

```

> M1 <- glm(cbind(ndeath,ntotal-ndeath) ~ 1 + dose, data=beetledata, family=binomial(link=logit))
> M2 <- glm(cbind(ndeath,ntotal-ndeath) ~ 1 + dose, data=beetledata, family=binomial(link=probit))
> M3 <- glm(cbind(ndeath,ntotal-ndeath) ~ 1 + dose, data=beetledata, family=binomial(link=cloglog))
> coef(summary(M1))
      Estimate Std. Error   z value    Pr(>|z|)
(Intercept) -60.71745    5.180701 -11.71993 1.007549e-31
dose         34.27033    2.912134  11.76811 5.698445e-32
> coef(summary(M2))
      Estimate Std. Error   z value    Pr(>|z|)
(Intercept) -34.93527    2.647879 -13.19368 9.541285e-40
dose         19.72794    1.487213  13.26504 3.692396e-40
> coef(summary(M3))
      Estimate Std. Error   z value    Pr(>|z|)
(Intercept) -39.57231    3.240290 -12.21258 2.662986e-34
dose         22.04117    1.799365  12.24942 1.692092e-34

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> pred.prob.M1 <- predict(M1, type = "response")
> pred.prob.M2 <- predict(M2, type = "response")
> pred.prob.M3 <- predict(M3, type = "response")
> pred <- cbind(pred.prob.M1*ntotal,pred.prob.M2*ntotal,pred.prob.M3*ntotal)
> colnames(pred) <- c("ndeath", "logistic", "probit", "extreme")
> pred
  ndeath logistic   probit  extreme
1     6  3.457461  3.357774  5.58945
2    13  9.841672 10.721610 11.28068
3    18 22.451378 23.481932 20.95422
4    28 33.897635 33.815505 30.36944
5    52 50.095822 49.615626 47.77642
6    53 53.290913 53.318874 54.14273
7    61 59.222159 59.664650 61.11331
8    60 58.742961 59.227967 59.94723

```

Table 7.4 Comparison of observed numbers killed with fitted *v* various dose-response models for the beetle mortality data. *De also given.*

Observed value of Y	Logistic model	Probit model	Extreme value model
6	3.46	3.36	5.59
13	9.84	10.72	11.28
18	22.45	23.48	20.95
28	33.90	33.82	30.37
52	50.10	49.62	47.78
53	53.29	53.32	54.14
61	59.22	59.66	61.11
60	58.74	59.23	59.95

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R-session from:
Logistic Regression
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Biometry Research Unit
Danish Institute of Agricultural Sciences

```
> library(dataRep)
> data(budworm)
> budworm
  sex dose ndead ntotal
1  male  1     1     20
2  male  2     4     20
3  male  4     9     20
4  male  8    13     20
5  male 16    18     20
6  male 32    20     20
7 female  1     0     20
8 female  2     2     20
9 female  4     6     20
10 female 8    10     20
11 female 16    12     20
12 female 32    16     20
>
> budworm$y <- cbind(budworm$ndead, budworm$ntotal - budworm$ndead)
> budworm$logdose <- log(budworm$dose)
> M0 <- glm(y ~ 1 + sex + logdose, data = budworm, family = binomial(link = logit))
> tab1 <- coef(summary(M0))
> tab2 <- confint(M0)
> tab.est <- cbind(tab1[, "Estimate"], tab2)
> colnames(tab.est) <- c("Estimate", colnames(tab2))
> tab.est
```

	Estimate	2.5 %	97.5 %
(Intercept)	-3.473155	-4.4582430	-2.613736
sexmale	1.100743	0.4192377	1.820464
logdose	1.535336	1.1872042	1.931893

