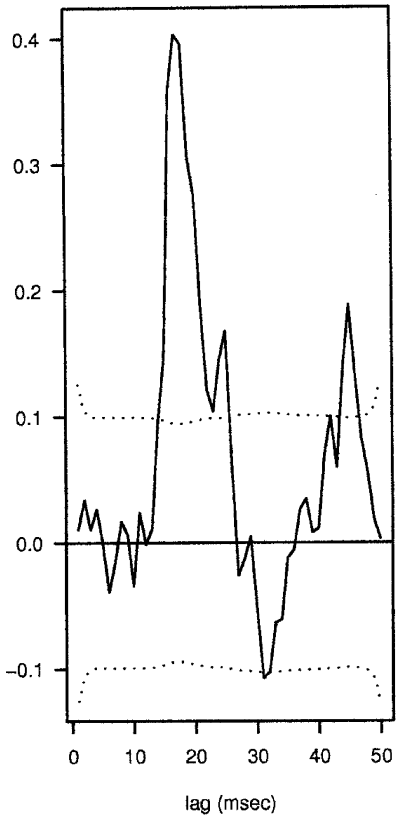
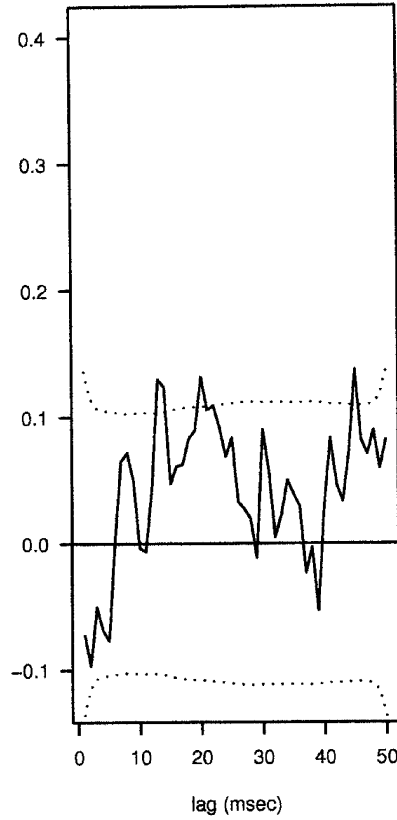


