```
> no.yes=c("No","Yes")
> smoking=gl(2,1,8,no.yes)
> obesity=gl(2,2,8,no.yes)
> snoring=gl(2,4,8,no.yes)
> n.tot=c(60,17,8,2,187,85,51,23)
> n.hyp=c(5,2,1,0,35,13,15,8)
> hypertension=data.frame(smoking,obesity,snoring,n.tot,n.hyp)
> hypertension
  smoking obesity snoring n.tot n.hyp
                               60
       No
                No
                                       5
                        No
                               17
      Yes
                No
                        No
       No
               Yes
                        No
                                8
                                       0
      Yes
               Yes
                        No
       No
                No
                              187
                                      35
                       Yes
6
                               85
                                      13
                       Yes
      Yes
                No
       No
               Yes
                       Yes
                               51
                                      15
                               23
8
      Yes
                                       8
               Yes
                       Yes
```

```
> hyp.table=cbind(hypertension$n.hyp,hypertension$n.tot-
+ hypertension$n.hyp)
> hyp.table
    [,1] [,2]
[1,] 5 55
[2,] 2 15
[3,] 1 7
[4,] 0
[5,] 35 152
[6,] 13 72
[7,] 15 36
[8,]
           15
> M1=glm(hyp.table~smoking+obesity+snoring,family =
binomial("logit"))
> summary(M1)
```

```
Call:
glm(formula = hyp.table ~ smoking + obesity + snoring, family =
binomial("logit"))
Deviance Residuals:
                         3
                                   4
                                                      6
7
-0.04344 0.54145 -0.25476 -0.80051 0.19759 -0.46602
-0.21262 0.56231
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.37766 0.38018 -6.254 4e-10 ***
smokingYes -0.06777 0.27812 -0.244 0.8075
obesityYes 0.69531 0.28509 2.439 0.0147 *
snoringYes 0.87194 0.39757 2.193 0.0283 *
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 14.1259 on 7 degrees of freedom
Residual deviance: 1.6184 on 4 degrees of freedom
AIC: 34.537
Number of Fisher Scoring iterations: 4
```

```
Alternatively, one can also provide the proportions instead
of the counts:
> prop.hyp=n.hyp/n.tot
> M1 2=glm(prop.hyp~smoking+obesity+snoring,family=binomial,
weights=n.tot)
> summary(M1 2)
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.37766 0.38018 -6.254 4e-10 ***
smokingYes -0.06777 0.27812 -0.244 0.8075
obesityYes 0.69531 0.28509 2.439 0.0147 *
snoringYes 0.87194 0.39757 2.193 0.0283 *
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 14.1259 on 7 degrees of freedom
Residual deviance: 1.6184 on 4 degrees of freedom
AIC: 34.537
```

Number of Fisher Scoring iterations: 4

 Null deviance corresponds to the deviance of a model that contains only the interval (and so, a fixed probability of success)

```
> M2=glm(hyp.table~obesity+snoring,family = binomial("logit"))
> summary(M2)
Coefficients:
           Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.3921 0.3757 -6.366 1.94e-10 ***
obesityYes 0.6954 0.2851 2.440 0.0147 *
snoringYes 0.8655 0.3967 2.182 0.0291 *
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 14.1259 on 7 degrees of freedom
Residual deviance: 1.6781 on 5 degrees of freedom
AIC: 32.597
```

