

# `exactLoglinTest`: A Program for Monte Carlo Conditional Analysis of Log-linear Models

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Nuisance parameters are parameters that are not of direct interest to the inferential question in hand. In a frequentist or likelihood paradigm, a common tool for eliminating nuisance parameters is to condition on their sufficient statistics. The same technique is useful (though rarely used) in a Bayesian settings, as it eliminates the need to put priors on nuisance parameters.

For log-linear models, conditional analysis suffers from two main drawbacks.

1. The set of lattice points contained in the conditional distribution is difficult to manage, computationally or analytically.
2. The sufficient statistics for the nuisance parameters are not ancillary to the parameters of interest.

In this manuscript we address only the first drawback using `exactLoglinTest`.

## 1 The Problem

The observed data,  $y = (y_1, \dots, y_n)$ , are modeled as Poisson counts with a means,  $\mu = (\mu_1, \dots, \mu_n)$ , satisfying

$$\log \mu = x\beta$$

under the null hypothesis. Here  $x$  is a full rank  $n \times p$  design matrix. It is easily shown that the sufficient statistics for  $\beta$  under the null hypothesis are  $x^t y$ , where a superscript  $t$  denotes a transpose. Let  $h$  be a test statistic of interest where larger values of  $h$  support the alternative hypothesis. Two examples are the Pearson Chi-Squared statistic and the deviance. An exact test relative to  $h$  can be performed via the conditional P-value

$$\text{Prob}\{h(y) \geq h(y_{obs}) | x^t y = x^t y_{obs}\} = \sum_{\{y \in \Gamma\}} \frac{I\{h(y) \geq h(y_{obs})\}}{C \prod y_i!}$$

where  $y_{obs}$  is the observed table,  $C$  is a normalizing constant and  $\Gamma = \{y | x^t y = x^t y_{obs}\}$  (often referred to as the reference set).

The term “exact” is used to refer to tests that guarantee the nominal type I error rate unconditionally. Thus a test that never rejects the null hypothesis is technically exact in any situation. Therefore, exactness is not in itself a sufficient condition for a test to be acceptable. Moreover, this example (never rejecting) is particularly relevant in our setting because  $\Gamma$  may contain one or few elements. Hence the conditional P-value will be exactly or near one regardless of the evidence in the data vis-a-vis the two hypotheses. However, it is also the case that the conservative conditional tests can produce P-values that are smaller than those calculated via Chi-squared approximations (see Subsection 3.2 for an example).

### 1.1 Binomial Calculations

Conditional inference for Poisson log-linear models contains conditional inference for binomial-logit models as a special case. Consider a binomial logit models of the form,  $b_i \sim \text{Bin}(n_i, p_i)$  for  $i = 1, \dots, k$  and

$$\text{logit}(p_i) = z_i \gamma + x'_i \beta, \quad (1)$$

where  $\gamma$  is a scalar and  $\beta$  is a  $p$  dimensional vector. Frequently,  $x'_i$  contains only a strata indicator and an intercept term. In this case conditioning on the sufficient statistic for  $\beta$  results in standard conditional

logistic regression. For this purpose, we suggest the `coxph` function as described in [7]. Instead we consider the more general case where  $\beta$  is arbitrary vector of nuisance parameters. However, the reader should again be warned that the loss of information from conditioning can sometimes be quite severe in these problems and hence produce useless results.

Consider testing  $H_0\gamma = 0$  versus some alternative. The following model model is equivalent to the null modell for (1):

$$y_{ij} \sim \text{Poisson}(\mu_{ij}) \quad \log(\mu_{i1}) = \alpha_i + x'_i \beta \quad \log(\mu_{i2}) = \alpha_i, \quad (2)$$

for  $j = 1, 2$  and  $i = 1, \dots, k$ . The sufficient statistics for the  $\alpha_i$  are  $y_{i1} + y_{i2} = y_{i+}$ . Then it is easy to show that the conditional distribution of  $y_{i1}|y_{i+}$  is precisely the model given by (1) where

$$\begin{aligned} p_i &= \mu_{i1}/\mu_{i+} \\ b_i &= y_{i1} \\ n_i &= y_{i+}. \end{aligned}$$

Therefore, conditioning out the nuisance parameters  $\{\alpha_i\}$  and  $\beta$  for the Poisson log-linear model yields exactly the same (null) conditional distribution as conditioning out  $\beta$  in model (1). Furthermore, this exercise indicates exactly how to perform the calculations, which is useful since `exactLoglinTest` only accepts models in the form of Poisson log-linear models.