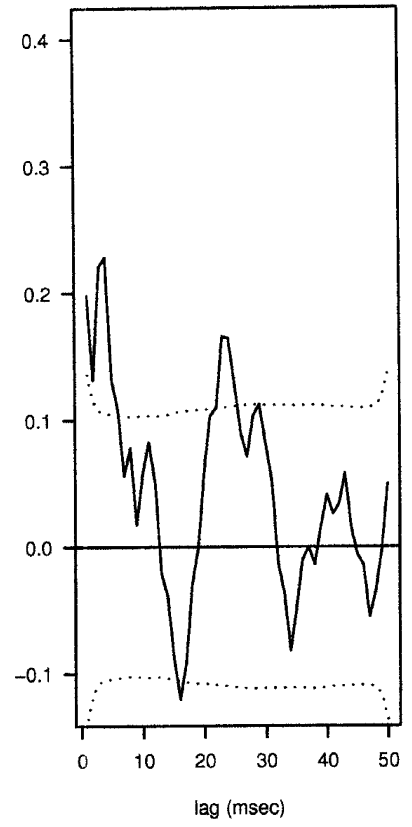
II from Ia, g1, g2 - g1 function



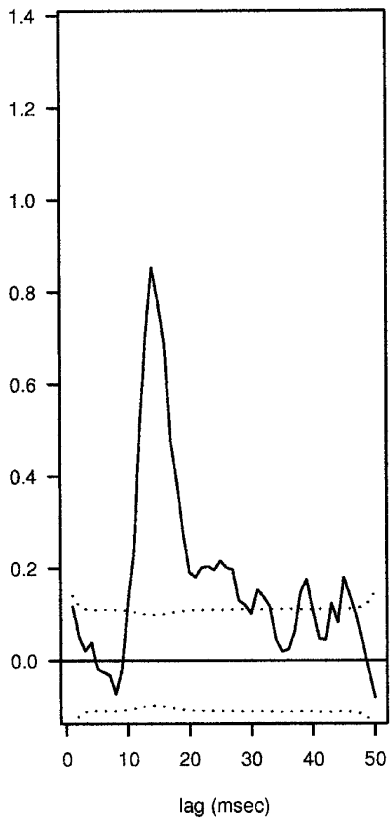
II from Ia, g1, g2 - g2 function



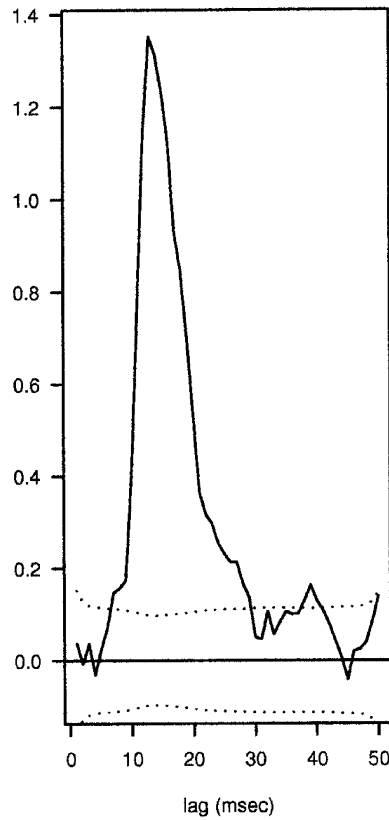
II from Ia, g1, g2 - Ia function



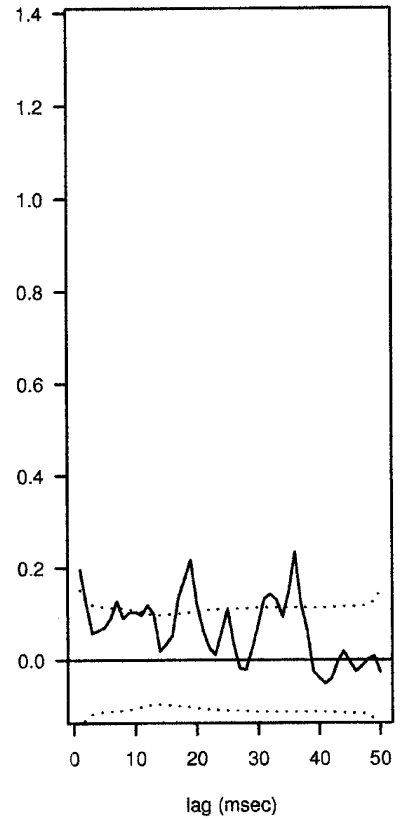
Ia from II, g1, g2 - g1 function



Ia from II, g1, g2 - g2 function



Ia from II, g1, g2 - II function



16 April 08

Scaled deviance

$$D = 2 \sum_{j=1}^n \{ \log f(y_j; \hat{\pi}_j) - \log f(y_j; \tilde{\pi}_j) \}$$

Model fits well $\hat{\pi}_j$ and $\tilde{\pi}_j$ are close.

Normal deviance

$$\log f(y_j; \pi_j, \varphi) = -\frac{1}{2} \log(2\pi\varphi) - (y_j - \pi_j)^2 / \varphi$$

$$\tilde{\pi}_j = y_j$$

$$\log f(y_j; \tilde{\pi}_j, \varphi) = -\frac{1}{2} \log 2\pi\varphi$$

$$D = \frac{1}{\varphi} \sum_{j=1}^n (y_j - \hat{\pi}_j)^2 = \frac{1}{\varphi} \text{RSS}$$

$$\text{If } \pi_j = x_j^T \beta, \text{ RSS} \sim \varphi \chi_{n-p}^2$$

$$\frac{\text{RSS}}{\varphi} \sim \chi_{n-p}^2$$

Check on fit

$$\beta \quad p \times 1$$

$$H_0: \beta_{g+1}, \dots, \beta_p = 0$$

Model B g β 's free to vary

Model A p β 's free to vary

B is nested within A

Likelihood ratio statistic

$$2 \sum_{j=1}^n \{ \log f(y_j; \hat{\eta}_j^A) - \log f(y_j; \hat{\eta}_j^B) \}$$

$$= D_B - D_A$$

$$\text{Under } H_0 \quad \chi^2_{p-g}$$

Normal case

$$D_B - D_A = \varphi^{-1} \sum_{j=1}^n \{ (y_j - \hat{\eta}_j^B)^2 - (y_j - \hat{\eta}_j^A)^2 \}$$

