

Table 9.10 *Log-linear models for the melanoma data in Table 9.4; coefficients, b, with standard errors in brackets.*

Term *	Saturated model (9.10)	Additive model (9.9)	Minimal model
Constant	3.091 (0.213)	1.754 (0.204)	3.507 (0.05)
<i>SSM</i>	-0.318 (0.329)	1.694 (0.187)	
<i>NOD</i>	-0.147 (0.313)	1.302 (0.193)	
<i>IND</i>	-0.693 (0.369)	0.499 (0.217)	
<i>TNK</i>	-2.398 (0.739)	0.444 (0.155)	
<i>EXT</i>	-0.788 (0.381)	1.201 (0.138)	
<i>SSM</i> * <i>TNK</i>	3.614 (0.792)		
<i>SSM</i> * <i>EXT</i>	2.761 (0.465)		
<i>NOD</i> * <i>TNK</i>	2.950 (0.793)		
<i>NOD</i> * <i>EXT</i>	2.134 (0.460)		
<i>IND</i> * <i>TNK</i>	2.833 (0.834)		
<i>IND</i> * <i>EXT</i>	1.723 (0.522)		
log-likelihood	-29.556	-55.453	-177.16
X^2	0.0	65.813	
<i>D</i>	0.0	51.795	

*Reference categories are: Hutchinson's melanotic freckle (*HMF*) and head and neck (*HNK*). Other categories are: for type, superficial spreading melanoma (*SSM*), nodular (*NOD*) and indeterminate (*IND*); for site, trunk (*TNK*) and extremities (*EXT*).

Table 9.9 *Conventional chi-squared test of independence for melanoma data in Table 9.4; expected frequencies are shown in brackets.*

Tumor type	Site			Total
	Head & Neck	Trunk	Extremities	
Hutchinson's melanotic freckle	22 (5.78)	2 (9.01)	10 (19.21)	34
Superficial spreading melanoma	16 (31.45)	54 (49.03)	115 (104.52)	185
Nodular	19 (21.25)	33 (33.13)	73 (70.62)	125
Indeterminate	11 (9.52)	17 (14.84)	28 (31.64)	56
Total	68	106	226	400

MINITAB analysis Table 9.6

Welcome to Minitab, press F1 for help.

Chi-Square Test: C1; C2; C3

Expected counts are printed below observed counts
Chi-Square contributions are printed below expected counts

	C1	C2	C3	Total
1	25	8	5	38
	16,14	13,53	8,33	
	4,868	2,263	1,330	
2	6	18	11	35
	14,86	12,47	7,67	
	5,285	2,457	1,444	
Total	31	26	16	73

Chi-Sq = 17,648; DF = 2; P-Value = 0,000

Table 9.11 Results of log-linear modelling of data in Table 9.7.

Terms in model	d.f.*	log-likelihood**
$GD + CC + GD \times CC$	4	-83.16
$GD + CC + GD \times CC + AP$	3	-30.70
$GD + CC + GD \times CC + AP + AP \times CC$	2	-25.08
$GD + CC + GD \times CC + AP + AP \times CC + AP \times GD$	1	-22.95

*d.f. denotes degrees of freedom = number of observations (8) minus number of parameters;

** maximum value of the log-likelihood function.

Table 9.12 Comparison of observed frequencies and expected frequencies obtained from the log-linear model with all two-way interaction terms for the data in Table 9.7; expected frequencies in brackets.

	Aspirin use		Total
	Non-user	User	
<i>Gastric ulcer</i>			
Controls	62 (58.53)	6 (9.47)	68
Cases	39 (42.47)	25 (21.53)	64
<i>Duodenal ulcer</i>			
Controls	53 (56.47)	8 (4.53)	61
Cases	49 (45.53)	8 (11.47)	57

R-analysis Table 9.6

```
> data94 <- read.table(file="Table9.4.txt",header=T)
> data96 <- read.table(file="Table9.6.txt",header=T)
> data96 <- data.frame(data96)
> data96
  vaccine response frequency
1      0         1        25
2      0         2         8
3      0         3         5
4      1         1         6
5      1         2        18
6      1         3        11
> attach(data96)
> data96$vaccine <- factor(vaccine)
> data96$response <- factor(response)
> msat <- glm(frequency ~ vaccine + response + vaccine*response,family=poisson,data=data96)
> madd <- glm(frequency ~ vaccine + response,family=poisson,data=data96)
```

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```
> summary(madd)

Call:
glm(formula = frequency ~ vaccine + response, family = poisson,
    data = data96)

Deviance Residuals:
    1     2     3     4     5     6 
2.040 -1.630 -1.247 -2.615  1.469  1.128 

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  2.78111    0.21184  13.129 <2e-16 ***
vaccine1     -0.08224    0.23428  -0.351  0.7256
response2    -0.17589    0.26593  -0.661  0.5083
response3    -0.66140    0.30783  -2.149  0.0317 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 23.807  on 5  degrees of freedom
Residual deviance: 18.643  on 2  degrees of freedom
AIC: 51.77

Number of Fisher Scoring iterations: 5
```

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```

> summary(msat)
Call:
glm(formula = frequency ~ vaccine + response + vaccine * response,
     family = poisson, data = data96)

Deviance Residuals:
[1] 0 0 0 0 0 0

Coefficients:
                Estimate Std. Error z value Pr(>|z|)
(Intercept)      3.2189     0.2000  16.094 < 2e-16 ***
vaccinel         -1.4271     0.4546  -3.139 0.001694 **
response2        -1.1394     0.4062  -2.805 0.005030 **
response3        -1.6094     0.4899  -3.285 0.001019 **
vaccinel:response2  2.2380     0.6223   3.597 0.000322 ***
vaccinel:response3  2.2156     0.7054   3.141 0.001684 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance:  2.3807e+01  on 5  degrees of freedom
Residual deviance: -4.4409e-16  on 0  degrees of freedom
AIC: 37.128

Number of Fisher Scoring iterations: 3

> predict(madd,type="response")
Error: syntax error in "predict(madd,type=")"
> predict(madd,type="response")
      1      2      3      4      5      6
16.136986 13.534247  8.328767 14.863014 12.465753  7.671233
> predict(msat,type="response")
 1  2  3  4  5  6
25 8  5  6 18 11

```

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R-analysis Table 9.7

```

> data97 <- read.table(file="Table9.7.txt",header=T)
> data97 <- data.frame(data97)
> data97
  case ulcer aspirin frequency
1    0    0      0         62
2    0    0      1          6
3    1    0      0         39
4    1    0      1         25
5    0    1      0         53
6    0    1      1          8
7    1    1      0         49
8    1    1      1          8
> m1 <- glm(freq ~ ulcer + case + ulcer*case, family=poisson,data=data97)
> m2 <- glm(freq ~ ulcer + case + ulcer*case + aspirin, family=poisson,data=data97)
> m3 <- glm(freq ~ ulcer + case + ulcer*case + aspirin + aspirin*case, family=poisson,data=data97)
> m4 <- glm(freq ~ ulcer + case + ulcer*case + aspirin + aspirin*case + aspirin*ulcer, family=poisson,data=data97)

```

DEVIANCES:

```

m1: Residual deviance: 126.71  on 4  degrees of freedom
m2: Residual deviance: 21.789  on 3  degrees of freedom
m3: Residual deviance: 10.538  on 2  degrees of freedom
m4: Residual deviance:  6.283  on 1  degrees of freedom

```

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