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```
> pred.prob <- predict(M0, type = "response")
> pred.prob
  1         2         3         4         5         6         7         8
0.08530076 0.21278854 0.43930479 0.69428515 0.86812073 0.95020002 0.03008577 0.08249341
  9         10        11        12
0.20673372 0.43032791 0.68647712 0.86388206
> pred.logits <- predict(M0, type = "link")
> pred.logits
  1         2         3         4         5         6         7         8
-2.3724119 -1.3081980 -0.2439840  0.8202300  1.8844439  2.9486579 -3.4731553 -2.4089413
  9         10        11        12
-1.3447274 -0.2805134  0.7837006  1.8479145
> plogis(pred.logits)
  1         2         3         4         5         6         7         8
0.08530076 0.21278854 0.43930479 0.69428515 0.86812073 0.95020002 0.03008577 0.08249341
  9         10        11        12
0.20673372 0.43032791 0.68647712 0.86388206
> new <- data.frame(sex = "female", logdose = log(27))
> pred.prob <- predict(M0, newdata = new, type = "response")
> pred.prob
[1] 0.8302024
> pred.eta <- predict(M0, newdata = new, type = "link", se = TRUE)
> CI <- pred.eta$fit + 1.96 * c(-1, 1) * pred.eta$se.fit
> CI
[1] 0.9410702 2.2330546
> plogis(CI)
[1] 0.7193158 0.9031788
```

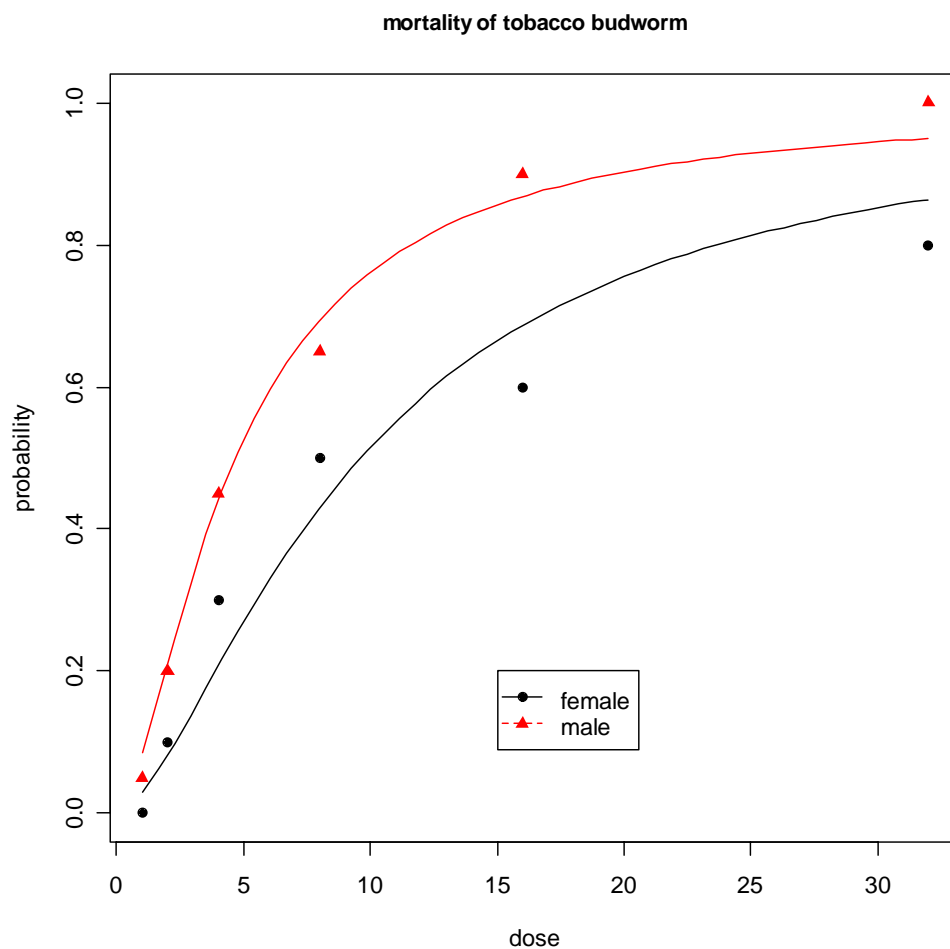
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> budworm$prop <- budworm$ndead/budworm$ntotal
> logdose = log(seq(1, 32, l = 50))
> new <- expand.grid(sex = c("male", "female"), logdose = logdose)
> pred.prob <- predict(M0, newdata = new, type = "response")
> plot(prop ~ dose, data = budworm, xlab = "dose", ylab = "probability",
+ type = "n", col = 1, pch = 16)
> points(prop ~ dose, data = budworm, subset = c(sex == "female"),
+ col = 1, pch = 16)
> points(prop ~ dose, data = budworm, subset = c(sex == "male"),
+ col = 2, pch = 17)
> dat <- data.frame(pred.prob = pred.prob, new, dose = exp(new$logdose))
> lines(pred.prob ~ dose, data = dat, subset = c(sex == "female"),
+ col = 1, pch = 16)
> lines(pred.prob ~ dose, data = dat, subset = c(sex == "male"),
+ col = 2, pch = 17)
> legend(15, 0.2, legend = c("female", "male"), col = c(1,
+ 2), pch = c(16, 17), lty = c(1, 2))
> title("mortality of tobacco budworm", cex.main = 0.9)

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> M0 <- glm(cbind(ndeath, ntotal - ndeath) ~ 1 + sex + logdose,
+ data = budworm, family = binomial)
> M1 <- glm(cbind(ndeath, ntotal - ndeath) ~ 1 + sex + logdose +
+ sex:logdose, data = budworm, family = binomial)
> anova(M0, M1, test = "Chisq")
Analysis of Deviance Table
Model 1: cbind(ndeath, ntotal - ndeath) ~ 1 + sex + logdose
Model 2: cbind(ndeath, ntotal - ndeath) ~ 1 + sex + logdose + sex:logdose
  Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1          9      6.7571
2          8      4.9937  1   1.7633   0.1842
> drop1(M1, test = "Chisq")
Single term deletions
Model:
cbind(ndeath, ntotal - ndeath) ~ 1 + sex + logdose + sex:logdose
      Df Deviance   AIC   LRT Pr(Chi)
<none>      4.994 43.104
sex:logdose  1   6.757 42.867  1.763  0.1842
> M0$deviance
[1] 6.757064
> res <- residuals(M0, type = "pearson")
> X2 <- sum(res^2)
> res
      1          2          3          4          5          6          7
-0.56517566 -0.13973857  0.09637356 -0.42987872  0.42135194  1.02381637 -0.78764207
      8          9          10         11         12
  0.28457864  1.02996982  0.62930558 -0.83362087 -0.83312277
> X2
[1] 5.306017
> M0$df.residual
[1] 9
> 1 - pchisq(X2, M0$df.residual)
[1] 0.8068578