$$\sim \chi^2_{p-g}$$

Logistic regression, neuro example

$$P_n(Y=1) = \pi = \frac{\exp\{x^T \beta\}}{1 + \exp\{x^T \beta\}}$$

$$P_n(Y=0) = 1 - \pi = \frac{1}{1 + \exp\{x^T \beta\}}$$

odds of success

$$\frac{P_n(Y=1)}{P_n(Y=0)} = \frac{\pi}{1-\pi} = \exp\{x^T \beta\}$$

log odds = $x^T \beta$

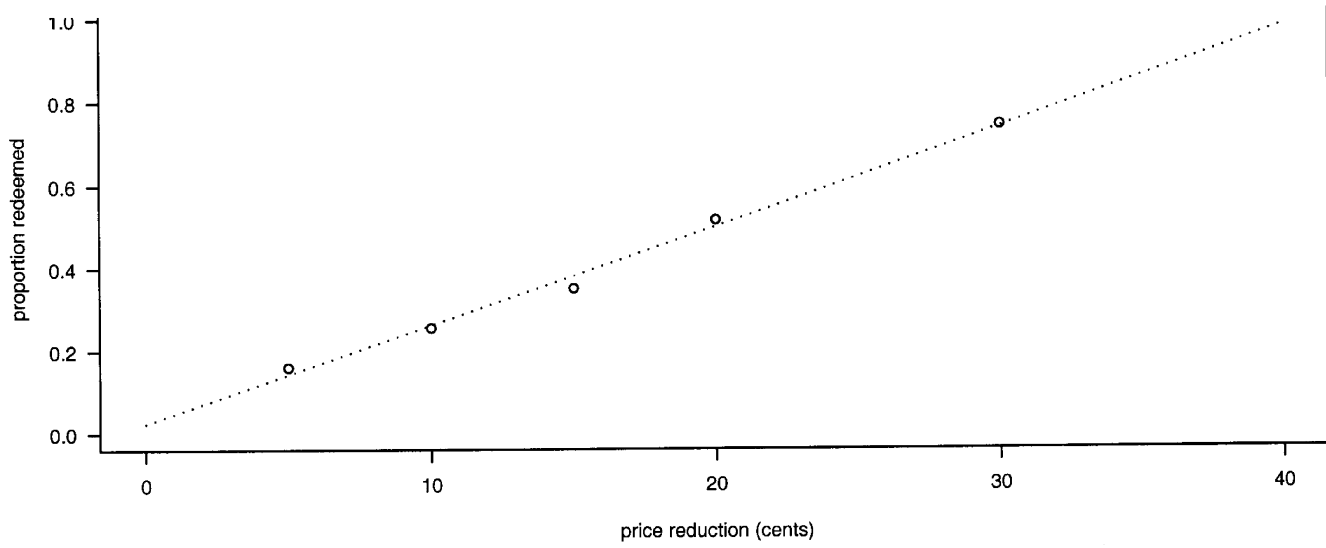
logit likelihood

$$\begin{aligned} L(\beta) &= \prod_{j=1}^n \left\{ \frac{\exp\{x_j^T \beta\}}{1 + \exp\{x_j^T \beta\}} \right\} \\ &= \frac{\exp\{\sum_j y_j x_j^T \beta\}}{\prod_j \{1 + \exp\{x_j^T \beta\}\}} \end{aligned}$$