Currently `exactLoglinTest` is useful for tests of  $\gamma = 0$ . With modifications, the central ideas could be used to calculate a Monte Carlo estimate of the conditional likelihood for  $\gamma$ . (It is possible to use `mceexact` as is for this purpose. However, we have had mixed success in this endeavor and it is best avoided due to numerical instability.)

## 2 exactLoglinTest

The software `exactLoglinTest` is an implementation of the algorithms presented in [2] and [3]. At the heart of both algorithms is a sequentially generated rounded normal approximation to the conditional distribution. We refer the reader to those papers for a more complete description.

You can obtain a copy of `exactLoglinTest` at as well as a no-web [6] version of this document at

<http://www.biostat.jhsph.edu/~bcaffo/downloads.htm>

You can install `exactLoglinTest` with R CMD INSTALL, on Unix and Linux, while the binaries are available for Windows. Assuming it is installed, one can load `mceexact` with

```
> library(exactLoglinTest)
> set.seed(1)
```

Here, the optional argument `lib.loc` is necessary if the package has been installed into one of the paths that R automatically checks. We also set the random number seed to a specific value which is a good practice for Monte Carlo procedures.

## 3 Examples

### 3.1 Residency Data

Assuming `exactLoglinTest` has been properly installed, the residency data can be obtained by the command

```
> data(residence.dat)
```

This data is a  $4 \times 4$  table of persons' residence in 1985 by their residence in 1980. See Table 1 for the complete data. The data frame, `residence.dat`, contains the counts stacked by the rows. The extra term `sym.pair` is used to fit a quasi-symmetry model. For details on the quasi-symmetry model see [1]. To obtain a Monte Carlo goodness of fit test of quasi-symmetry versus a saturated model involves the following command

```

> resid.mcx <- mceexact(y ~ res.1985 + res.1980 + factor(sym.pair),
+                         data = residence.dat,
+                         nosim = 10 ^ 2,
+                         maxiter = 10 ^ 4)
> resid.mcx

      deviance    Pearson
observed.stat 2.98596233 2.98198696
pvalue         0.43615976 0.43615976
mcse          0.03240488 0.03240488

```

The default method is the importance sampling of [2]. Using this method, the number of desired simulations `nosim` may not be met in `maxiter` iterations and no warning is issued if this occurs. The returned value is a list storing the results of the Monte Carlo simulation and all of the relevant information necessary to restart the simulation. More information can be obtained with `summary`

```

> summary(resid.mcx)

$conde1
      15       14       10
294.8800 166.8939 238.3175

$condv1
  56.78443 -39.34468 36.79749
-39.34468  51.14382 -39.59345
  36.79749 -39.59345 59.74533

$dens
function (y)
sum(-lgamma(y + 1))
<environment: namespace:exactLoglinTest>

$doobs
[1] 2.985962 2.981987

$mu.hat
      15       14       10       16       13       12
294.87999 166.89392 238.31746 10192.00000 63.22609 261.12001
      11        9        8        7        6        5
17819.00000 167.56253 311.10608 501.68254 13677.00000 91.21138
      4        3        2        1
123.77391 370.43747 95.78862 11607.00000

$n
[1] 16

$n1
[1] 3

$nosim
[1] 100

$s
      [,1]
(Intercept) 55981
res.1985NE 11929
res.1985S 18986
res.1985W 10888