```

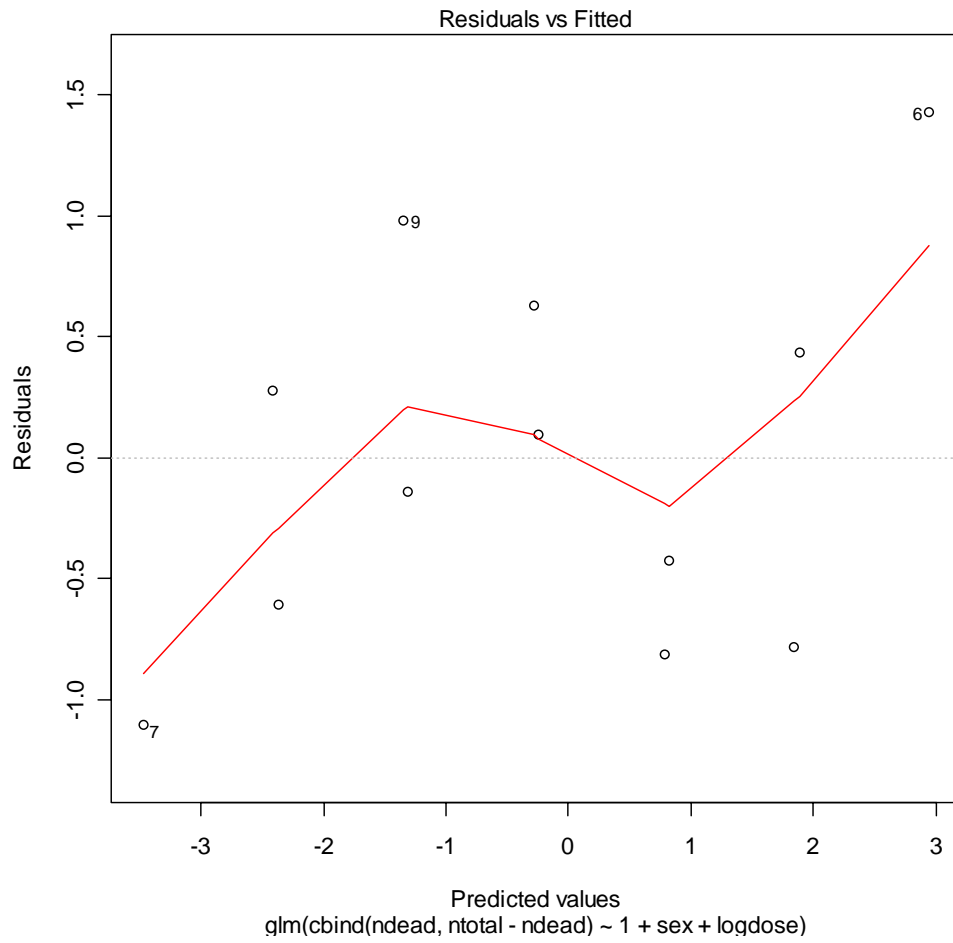
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```

