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> data94 <- read.table(file="Table9.4.txt",header=T)
> data94 <- data.frame(data94)
> data94
  type site frequency
1     1     1         22
2     1     2          2
3     1     3         10
4     2     1         16
5     2     2         54
6     2     3        115
7     3     1         19
8     3     2         33
9     3     3         73
10    4     1         11
11    4     2         17
12    4     3         28
> attach(data94)
> data94$site <- factor(site)
> data94$type <- factor(type)
> madd <- glm(frequency ~ type + site,family=poisson,data=data94)
> summary(madd)

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Call:
glm(formula = frequency ~ type + site, family = poisson, data = data94)
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.0453  -1.0741   0.1297   0.5857   5.1354
Coefficients:
            Estimate Std. Error  z value Pr(>|z|)
(Intercept)   1.7544     0.2040   8.600 < 2e-16 ***
type2         1.6940     0.1866   9.079 < 2e-16 ***
type3         1.3020     0.1934   6.731 1.68e-11 ***
type4         0.4990     0.2174   2.295  0.02173 *
site2         0.4439     0.1554   2.857  0.00427 **
site3         1.2010     0.1383   8.683 < 2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for poisson family taken to be 1)
    Null deviance: 295.203  on 11  degrees of freedom
Residual deviance:  51.795  on  6  degrees of freedom
AIC: 122.91
Number of Fisher Scoring iterations: 5

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> predict(madd,type="response")
  1      2      3      4      5      6      7      8      9     10
5.780  9.010 19.210 31.450 49.025 104.525 21.250 33.125 70.625  9.520
 11     12
14.840 31.640
> msat <- glm(frequency ~ type + site+ type*site,family=poisson,data=data94)
> summary(msat)
Call:
glm(formula = frequency ~ type + site + type * site, family = poisson,
     data = data94)
Deviance Residuals:
 [1]  0  0  0  0  0  0  0  0  0  0  0  0  0
Coefficients:
              Estimate Std. Error  z value Pr(>|z|)
(Intercept)   3.0910     0.2132  14.4981 < 2e-16 ***
type2         -0.3185     0.3286  -0.969 0.332432
type3         -0.1466     0.3132  -0.468 0.639712
type4         -0.6931     0.3693  -1.877 0.060511 .
site2         -2.3979     0.7385  -3.247 0.001167 **
site3         -0.7885     0.3814  -2.067 0.038701 *
type2:site2    3.6143     0.7915   4.566 4.96e-06 ***
type3:site2    2.9500     0.7927   3.721 0.000198 ***
type4:site2    2.8332     0.8338   3.398 0.000679 ***
type2:site3    2.7608     0.4655   5.931 3.00e-09 ***
type3:site3    2.1345     0.4602   4.638 3.52e-06 ***
type4:site3    1.7228     0.5216   3.303 0.000957 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for poisson family taken to be 1)
Null deviance:  2.9520e+02 on 11 degrees of freedom
Residual deviance: -2.3981e-14 on  0 degrees of freedom
AIC: 83.111
Number of Fisher Scoring iterations: 3
> predict(msat,type="response")
  1  2  3  4  5  6  7  8  9 10 11 12
22  2 10 16 54 115 19 33 73 11 17 28

```