

ORIGIN := 0

Logistic Regression for Binary Response Variable

Logistic Regression applies in situations where the response (i.e., dependent) variable is qualitative with only two possible outcomes (0 vs 1, "yes" vs "no", "absent" vs "present" etc.). Because of this, the response and error terms follow the Binomial Distribution. If, as is often the case in regression, there is only one response for each set of independent variables (i.e., no replication) then the Binomial distribution is $\sim B(1,p)$ with number of trials = 1 and p = probability of success. This special case is known as the Bernoulli distribution. Since the response variable is binary, modeling response involves modeling the probability π that the response variable Y takes one of the two values (e.g., Y=1 versus 0). The alternative probability P(Y=0) is therefore $(1-\pi)$. Kutner et al. (KNNL) in *Applied Linear Statistical Models 5th ed.* p. 557 list three "special problems" arising from this: 1) non-Normal Distribution of error terms, 2) non-constant variance associated with values of the independent variables X, and 3) the requirement that π must be bound between (0,1). All three rule out use of standard linear models involving the Normal (Gaussian) distribution.

The requirement that π remain bound between (0,1) suggest use of a sigmoidal function as the natural description of probability. Currently three functions are in common use: Logistic, Probit & Clog-log. The first two are symmetric, intended for modeling more-or-less equal numbers of each response in the dataset, whereas the last is asymmetric useful with unequal numbers. Although all are easily available in R as options, by far the most commonly used is the Logistic function shown in more detail here. Logistic Regression is one example of the class of Generalized Linear Models (GLM) in which "best fit" linear coefficients for the independent variables X (also termed the "systematic component") are estimated for transformed values of the response variable π , with the function describing the transformation termed the "link function". When the relationship between π and X is expressed directly in Logistic Regression, the equation describes a non-linear function with sigmoidal shape. Zuur et al. 2009 (Za) in *Mixed Effects Models and Extensions in Ecology with R* usefully describe all GLM's as having three formal components: 1 - a statement of the distribution of Y, 2 - a statement of the expected value of Y, $\exp(Y)$ and variance of Y, $\text{var}(Y)$, and 3 - a description of the link function. I'll follow their format here.

Assumptions:

Regression depends on specifying Response & Independent variables in advance:

Y = vector of binary response variable (0 or 1), each row of Y indicated by index i .

X = matrix independent variables (columns) with observations of X_i (rows) matched to Y_i (rows of Y).

β = vector of linear coefficients and $X\beta$ is the linear predictor (systematic component) of the model.

Cases Y_i are independent.

Model:

$$Y_i \sim B(1, \pi_i) \quad < Y_i's are Bernoulli distributed with probability \pi_i for each case.$$

$$E(Y_i) = \pi_i, \text{ and } \text{var}(Y_i) = \pi_i(1-\pi_i) \quad < \text{mean and variance defined.}$$

$$\text{logit}(\pi_i) = X\beta \text{ where } \text{logit}(\pi_i) = \pi_i/(1-\pi_i) \quad < \text{for logit link to } \pi_i \text{ for Logistic Regression}$$

$$\text{alternatively: } \pi_i = e^{(X\beta)} / (1+e^{(X\beta)})$$

Estimation of Regression Coefficients:

Estimation is based on determining the maximum likelihood function given the data. Since a closed-form solution doesn't exist, this requires iterative computation, here using `glm()` in the `{nlme}` package in R.