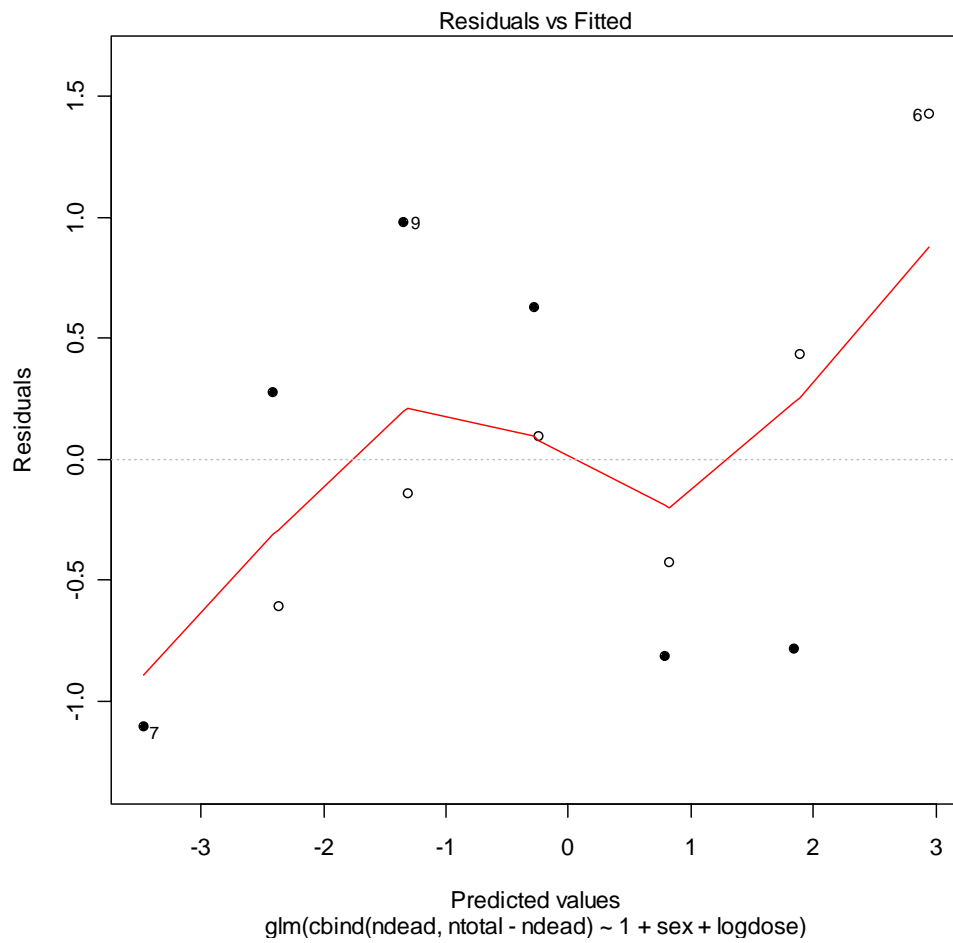
> plot(M0, which = 1)
> plot(M0, which = 1, pch = c(16, 1)[budworm$sex])

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