Number of Fisher Scoring iterations: 4

```
> anova(M2)
Analysis of Deviance Table

Model: binomial, link: logit

Response: hyp.table

Terms added sequentially (first to last)
```

```
Df Deviance Resid. Df Resid. Dev NULL 7 14.1259 obesity 1 6.8260 6 7.2999 snoring 1 5.6218 5 1.6781
```

```
> M2=glm(hyp.table~obesity+snoring,family = binomial("logit"))
> anova(M2,test="Chisq")
Analysis of Deviance Table
Model: binomial, link: logit
Response: hyp.table
Terms added sequentially (first to last)
       Df Deviance Resid. Df Resid. Dev Pr(>Chi)
                                14.1259
NULL
obesity 1 6.8260
                        6 7.2999 0.008984 **
snoring 1 5.6218
                                 1.6781 0.017738 *
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Odds-estimates

- Odds ratio per unit change in the covariate. For example, if
 we consider obesity, the odds ratio associated with obesity
 is approx 2.0. We refer to the "odds ratio" as the ratio of the
 odds of developing the disease given exposure and the
 odds of developing the disease given the non-exposure.
- An odds ratio of 1 indicates the condition is equally likely to occur in both groups.

Example: experiment on the toxicity to the tobacco budworm Heliothis virescens of doses of a pyrethroid (insecticide). Batches of 20 moths of each sex were exposed for 3 days and the number in each batch that were dead or knocked down was recorded.

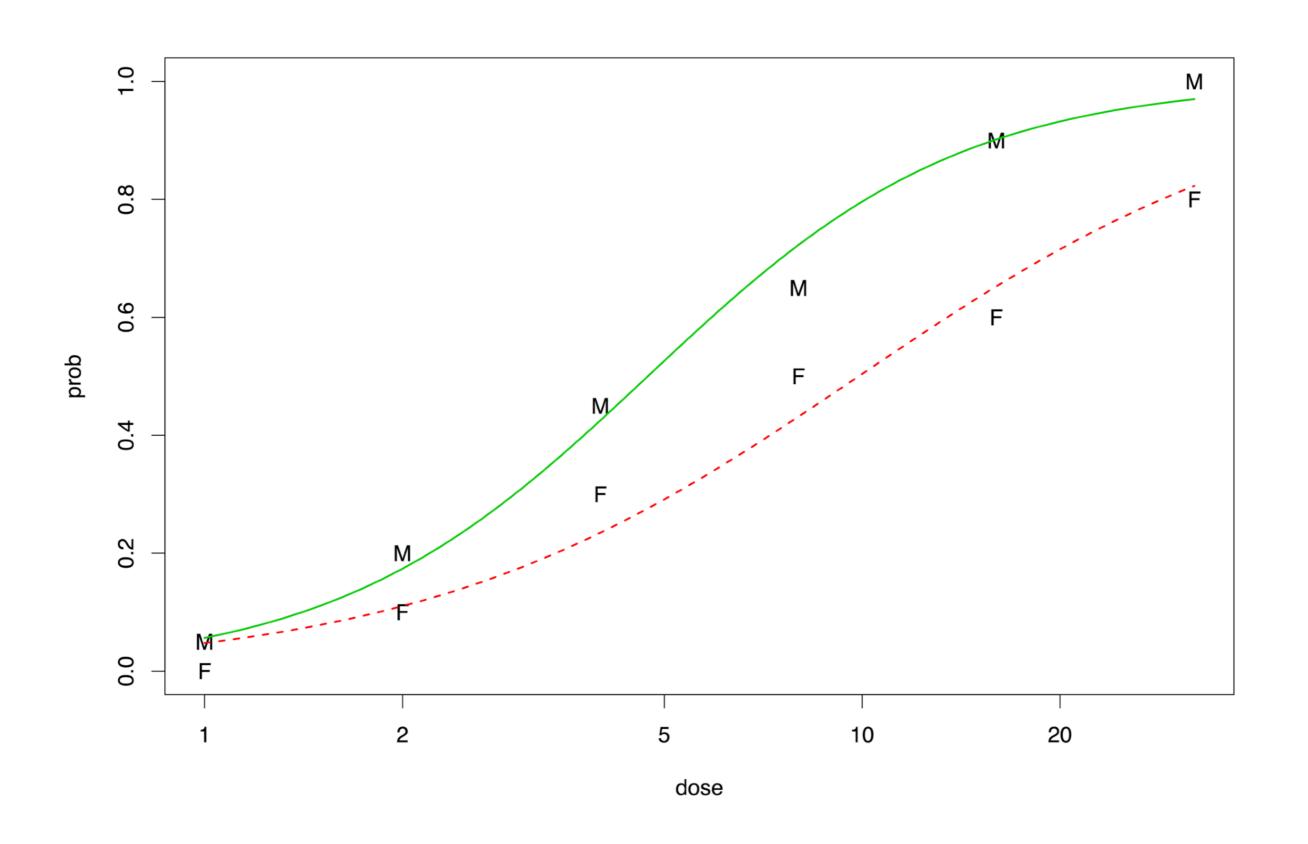
Sex	Dose					
	1	2	4	8	16	32
Male	1	4	9	13	18	20
Female	0	2	6	10	12	16