#GLM 020 LOGISTIC REGRESSION

```
library(nlme)
setwd("c:/DATA/Models")
D=read.table("KNNL1401.txt",header=T)
D
FM1=glm(Y~X,data=D,family=binomial)
summary(FM1)
```

> summary(FM1)

Call:

glm(formula = Y ~ X, family = binomial, data = D)

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.8992	-0.7509	-0.4140	0.7992	1.9624

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.05970	1.25935	-2.430	0.0151 *
X	0.16149	0.06498	2.485	0.0129 *

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 34.296 on 24 degrees of freedom

Residual deviance: 25.425 on 23 degrees of freedom

AIC: 29.425

Number of Fisher Scoring iterations: 4

Fitted Values:

Results=cbind(X=D\$X,Y=D\$Y,Fitted=fitted(FM1))

Results

Example for first point $X_1 = 14$: $X_1 := 14 \quad Y_1 := 0$ < observed values of X & Y for the first case $\beta_0 := -3.05970 \quad \beta_1 := 0.16149$ < regression coefficients from above

$$\pi_1 := \frac{e^{(\beta_0 + \beta_1 X_1)}}{1 + e^{(\beta_0 + \beta_1 X_1)}} \quad \pi_1 = 0.3103 \quad < \text{fitted value for the first case } \pi_1$$

Odds & Odds Ratio:

$$\text{Odds}_1 := \frac{\pi_1}{1 - \pi_1} \quad \text{Odds}_1 = 0.45 \quad = \text{Odds (ratio of probability } \pi_1 \text{ and its complement)}$$

 $X_2 := X_1 + 1$ < unit increase in independent variable X

$$\pi_2 := \frac{e^{(\beta_0 + \beta_1 X_2)}}{1 + e^{(\beta_0 + \beta_1 X_2)}} \quad \pi_2 = 0.346$$

data from KNNL Table 14.1

Y is the response variable (0 or 1)
X is the independent variable

> D

	X	Y	fittedY
1	14	0	0.310262
2	29	0	0.835263
3	6	0	0.109996
4	25	1	0.726602
5	18	1	0.461837
6	4	0	0.082130
7	18	0	0.461837
8	12	0	0.245666
9	22	1	0.620812
10	6	0	0.109996
11	30	1	0.856299
12	11	0	0.216980
13	30	1	0.856299
14	5	0	0.095154
15	20	1	0.542404
16	13	0	0.276802
17	9	0	0.167100
18	32	1	0.891664
19	24	0	0.693379
20	13	1	0.276802
21	19	0	0.502134
22	4	0	0.082130
23	28	1	0.811825
24	22	1	0.620812
25	8	1	0.145815

> Results

	X	Y	Fitted
1	14	0	0.31026237
2	29	0	0.83526292
3	6	0	0.10999616
4	25	1	0.72660237
5	18	1	0.46183704
6	4	0	0.08213002
7	18	0	0.46183704
8	12	0	0.24566554
9	22	1	0.62081158
10	6	0	0.10999616
11	30	1	0.85629862
12	11	0	0.21698039
13	30	1	0.85629862
14	5	0	0.09515416
15	20	1	0.54240353
16	13	0	0.27680234
17	9	0	0.16709980
18	32	1	0.89166416
19	24	0	0.69337941
20	13	1	0.27680234
21	19	0	0.50213414
22	4	0	0.08213002
23	28	1	0.81182461
24	22	1	0.62081158
25	8	1	0.14581508

$$\text{Odds}_2 := \frac{\pi_2}{1 - \pi_2} \quad \text{Odds}_2 = 0.529$$

$$\frac{\text{Odds}_2}{\text{Odds}_1} = 1.175 \quad e^{\beta_1} = 1.175 \quad = \text{Odds Ratio}$$

^ A unit increase in the independent variable X results in a 17.5% increase in the odds of Y (completing the task in this example).

c := 15 < an arbitrary number of units in X (for estimating changes over a larger interval of X)

$$e^{c\beta_1} = 11.272 \quad < \text{Odds increase 11-fold over 15 months}$$

```
Residuals=cbind(X=D$X,Y=D$Y,
Pearson=resid(FM1,type="pearson"),
Deviance=resid(FM1,type="deviance"))
Residuals
```

Pearson Residuals:

$$r_p := \frac{Y_1 - \pi_1}{\sqrt{\pi_1 \cdot (1 - \pi_1)}} \quad r_p = -0.6707 \quad < \text{pearson residual for the first case}$$

