

OUTPUT 1

```
1 > summary(glm(cbind(z,m-z)~Dose,family=binomial))
2
3 Call: glm(formula = cbind(z, m - z) ~ Dose, family = binomial)
4
5 Coefficients:
6             Estimate Std. Error z value Pr(>|z|)
7 (Intercept) -2.564549   0.363907  -7.047 1.82e-12 ***
8 Dose         0.020983   0.002866   7.321 2.46e-13 ***
9 ---
10 Signif. codes:  0   ***  0.001  **  0.01  *  0.05  .  0.1    1
11
12 (Dispersion parameter for binomial family taken to be 1)
13
14 Null deviance: 147.3237  on 7  degrees of freedom
15 Residual deviance:  3.8835  on 6  degrees of freedom
16 AIC: 29.255
17
18 Number of Fisher Scoring iterations: 5
```

OUTPUT 2

```
1 > mod1<-glm(cbind(z,m-z)~Dose+Sex,family=binomial)
2 > mod2<-glm(cbind(z,m-z)~Dose*Sex,family=binomial)
3
4 > summary(mod1)
5
6 Call:glm(formula = cbind(z, m - z) ~ Dose + Sex, family = binomial)
7
8 Coefficients:
9             Estimate Std. Error z value Pr(>|z|)
10 (Intercept) -2.645127   0.279690  -9.457  <2e-16 ***
11 Dose         0.022938   0.002004  11.445  <2e-16 ***
12 SexMale      -0.848825   0.253184  -3.353   8e-04 ***
13 ---
14 Signif. codes:  0   ***  0.001  **  0.01  *  0.05  .  0.1    1
15
16 (Dispersion parameter for binomial family taken to be 1)
17
18 Null deviance: 289.4726  on 15  degrees of freedom
19 Residual deviance:  6.0427  on 13  degrees of freedom
20 AIC: 56.087
21
22 Number of Fisher Scoring iterations: 5
23
24
25
26
27
28
29
```

```

30 > summary(mod2)
31
32 Call:glm(formula = cbind(z, m - z) ~ Dose * Sex, family = binomial)
33
34 Coefficients:
35             Estimate Std. Error z value Pr(>|z|)
36 (Intercept) -3.068135   0.405221  -7.572 3.69e-14 ***
37 Dose         0.026853   0.003288   8.166 3.19e-16 ***
38 SexMale     -0.072372   0.537098  -0.135  0.893
39 Dose:SexMale -0.006721   0.004134  -1.626  0.104
40 ---
41 Signif. codes:  0   ***  0.001  **  0.01  *  0.05  .  0.1    1
42
43 (Dispersion parameter for binomial family taken to be 1)
44
45     Null deviance: 289.4726  on 15  degrees of freedom
46 Residual deviance:  3.3273  on 12  degrees of freedom
47 AIC: 55.372
48
49 Number of Fisher Scoring iterations: 5

```

Recall that the deviance test for model comparison uses the $(1 - \alpha)$ quantile of the χ_r^2 distribution, for $\alpha = 0.05$ or $\alpha = 0.01$, where

$$r = p_B - p_A$$

and rejects the relevant null hypothesis if the test statistic exceeds the quantile value. The following table contains the quantiles for $\alpha = 0.05$ for a range of values of r :

r	Quantile
1	3.8415
2	5.9915
3	7.8147
4	9.4877
5	11.0705
6	12.5916
7	14.0671
8	15.5073
9	16.9190
10	18.3070
11	19.6751
12	21.0261
13	22.3620
14	23.6848
15	24.9958
16	26.2962