```
>ldose=rep(0:5,2)
>numdead=c(1,4,9,13,18,20,0,2,6,10,12,16)
>sex=factor(rep(c("M", "F"), c(6,6)))
>SF=cbind(numdead,numalive=20-numdead)
>M1=glm(SF~sex*ldose,family=binomial)
>summary(M1)
Call:
glm(formula = SF ~ sex * ldose, family = binomial)
Deviance Residuals:
    Min
                10 Median
                                    3Q
                                             Max
-1.39849 -0.32094 -0.07592 0.38220 1.10375
```

increase in "intercept" for males

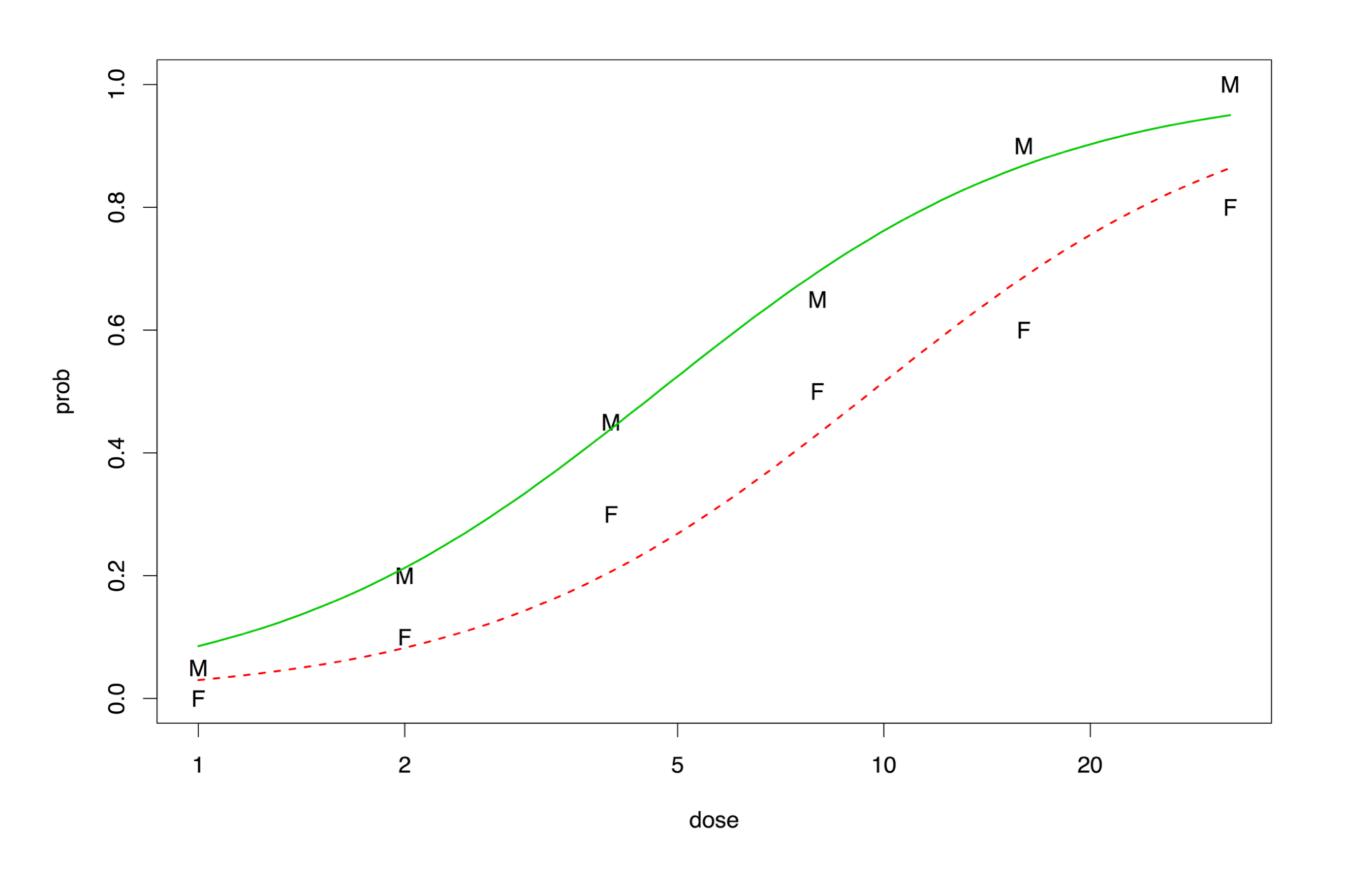
```
Coefficients:
          Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.9935
                      0.5527 -5.416 6.09e-08 ***
sexM 0.1750
                      0.7783 0.225 0.822
     0.9060 0.1671 5.422 5.89e-08 ***
ldose
sexM:ldose 0.3529 0.2700 1.307 0.191
Signif. codes 0 '***' 0.001 '**' 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: 43.10A
Number of Fisher Scoring iterations: 4
```

increase in "slope" for males



```
> M2=glm(SF~sex+ldose,family=binomial)
> summary(M2)
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 ***
sexM 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: 124.8756 on 11 degrees of freedom
Residual deviance: 6.7571 on 9 degrees of freedom
AIC: 42.867
```

Number of Fisher Scoring iterations: 4



Titanic Data. The Titanic sank on April 15, 1912, killing 1502 out of 2224 passengers and crews. There were not enough lifeboats. Some groups of people were more likely to survive than others, such as women, children, and the upper class. The data is from Kaggle, but available in **R**.