Deviance Residuals:

$$r_{dev1} := \text{sign}(Y_1 - \pi_1) \cdot \sqrt{-2 \cdot [Y_1 \cdot \ln(\pi_1) + (1 - Y_1) \cdot \ln(1 - \pi_1)]}$$

$$\text{sign}(Y_1 - \pi_1) = -1 \quad < \text{function for sign}$$

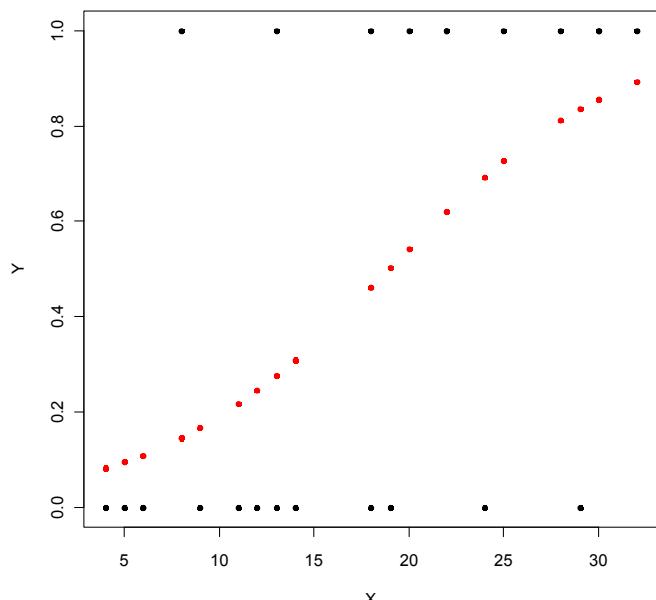
$$r_{dev1} = -0.8619 \quad < \text{deviance residual for the first case}$$

#PLOTTING CURVE:

```
M=data.frame(X=D$X) #USING ORIGINAL INDEPENDENT VALUES
M=na.omit(M)
Pred=predict(FM1,newdata=M,type="response")
plot(x=D$X,y=D$Y,xlab="X",ylab="Y",pch=20)
points(M$X,Pred,pch=20,col="red")
```

> Residuals

	X	Y	Pearson	Deviance
1	14	0	-0.6706912	-0.8619095
2	29	0	-2.2517280	-1.8991601
3	6	0	-0.3515546	-0.4827618
4	25	1	0.6134073	0.7992195
5	18	1	1.0794748	1.2430150
6	4	0	-0.2991303	-0.4140037
7	18	0	-0.9263764	-1.1131881
8	12	0	-0.5706767	-0.7508920
9	22	1	0.7815336	0.9764504
10	6	0	-0.3515546	-0.4827618
11	30	1	0.4096546	0.5570209
12	11	0	-0.5264098	-0.6994248
13	30	1	0.4096546	0.5570209
14	5	0	-0.3242848	-0.4471928
15	20	1	0.9185019	1.1061148
16	13	0	-0.6186662	-0.8050748
17	9	0	-0.4479107	-0.6047172
18	32	1	0.3485663	0.4788856
19	24	0	-1.5037818	-1.5376242
20	13	1	1.6163806	1.6027798
21	19	0	-1.0042774	-1.1810373
22	4	0	-0.2991303	-0.4140037
23	28	1	0.4814490	0.6457104
24	22	1	0.7815336	0.9764504
25	8	1	2.4203309	1.9623537