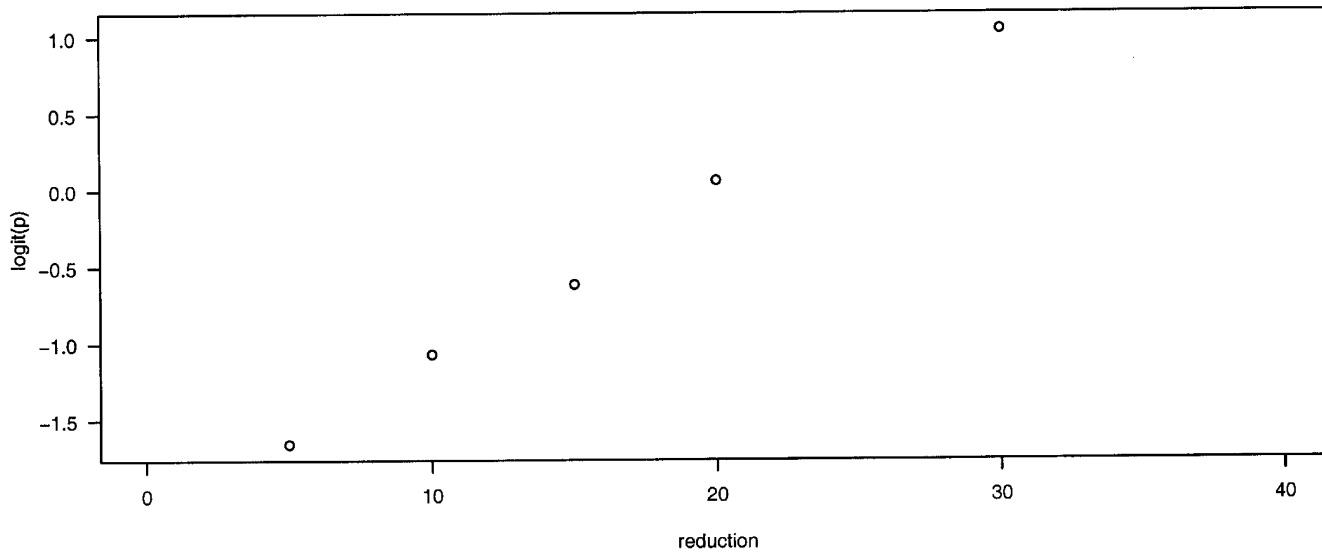
$S = \sum y_j x_j$ is sufficient

```
postscript(file="Po.ps",hor=F)
par(mfrow=c(3,1))
n<-c(200,200,200,200,200)
r<-c(32,51,70,103,148)
y<-r/n
x<-c(5,10,15,20,30)
plot(x,y,main="Coupon effectiveness study - proportion redeemed",xlab="price reduction (cents)",ylab="proportion redeemed",las=1,xlim=c(0,40),cex=1.,ylim=c(0,1))
junk1<-lm(y~x)
xaxis<-c(0:40)
ylin<-junk1$coef[1]+junk1$coef[2]*xaxis
lines(xaxis,ylin,lty=3)
plot(x,log(y/(1-y)),main="Logit plot",xlab="reduction",ylab="logit(p)",las=1,xlim=c(0,40),cex=1.)
junk<-glm(y~x,wei=n,family=binomial)
summary(junk)
anova(junk)
xaxis<-c(0:40)
ylin<-junk$coef[1]+junk$coef[2]*xaxis
ypred<-exp(ylin)/(1+exp(ylin))
plot(x,y,main="Fitted function",xlab="price reduction (cents)",ylab="proportion redeemed",las=1,xlim=c(0,40),ylim=c(0,1),cex=1.)
lines(xaxis,ypred)
junk2<-residuals(junk,type="pearson")
X2<-sum(junk2^2)
pval<-1-pchisq(X2,3)
print(c(X2,pval))
graphics.off()
q()
```

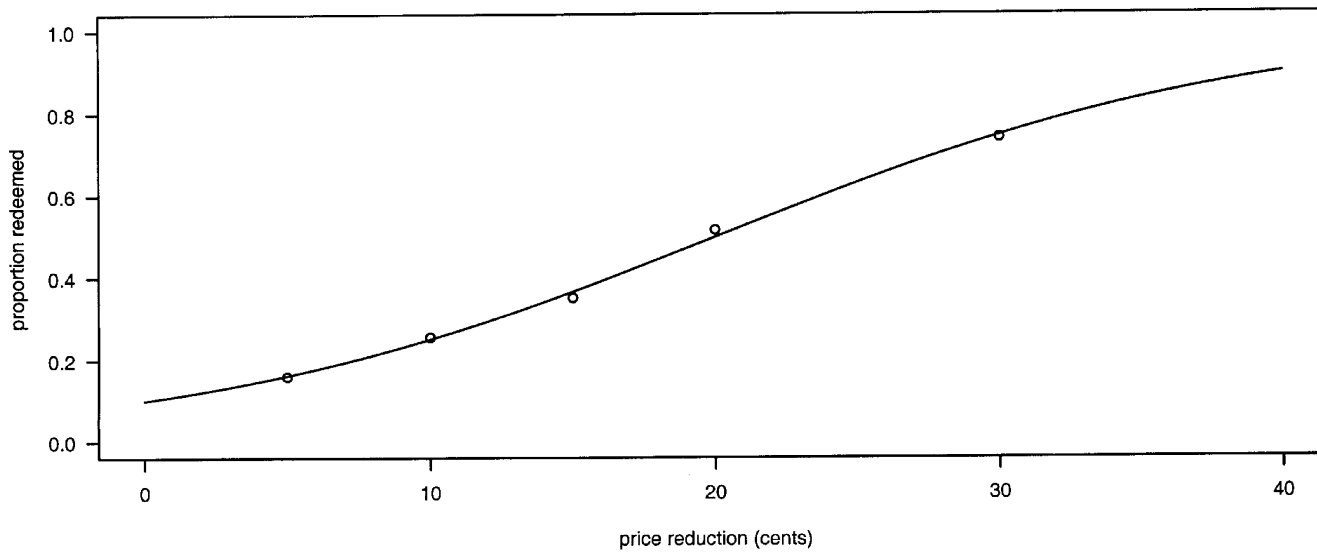
Effectiveness of coupons offering a price reduction
1000 homes selected
coupon and advertising mailed
price reductions of 5, 10, 15, 20, 30
200 homes assigned at random to each price reduction, X
 $Y=1$ coupon redeemed within 6 months
 0 not