```

```

res.1980NE      12197
res.1980S       18486
res.1980W       10717
factor(sym.pair)2   187
factor(sym.pair)3   538
factor(sym.pair)4   187
factor(sym.pair)5 13677
factor(sym.pair)6   740
factor(sym.pair)8 17819

$stat
function (y = NULL, mu = NULL, rowlabels = FALSE)
{
  if (rowlabels)
    c("deviance", "Pearson")
  else {
    temp <- y != 0
    c(2 * sum(y[temp] * log(y[temp]/mu[temp])), sum((y -
      mu)^2/mu))
  }
}
<environment: namespace:exactLoglinTest>

$tdf
[1] 3

$x
  (Intercept) res.1985NE res.1985S res.1985W res.1980NE res.1980S res.1980W
15          1         0         1         0         0         0         1
14          1         0         0         0         0         0         1
10          1         0         0         0         0         1         0
16          1         0         0         1         0         0         1
13          1         1         0         0         0         0         1
12          1         0         0         1         0         1         0
11          1         0         1         0         0         1         0
9           1         1         0         0         0         1         0
8           1         0         0         1         0         0         0
7           1         0         1         0         0         0         0
6           1         0         0         0         0         0         0
5           1         1         0         0         0         0         0
4           1         0         0         1         1         0         0
3           1         0         1         0         1         0         0
2           1         0         0         0         1         0         0
1           1         1         0         0         1         0         0
  factor(sym.pair)2 factor(sym.pair)3 factor(sym.pair)4 factor(sym.pair)5
15          0         0         0         0
14          0         0         0         0
10          0         0         0         0
16          0         0         0         0
13          0         0         1         0
12          0         0         0         0
11          0         0         0         0
9           0         1         0         0
8           0         0         0         0
7           0         0         0         0
6           0         0         0         1
5           1         0         0         0
4           0         0         0         1

```

```

3          0          1          0          0
2          1          0          0          0
1          0          0          0          0
  factor(sym.pair)6 factor(sym.pair)8
15         0          0
14         0          0
10         1          0
16         0          0
13         0          0
12         0          0
11         0          1
9          0          0
8          0          0
7          1          0
6          0          0
5          0          0
4          0          0
3          0          0
2          0          0
1          0          0

$x1
  (Intercept) res.1985NE res.1985S res.1985W res.1980NE res.1980S res.1980W
15         1          0          1          0          0          0          1
14         1          0          0          0          0          0          1
10         1          0          0          0          0          1          0
  factor(sym.pair)2 factor(sym.pair)3 factor(sym.pair)4 factor(sym.pair)5
15         0          0          0          0
14         0          0          0          0
10         0          0          0          0
  factor(sym.pair)6 factor(sym.pair)8
15         0          0
14         0          0
10         1          0

$x2invt
  (Intercept) res.1985NE res.1985S res.1985W res.1980NE res.1980S res.1980W
16        -1         0.5         0         1         0.5         0         1
13         1        -0.5         0        -1        -0.5         0         0
12         0         0.0         1         0         0.0         1         0
11         0         0.0         0         0         0.0         0         0
9          0         0.0        -1         0         0.0         0         0
8          2        -1.0        -1        -1        -1.0        -1        -1
7          0         0.0         0         0         0.0         0         0
6          0         0.0         0         0         0.0         0         0
5         -1         1.0         1         1         0.0         0         0
4         -1         0.5         0         1         0.5         0         0
3          0         0.0         1         0         0.0         0         0
2          1        -1.0        -1        -1         0.0         0         0
1          0         0.5         0         0         0.5         0         0
  factor(sym.pair)2 factor(sym.pair)3 factor(sym.pair)4 factor(sym.pair)5
16         0.5         0.5        -0.5         1
13        -0.5        -0.5         0.5        -1
12         0.0        -1.0         0.0         0
11         0.0         0.0         0.0         0
9          0.0         1.0         0.0         0
8        -1.0         0.0         0.0        -2
7          0.0         0.0         0.0         0