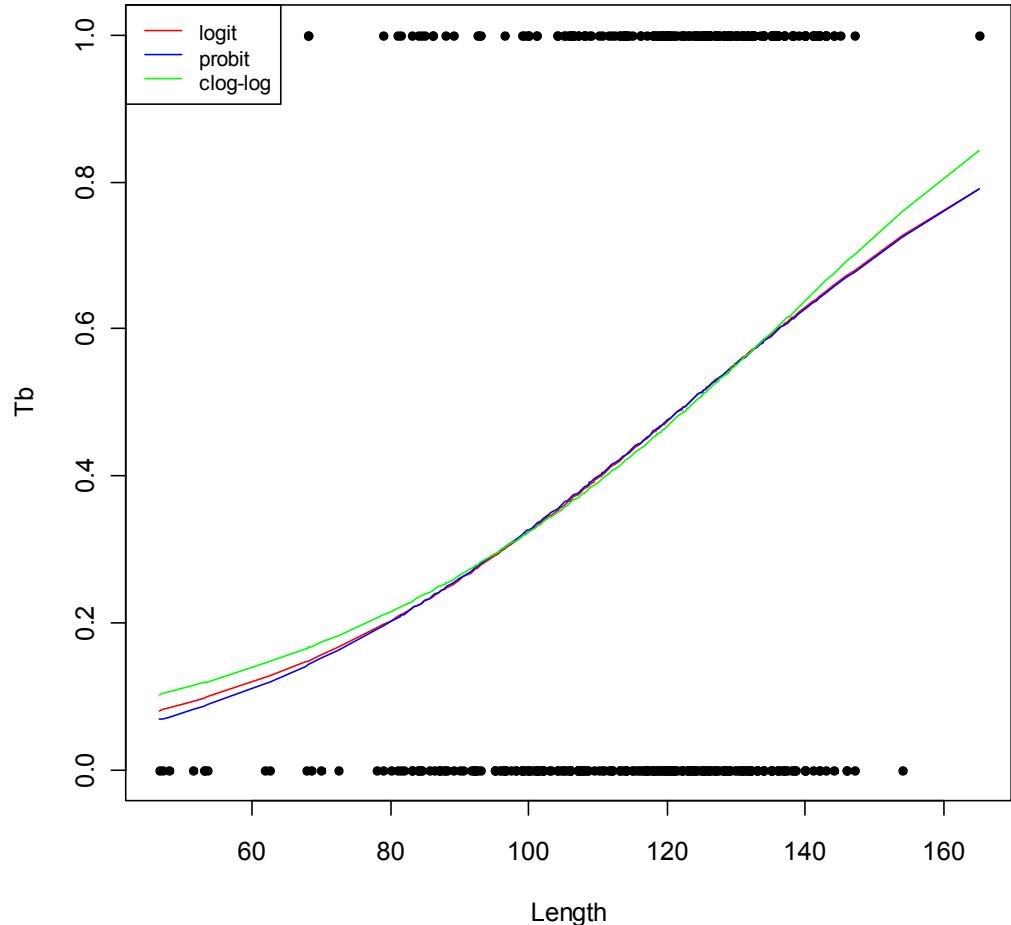


Comparison of Logistic, Probit & Clog-log fits:

```
B=read.table("Boar.txt",header=T)
B
FM2=glm(Tb~LengthCT,family=binomial(link="log it"),data=B) #(link="logit") DEFAULT
FM3=glm(Tb~LengthCT,family=binomial(link="probit"),data=B)
FM4=glm(Tb~LengthCT,family=binomial(link="clog log"),data=B)

#PLOTTING CURVES:
M=data.frame(LengthCT=B$LengthCT) #USING ORIGINAL INDEPENDENT VALUES
M=na.omit(M)
#M=data.frame(LengthCT=seq(from=46.5,to=165,by=1)) #USING NEW SEQUENCE
Pred2=predict(FM2,newdata=M,type="response")
Pred3=predict(FM3,newdata=M,type="response")
Pred4=predict(FM4,newdata=M,type="response")
plot(x=B$LengthCT,y=B$Tb,xlab="Length",ylab="Tb",pch=20)
lines(M$LengthCT,Pred2,col="red")
lines(M$LengthCT,Pred3,col="blue")
lines(M$LengthCT,Pred4,col="green")
legend("topleft",legend=c("logit","probit","clog-log"),
lty=c(1,1,1),col=c("red","blue","green"),cex=0.8)
```

data from Za boar.txt data:
Tb - Response Variable
LengthCT - Independent Variable