Logit plot



Fitted function



junk Wed Apr 16 17:50:30 2008 1

Call:
glm(formula = y ~ x, family = binomial, weights = n)

Deviance Residuals:
1 2 3 4 5
-0.08476 0.16111 -0.43523 0.50294 -0.18626

Coefficients:
Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.185505 0.164667 -13.27 <2e-16 ***
x 0.108719 0.008843 12.29 <2e-16 ***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 180.94751 on 4 degrees of freedom
Residual deviance: 0.51021 on 3 degrees of freedom
AIC: 32.025

Number of Fisher Scoring iterations: 3

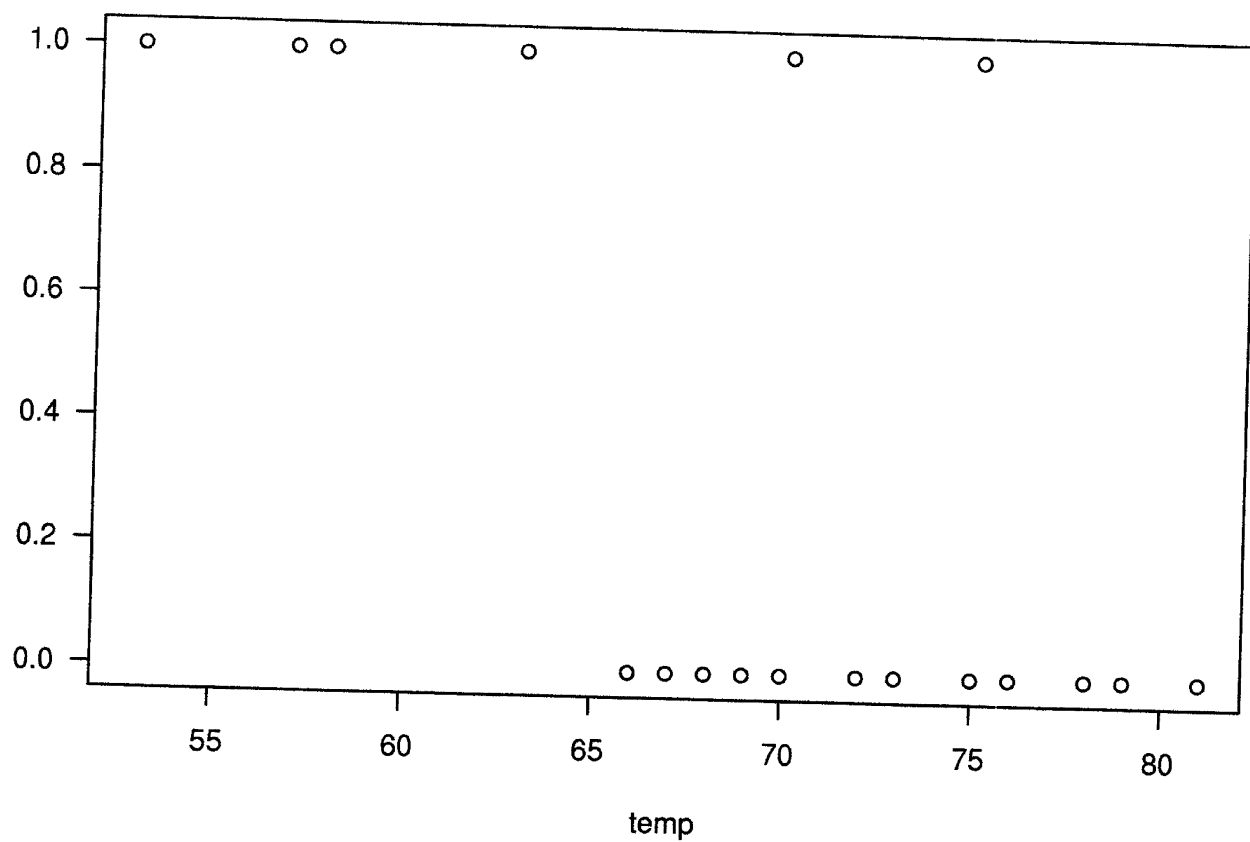
> anova(junk)
Analysis of Deviance Table

