[!male],budworm$p[!male],pch=2)
> lines(ldose0,
+ expit( (coef(m1)[1]+coef(m1)[3])+(coef(m1)[2]+coef(m1)[4])*ldose0),lty=2)
> lines(ldose0,
+ expit( (coef(m1)[1])+(coef(m1)[2])*ldose0),lty=1)
> legend(locator(1),legend=c("males","females"),lty=c(2,1),pch=c(1,2))
```



```

>
>
> plot(budworm$Ildose[male],budworm$samplogit[male],xlab="Log2(dose)",
+ ylab="Log Odds",
+ main="Fitted log odds from model m1",pch=1, sub="Plot (e)")
> points(budworm$Ildose[!male],budworm$samplogit[!male],pch=2)
> lines(Ildose0,
+ (coef(m1)[1]+coef(m1)[3])+(coef(m1)[2]+coef(m1)[4])*Ildose0,lty=2)
> lines(Ildose0,
+ (coef(m1)[1])+(coef(m1)[2])*Ildose0,lty=1)
> legend(locator(1),legend=c("males","females"),lty=c(2,1),pch=c(1,2))

```



```
>
>
> budworm$Ildosec <- budworm$Ildose-2.5
> m3 <- glm(p~Ildosec*male,data=budworm,weights=rep(20,12),
+ family=binomial(link="logit"))
>
> summary(m3)
```

Call:  
 glm(formula = p ~ Ildosec \* male, family = binomial(link = "logit"),  
 data = budworm, weights = rep(20, 12))

Deviance Residuals:  
 Min 1Q Median 3Q Max  
 -1.39849 -0.32094 -0.07592 0.38220 1.10375

Coefficients:  
 Estimate Std. Error z value Pr(>|z|)  
 (Intercept) -0.7285 0.2455 -2.967 0.00301 \*\*  
 Ildosec 0.9060 0.1671 5.422 5.89e-08 \*\*\*  
 male 1.0573 0.3581 2.952 0.00316 \*\*  
 Ildosec:male 0.3529 0.2700 1.307 0.19117  
 ---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 124.8756 on 11 degrees of freedom  
 Residual deviance: 4.9937 on 8 degrees of freedom  
 AIC: 43.104



Number of Fisher Scoring iterations: 4

```
>
> m4 <- glm(p~male+ldose,data=budworm,weights=rep(20,12),
+ family=binomial(link="logit"))
> anova(m4,m1,test="Chisq")
Analysis of Deviance Table
```

```
Model 1: p ~ male + ldose
Model 2: p ~ ldose * male
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1     9    6.7571
2     8    4.9937 1  1.7633  0.1842
> anova(m4,m3,test="Chisq")
Analysis of Deviance Table
```

```
Model 1: p ~ male + ldose
Model 2: p ~ ldosec * male
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1     9    6.7571
2     8    4.9937 1  1.7633  0.1842
>
> summary(m4)
```

```
Call:
glm(formula = p ~ male + ldose, family = binomial(link = "logit"),
    data = budworm, weights = rep(20, 12))
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.10540 -0.65343 -0.02225  0.48471  1.42944
```

```
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.4732    0.4685  -7.413 1.23e-13 ***
male         1.1007    0.3558   3.093 0.00198 **
ldose        1.0642    0.1311   8.119 4.70e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 124.876 on 11 degrees of freedom
Residual deviance: 6.757 on 9 degrees of freedom
AIC: 42.867
```

Number of Fisher Scoring iterations: 4

```

>
> m5 <- glm(p~factor(male)+ldose-1,data=budworm,weights=rep(20,12),
+ family=binomial(link="logit"))
> summary(m5)

```

Call:

```

glm(formula = p ~ factor(male) + ldose - 1, family = binomial(link = "logit"),
    data = budworm, weights = rep(20, 12))

```

Deviance Residuals:

```

    Min      1Q  Median      3Q     Max
-1.10540 -0.65343 -0.02225  0.48471  1.42944

```

Coefficients:

```

      Estimate Std. Error z value Pr(>|z|)
factor(male)0 -3.4732    0.4685  -7.413 1.23e-13 ***
factor(male)1 -2.3724    0.3855  -6.154 7.56e-10 ***
ldose          1.0642    0.1311   8.119 4.70e-16 ***
---

```

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

```

Null deviance: 126.227 on 12 degrees of freedom
Residual deviance: 6.757 on 9 degrees of freedom
AIC: 42.867

```

Number of Fisher Scoring iterations: 4

```

>
> coef(m4)
(Intercept)  male  ldose
-3.473155  1.100743  1.064214
> coef(m5)
factor(male)0 factor(male)1  ldose
-3.473155  -2.372412  1.064214
>
>
> #LD50 and Wald confidence interval: females
> # if natural log of dose had been used instead of log2(dose), then
> # use exp() instead of 2^() below to invert the logarithm
> varbetahat <- summary(m5)$cov.scaled
>
> ILD50 <- (0-coef(m5)[1])/coef(m5)[3]
> se.ILD50 <- sqrt((coef(m5)[3]^(-2))* t(c(1,0,ILD50))%*%varbetahat%*%c(1,0,ILD50))
> ILD50
factor(male)0

```

```

3.263587
> se.ILD50
      [,1]
[1,] 0.2297539
>
> #The same result can be obtained using the dose.p function in the MASS library
> library(MASS)
> dose.p(m5,cf=c(1,3),p=c(.5,.9))
      Dose      SE
p = 0.5: 3.263587 0.2297539
p = 0.9: 5.328233 0.3611835
>
> Lower.LD50 <- 2^(ILD50-1.96*se.ILD50)
> Upper.LD50 <- 2^(ILD50+1.96*se.ILD50)
> LD50interval.females.Wald <- cbind(Lower.LD50,2^(ILD50),Upper.LD50)
> LD50interval.females.Wald
      [,1] [,2] [,3]
factor(male)0 7.028758 9.60368 13.12190
>
> # if you wanted the LD90, you'd do the following
> # ILD90 <- (logit(.9)-coef(m5)[1])/coef(m5)[3]
> # se.ILD90 <- sqrt((coef(m5)[3]^(-2))* t(c(1,0,ILD90))%%varbetahat%%c(1,0,ILD90))
>
> #LD50 and Wald confidence interval: males
> dose.p(m5,cf=c(2,3),p=c(.5,.9))
      Dose      SE
p = 0.5: 2.229262 0.2259649
p = 0.9: 4.293908 0.3336275
>
> ILD50 <- (0-coef(m5)[2])/coef(m5)[3]
> se.ILD50 <- sqrt((coef(m5)[3]^(-2))* t(c(0,1,ILD50))%%varbetahat%%c(0,1,ILD50))
>
> Lower.LD50 <- 2^(ILD50-1.96*se.ILD50)
> Upper.LD50 <- 2^(ILD50+1.96*se.ILD50)
> LD50interval.males.Wald <- cbind(Lower.LD50,2^(ILD50),Upper.LD50)
> LD50interval.males.Wald
      [,1] [,2] [,3]
factor(male)1 3.449461 4.688941 6.373798
>
>
> quad.form <- function(a,b,c){
+ l <- (-b - sqrt(b^2-4*a*c))/(2*a)
+ u <- (-b + sqrt(b^2-4*a*c))/(2*a)
+ c(l,u)
+ }
> z <- qnorm(1-.05/2,0,1)
> a <- coef(m5)[3]^2-(z^2)*varbetahat[3,3]
> b <- 2*coef(m5)[3]*coef(m5)[2]-2*(z^2)*varbetahat[2,3]

```

```
> c <- coef(m5)[2]^2-(z^2)*varbetahat[2,2]
> LD50interval.males.Fieller <- quad.form(a,b,c)
> LD50interval.males.Fieller <- 2^LD50interval.males.Fieller
> LD50interval.males.Fieller
  ldose  ldose
1.768493 2.681297
> LD50interval.males.Fieller
  ldose  ldose
3.406979 6.414322
>
>
```