Multiple Logistic Regression:

```
C=read.table("ParasiteCod.txt",header=T)
C=na.omit(C)
C$fArea=factor(C$Area)
C$fYear=factor(C$Year)
FM5=glm(Prevalence~fArea*fYear+Length,family=binomial,data=C)
summary(FM5)
```

Wald Test of single β :

Hypotheses:

$$H_0: \beta = 0$$

$$H_1: \beta \neq 0$$

Test Statistic:

$$z = \text{Estimate}/\text{std.error}$$

Example calculations:

$$\beta_1 := -1.185849 \quad s_{\beta_1} := 0.276897$$

$$z_1 := \frac{\beta_1}{s_{\beta_1}} \quad z_1 = -4.283$$

$$\beta_6 := 0.008516 \quad s_{\beta_6} := 0.004585$$

$$z_6 := \frac{\beta_6}{s_{\beta_6}} \quad z_6 = 1.857$$

Sampling Distribution:

If Assumptions hold and H_0 is true,
then $z \sim N(0,1)$

> summary(FM5)

```
Call:
glm(formula = Prevalence ~ fArea * fYear + Length, family =
binomial, data = C)

Deviance Residuals:
Min      1Q   Median      3Q     Max 
-2.0922 -0.9089 -0.4545  0.9678  2.2394 

Coefficients:
            Estimate Std. Error z value Pr(>|z|)    
(Intercept) 0.003226  0.291973  0.011  0.99118    
fArea2      -1.185849  0.276897 -4.283 1.85e-05 ***
fArea3      -1.136105  0.231248 -4.913 8.97e-07 ***
fArea4       0.728736  0.261815  2.783  0.00538 **  
fYear2000    0.383756  0.343877  1.116  0.26444    
fYear2001    -2.655704  0.433542 -6.126 9.03e-10 ***
Length       0.008516  0.004585  1.858  0.06324 .  
fArea2:fYear2000 -0.209035  0.503494 -0.415  0.67802    
fArea3:fYear2000  0.561158  0.443733  1.265  0.20600    
fArea4:fYear2000  0.451582  0.588318  0.768  0.44274    
fArea2:fYear2001  2.595866  0.528472  4.912 9.01e-07 ***
fArea3:fYear2001  2.403050  0.493512  4.869 1.12e-06 *** 
fArea4:fYear2001  2.115534  0.513489  4.120 3.79e-05 *** 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1727.8 on 1247 degrees of freedom
Residual deviance: 1495.2 on 1235 degrees of freedom
(6 observations deleted due to missingness)
AIC: 1521.2
```

Probability:

$$P_1 := \min\left[2 \cdot \text{pnorm}(z_1, 0, 1), 2 \cdot (1 - \text{pnorm}(z_1, 0, 1))\right] \quad P_1 = 1.8469 \times 10^{-5}$$

$$P_6 := \min\left[2 \cdot \text{pnorm}(z_6, 0, 1), 2 \cdot (1 - \text{pnorm}(z_6, 0, 1))\right] \quad P_6 = 0.0633$$

Decision Rule:

IF $P < \alpha$ THEN REJECT H_0 , OTHERWISE ACCEPT H_0

The Wald test is a marginal test of single regression coefficients having a function similar to t-test in standard Linear Regression.

Note: Regression coefficients and standard errors are obtained from the maximum likelihood fit as first and second partial derivatives of the likelihood function. Summary information is obtained from the summary() wrapper of an object made by glm(). No attempt has been made to replicate the calculations here.

Za ParasiteCod data:

Prevalence of parasite = response.

Multiple independent variables X evaluated for a "best fit" model as in standard Linear Regression.