Model: binomial, link: logit

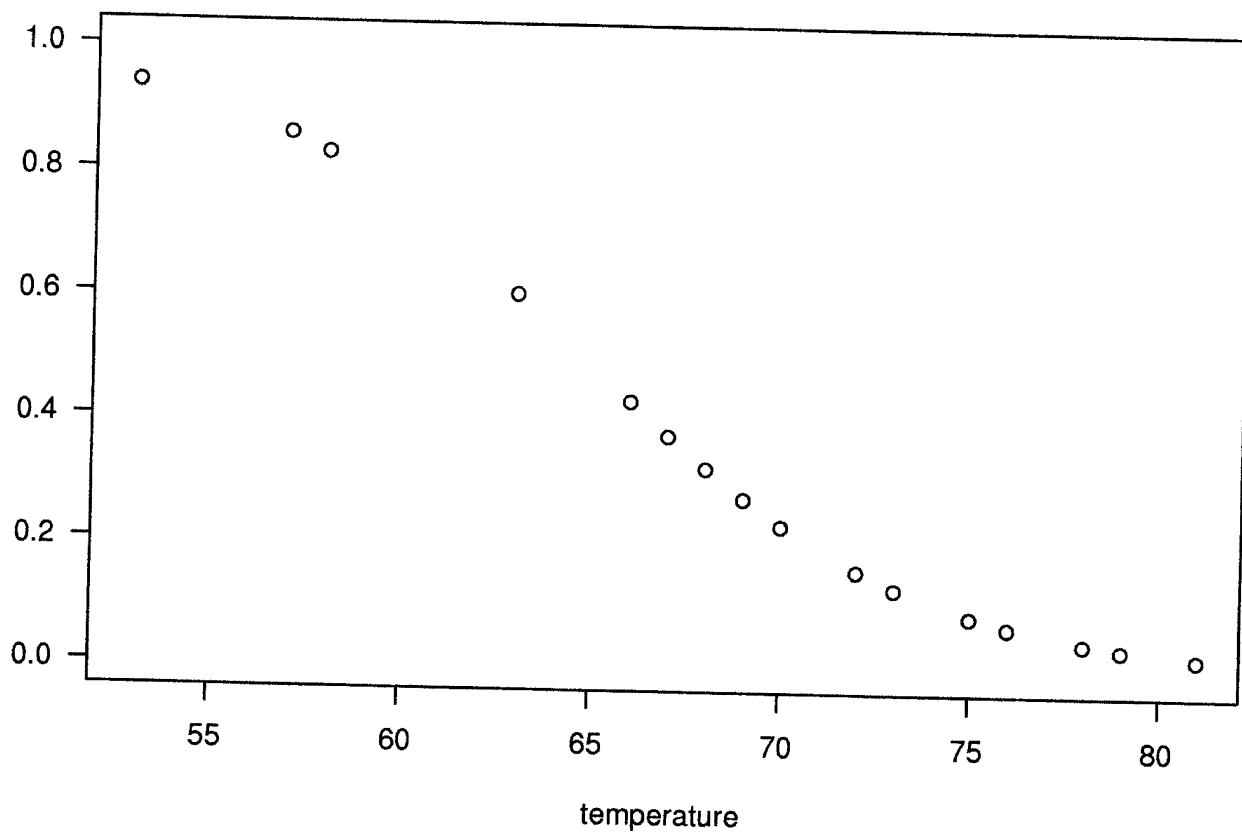
Response: y

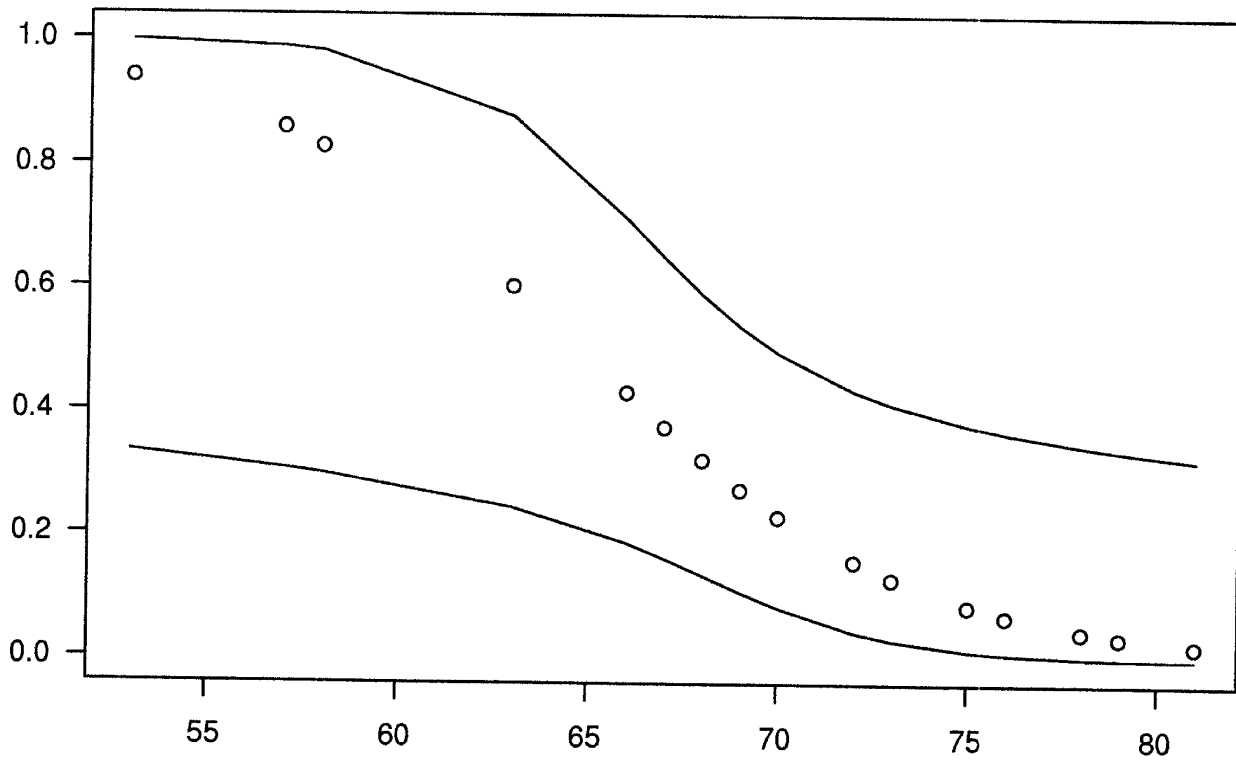
Terms added sequentially (first to last)

	Df	Deviance	Resid.	Df	Resid.	Dev
NULL				4		180.95
x	1	180.44		3		0.51
[1]		0.5093288			0.9168372	