```
> library(titanic)
> str(titanic train)
'data.frame': 891 obs. of 12 variables:
$ PassengerId: int 1 2 3 4 5 6 7 8 9 10 ...
$ Survived : int 0 1 1 1 0 0 0 0 1 1 ...
$ Pclass : int 3 1 3 1 3 3 1 3 3 2 ...
         : chr "Braund, Mr. Owen Harris" "Cumings, Mrs.
 $ Name
John Bradley (Florence Briggs Thayer)" "Heikkinen, Miss. Laina"
"Futrelle, Mrs. Jacques Heath (Lily May Peel)" ...
             : chr "male" "female" "female" ...
$ Sex
             : num 22 38 26 35 35 NA 54 2 27 14 ...
$ Age
$ SibSp : int 1 1 0 1 0 0 0 3 0 1 ...
$ Parch : int 0 0 0 0 0 0 1 2 0 ...
 $ Ticket : chr "A/5 21171" "PC 17599" "STON/O2. 3101282"
"113803" ...
```

Variables:

- Survival: 1 (Yes) and 0 (No)
- Pclass: 1st, 2nd and 3rd
- Sex: male, female
- Age
- Passenger ID
- Name
- SibSp: #siblings/spouses
- Parch: #of parents/children aboard
- Ticket: Ticket number
- Embarked: Port of embarkation (C=Cherbourg, Q=Queenstown, S=Southampton)
- Fare
- Cabin: cabin number

We consider a subset of 800 passengers and some variables:

```
> sapply(titanic train,function(x) sum(is.na(x)))
               Survived
PassengerId
                              Pclass
                                                          Sex
                                            Name
                                                                      Age
                       0
                                   0
                                               0
          0
                                                            0
                                                                      177
                              Ticket
      SibSp
                                                                 Embarked
                                                        Cabin
               Parch
                                            Fare
                                               0
```

```
>my_titanic=data.frame(Survived=Survived[1:800],
Pclass=Pclass[1:800],Age=Age[1:800],SibSp=SibSp[1:800],
Sex=Sex[1:800],Parch=Parch[1:800],Fare=Fare[1:800])
>M1=glm(Survived~.,family=binomial,data=my_titanic)
>summary(M1)
```

We will also consider some test data:

```
> my_titanic_test=data.frame(Survived=Survived[801:891],
+Pclass=as.factor(Pclass[801:891]),Age=Age[801:891],SibSp=SibSp[801:891],
+Sex=Sex[801:891],Parch=Parch[801:891],Fare=Fare[801:891])
> missing_index=(1:91)[apply(apply((my_titanic_test),2,is.na),1,sum)==1]
> my_titanic_test=my_titanic_test[-missing_index,]
> length(my_titanic_test$Survived)
> 7
```

```
> summary(M1)
Call:
glm(formula = Survived ~ ., family = binomial, data = my titanic)
Deviance Residuals:
   Min 1Q Median 3Q Max
-2.7382 \quad -0.6477 \quad -0.3944 \quad 0.6375 \quad 2.4249
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 4.119120 0.528061 7.800 6.17e-15 ***
Pclass2 -1.233680 0.338641 -3.643 0.000269 ***
Pclass3 -2.482686 0.355952 -6.975 3.06e-12 ***
Age -0.041966 0.008630 -4.863 1.16e-06 ***
SibSp -0.338228 0.133493 -2.534 0.011287 *
Sexmale -2.645685 0.233589 -11.326 < 2e-16 ***
Parch -0.097362 0.132937 -0.732 0.463927
Fare 0.001470 0.002518 0.584 0.559173
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 860.71 on 636 degrees of freedom
Residual deviance: 569.54 on 629 degrees of freedom
  (163 observations deleted due to missingness)
AIC: 585.54
Number of Fisher Scoring iterations: 5
```

```
> M2=qlm(Survived~Pclass+Age+SibSp+Sex,family=binomial,data=my titanic)
> summary(M2)
Deviance Residuals:
             1Q Median
   Min
                             30
                                     Max
-2.7543 -0.6436 -0.3904 0.6268 2.4376
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) 4.213846 0.469989 8.966 < 2e-16 ***
Pclass2 -1.326588 0.298966 -4.437 9.11e-06 ***
Pclass3 -2.601180 0.299387 -8.688 < 2e-16 ***
Age -0.042482 0.008573 -4.955 7.23e-07 ***
SibSp -0.358688 0.127083 -2.822 0.00477 **
Sexmale -2.619322 0.227509 -11.513 < 2e-16 ***
(Dispersion parameter for binomial family taken to be 1)
   Null deviance: 860.71 on 636 degrees of freedom
Residual deviance: 570.28 on 631 degrees of freedom
  (163 observations deleted due to missingness)
AIC: 582.28
Number of Fisher Scoring iterations: 5
```

```
> fitted_results=predict(M2,my_titanic_test,type='response')
> fitted_results<-ifelse(fitted_results>0.5,1,0)
> mean(fitted_results==my_titanic_test$Survived)
[1] 0.8181818
```