Confidence Interval for β :

$$\alpha := 0.05$$

$$C := \left| qnorm\left(1 - \frac{\alpha}{2}, 0, 1\right) \right| \quad C = 1.96$$

	estimate	confidence interval
$CI_1 := (\beta_1 - C \cdot s_{\beta_1}, \beta_1 + C \cdot s_{\beta_1})$	$\beta_1 = -1.186$	$CI_1 = (-1.729 \quad -0.643)$
$CI_6 := (\beta_6 - C \cdot s_{\beta_6}, \beta_6 + C \cdot s_{\beta_6})$	$\beta_6 = 0.00852$	$CI_6 = (-0.00047 \quad 0.0175)$

Likelihood Ratio Test:

The Likelihood Ratio Test in GLM models serves a function similar to that of the General F Ratio test of Full Model (FM) versus Reduced Model (RM). Since model likelihoods are not reported by `summary.glm` or `anova.glm`, the Likelihood Ratio test of is conducted by consulting the Analysis of Deviance Table in `anova(RM,FM)` (for serial testing) or `drop1` (for marginal testing).

C

```
anova(FM5,test="Chisq")
drop1(FM5,test="Chisq")
```

> C

	Sample	Intensity	Prevalence	Year	Depth	Weight	Length	Sex	Stage	Age	Area	fArea	fYear
1	1	0	0	1999	220	148	26	0	0	0	2	2	1999
2	2	0	0	1999	220	144	26	0	0	0	2	2	1999
3	3	0	0	1999	220	146	27	0	0	0	2	2	1999
4	4	0	0	1999	220	138	26	0	0	0	2	2	1999
5	5	0	0	1999	220	40	17	0	0	0	2	2	1999
...													
1248	1248	84	1	2001	260	910	48	2	1	4	2	2	2001
1249	1249	89	1	2001	260	1414	56	1	1	6	2	2	2001
1250	1250	90	1	2001	228	224	31	1	1	2	4	4	2001
1251	1251	104	1	2001	140	690	43	2	1	3	4	4	2001
1252	1252	125	1	2001	140	754	44	2	1	3	4	4	2001
1253	1253	128	1	2001	140	1270	55	2	4	7	4	4	2001
1254	1254	257	1	2001	228	370	35	2	1	3	4	4	2001

Hypotheses:

H_0 : a specified subset of β 's = 0

H_1 : same subset of β 's $\neq 0$

Test Statistic:

$$G^2 = -2\ln[L(R)/L(F)] = -2\ln(L(R) - 2\ln(L(F)) = dev_F - dev_R$$

< where dev_F & dev_R are residual deviances calculated from the Maximum Likelihood fits of FM & RM

Sampling Distribution:

If Assumptions hold and H_0 is true,

then $G^2 \sim \chi^2(df_F - df_R)$ < where df_F & df_R are degrees of freedom of FM & RM

Probability:

$$P = 1 - pchisq(\Delta dev, \Delta df) < \text{where } \Delta dev \& \Delta df \text{ are differences in values between FM \& RM}$$

Decision Rule:

IF $P < \alpha$ THEN REJECT H_0 , OTHERWISE ACCEPT H_0

Example Calculations:

For Interaction term (blue in table):

$$\begin{aligned} \text{dev}_F &:= 1422.7 & \text{dev}_R &:= 1474.7 \\ \Delta\text{dev} &:= \text{dev}_R - \text{dev}_F & \Delta\text{dev} &= 52 \\ \text{df}_F &:= 1178 & \text{df}_R &:= 1184 \\ \Delta\text{df} &:= \text{df}_R - \text{df}_F & \Delta\text{df} &= 6 \\ P &:= 1 - \text{pchisq}(\Delta\text{dev}, \Delta\text{df}) \\ && P &= 1.865 \times 10^{-9} \end{aligned}$$

For factor Length (green):

$$\begin{aligned} \text{dev}_F &:= 1422.7 & \text{dev}_R &:= 1424.9 \\ \Delta\text{dev} &:= \text{dev}_R - \text{dev}_F & \Delta\text{dev} &= 2.2 \\ \text{df}_F &:= 1178 & \text{df}_R &:= 1179 \\ \Delta\text{df} &:= \text{df}_R - \text{df}_F & \Delta\text{df} &= 1 \\ P &:= 1 - \text{pchisq}(\Delta\text{dev}, \Delta\text{df}) \\ && P &= 0.138 \end{aligned}$$