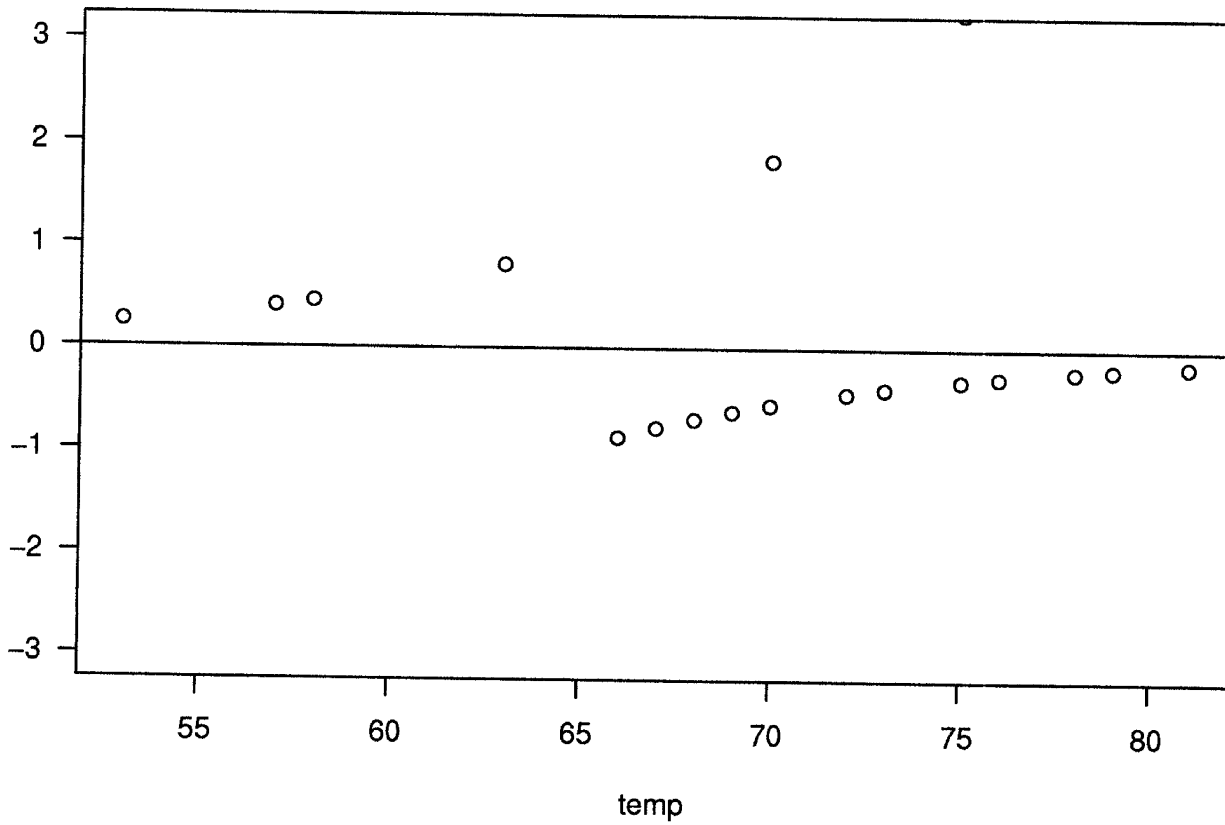
Fitted probabilities





temperature
 95% CI for risk at 31 degrees F is (.441,1.00)

Pearson residuals



Model Checking

Residuals

deviance residual

$$d_j = \text{sign}(\tilde{n}_j - \hat{\pi}_j) [2\{l_j(\tilde{n}_j; \varphi) - l_j(\hat{\pi}_j; \varphi)\}]^{1/2}$$

Pearson residual

$$\frac{1}{\sqrt{a_j}} \frac{y_j - \hat{\pi}_j}{\sqrt{\hat{\pi}_j / a_j}}$$

Terms	df	Deviance reduction	Terms	df	Deviance reduction
Species (unadj. for Colour)	5	19.64	Species (adj. for Colour)	5	41.18
Colour (adj. for Species)	7	47.31	Colour (unadj. for Species)	7	25.78
Species (unadj. for Colour)	4	27.63	Species (adj. for Colour)	4	35.18
Colour (adj. for Species)	7	18.03	Colour (unadj. for Species)	7	10.48

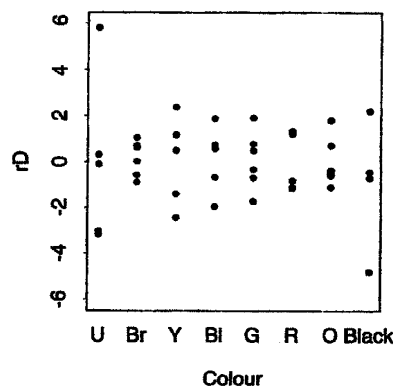
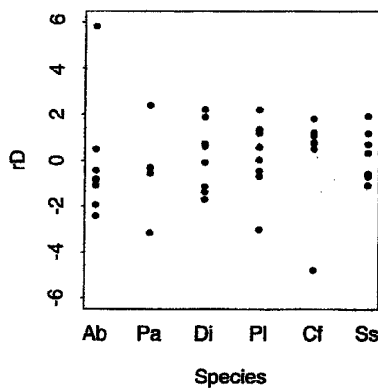


Figure 10.5
Standardized deviance
residuals r_D for binomial
two-way layout fitted
jacamar data.

2 x 2 table

patients

treatment or control

success or failure

		Success	Failure	Total
m_1	Treated	R_1	$m_1 - R_1$	m_1
m_0	Control	R_0	$m_0 - R_0$	m_0
	Total	$R_1 + R_0$	$m_1 + m_0 - R_1 - R_0$	$m_1 + m_0$

Treatments assigned randomly

One model

$$\pi_1 = \frac{e^{\lambda + \gamma}}{1 + e^{\lambda + \gamma}}, \quad \pi_0 = \frac{e^{\lambda}}{1 + e^{\lambda}}$$

$$\frac{\pi}{1 - \pi} = e^{\lambda + \gamma}, \quad \frac{\pi_0}{1 - \pi_0} = e^{\lambda}$$

$$\log \frac{\frac{\pi}{1 - \pi}}{\frac{\pi_0}{1 - \pi_0}} = \gamma$$