Note: slight differences here are due to rounding differences in hand calculation.

```
RM1=glm(Prevalence~fArea+fYear+Length,family=binomial,data=C)
anova(RM1,FM5,test="Chisq")
```

```
RM2=glm(Prevalence~fArea*fYear,family=binomial,data=C)
anova(RM2,FM5,test="Chisq")
```

Explicit Test for Interaction:

```
> anova(RM1,FM5,test="Chisq")
Analysis of Deviance Table

Model 1: Prevalence ~ fArea + fYear + Length
Model 2: Prevalence ~ fArea * fYear + Length
Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1      1184    1474.7
2      1178    1422.7  6   52.031  1.838e-09 ***
---
Signif. codes: 0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Explicit test for factor Length:

```
> anova(RM2,FM5,test="Chisq")
Analysis of Deviance Table

Model 1: Prevalence ~ fArea * fYear
Model 2: Prevalence ~ fArea * fYear + Length
Resid. Df Resid. Dev Df Deviance P(>|Chi|)
1      1179    1424.9
2      1178    1422.7  1   2.2313   0.1352
---
```

Serial report of Likelihood Ratio Tests:

```
> anova(FM5,test="Chisq")
Analysis of Deviance Table

Model: binomial, link: logit

Response: Prevalence

Terms added sequentially (first to last)

Df Deviance Resid. Df Resid. Dev P(>|Chi|)
NULL                      1190    1640.7
fArea                     3   113.171   1187    1527.5 < 2.2e-16 ***
fYear                     2    49.406   1185    1478.1 1.869e-11 ***
Length                    1    3.446    1184    1474.7   0.0634 .
fArea:fYear               6   52.031   1178    1422.7  1.838e-09 ***
---
Signif. codes: 0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Marginal report of Likelihood Ratio Tests:

```
> drop1(FM5,test="Chisq")
Single term deletions

Model:
Prevalence ~ fArea * fYear + Length
Df Deviance AIC      LRT Pr(Chi)
<none>        1422.7 1448.7
Length         1   1424.9 1448.9  2.231   0.1352
fArea:fYear    6   1474.7 1488.7 52.031  1.838e-09 ***
---
Signif. codes: 0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

summary(FM5)

Note: P-values reported by Wald Test and Likelihood Ratio test for a single β will not necessarily be equal.

As in linear regression, summary() are marginal reports.

> summary(FM5)

```

Call:
glm(formula = Prevalence ~ fArea * fYear + Length, family = binomial,
     data = C)

Deviance Residuals:
    Min      1Q   Median      3Q      Max 
-2.0858 -0.8626 -0.4865  0.9625  2.2218 

Coefficients:
                                         Estimate Std. Error z value Pr(>|z|)    
(Intercept)                      0.085255  0.295024  0.289   0.7726    
fArea2                           -1.321373  0.285258 -4.632 3.62e-06 ***  
fArea3                           -1.449183  0.243884 -5.942 2.81e-09 ***  
fArea4                            0.300728  0.271107  1.109   0.2673    
fYear2000                        0.395069  0.343814  1.149   0.2505    
fYear2001                        -2.652010  0.433369 -6.120 9.39e-10 ***  
Length                            0.006933  0.004653  1.490   0.1362    
fArea2:fYear2000                 -0.080344  0.507968 -0.158   0.8743    
fArea3:fYear2000                  0.870585  0.450273  1.933   0.0532 .  
fArea4:fYear2000                  0.864622  0.592386  1.460   0.1444    
fArea2:fYear2001                  2.737488  0.532881  5.137 2.79e-07 ***  
fArea3:fYear2001                  2.718986  0.499459  5.444 5.21e-08 ***  
fArea4:fYear2001                  2.541437  0.518224  4.904 9.38e-07 ***  
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 1640.7  on 1190  degrees of freedom
Residual deviance: 1422.7  on 1178  degrees of freedom
AIC: 1448.7

Number of Fisher Scoring iterations: 4

```