```

```

6          0.0          0.0          0.0          1
5          1.0          0.0          0.0          1
4          0.5          0.5          0.5          1
3          0.0          0.0          0.0          0
2          0.0          0.0          0.0         -1
1         -0.5         -0.5         -0.5          0
  factor(sym.pair)6 factor(sym.pair)8
16          1            1
13         -1           -1
12         -1           -2
11          0            1
9           1            1
8           -1           0
7            1            0
6            0            0
5            0            0
4            1            1
3           -1           -1
2            0            0
1            0            0

$y
  15   14   10   16   13   12   11    9    8    7    6    5    4
 286  176  225 10192   63   270 17819   172   302   515 13677   87   124
  3     2     1
 366  100 11607

$ord
 [1] 15 14 10 16 13 12 11  9  8  7  6  5  4  3  2  1

$glm.fit
Call: glm(formula = formula, family = poisson, data = data, x = TRUE,
y = TRUE)

Coefficients:
(Intercept)      res.1985NE      res.1985S      res.1985W
              1.6281        3.8411        0.5692        4.1120
res.1980NE      res.1980S      res.1980W factor(sym.pair)2
              3.8901       -0.1752        3.4892       -0.9561
factor(sym.pair)3 factor(sym.pair)4 factor(sym.pair)5 factor(sym.pair)6
             -0.1728       -4.8118        7.8953        4.0206
factor(sym.pair)7 factor(sym.pair)8 factor(sym.pair)9 factor(sym.pair)10
                  NA          7.7658          NA          NA

Degrees of Freedom: 15 Total (i.e. Null);  3 Residual
Null Deviance:           131000
Residual Deviance: 2.986          AIC: 159.2

$maxiter
[1] 10000

$startiter
[1] 101

$sumdw
[1] 18.64563 18.64563

```

```

$sumdwsq
[1] 19.12212 19.12212

$sumw
[1] 42.74954

$sumwsq
[1] 42.36458

$impconst
[1] -466390.4

$phat
[1] 0.4361598 0.4361598

$mcse
[1] 0.03240488 0.03240488

$perpos
[1] 1

attr(,"class")
[1] "babSummary"

```

The  $t$  degrees of freedom refers to degrees of freedom used as a tuning parameter within the algorithm while the `df` refers to the model degrees of freedom. In this case, the Monte Carlo standard error, `mcse`, seems too large. As mentioned previously, `mcexact` , stores the relevant information for restarting the simulation

```

> resid.mcx <- update(resid.mcx, nosim = 10 ^ 4, maxiter = 10 ^ 6)
> resid.mcx

      deviance      Pearson
observed.stat 2.985962330 2.981986964
pvalue        0.400636040 0.400930887
mcse         0.003196472 0.003196835

```

It is important to note that `update` only resumes the simulation with changes to simulation-specific parameters. It will not allow users to change the model formulation; one must rerun `mcexact` independently to do that.

This example illustrates the point that the underlying algorithms are very efficient when the cell counts are large. Of course, when this is the case, the large sample approximations are nearly identical to the conditional results

```

> pchisq(c(2.986, 2.982), 3, lower.tail = FALSE)
[1] 0.3937887 0.3944088

```

### 3.2 Pathologists' Tumor Ratings

The following example is interesting in that the large sample results differ drastically from the conditional results. Moreover, the conditional results are less conservative. The data, given in Table 2 can be obtained via

```
> data(pathologist.dat)
```

A uniform association model accounts for the ordinal nature of the ratings by associating ordinal scores with the pathologist's ratings [see 1]. Specifically, we can test a uniform association model against the saturated model with

```

> path.mcx <- mcexact(y ~ factor(A) + factor(B) + I(A * B),
+                         data = pathologist.dat,
+                         nosim = 10 ^ 4,
+                         maxiter = 10 ^ 4)
> summary(path.mcx)

$conde1
      20          19          18          17          15          14
6.344616e-01 3.692094e+00 1.749242e+01 1.770945e-01 2.998565e-02 1.123799e+00
           13          12          10          9          8          25
3.429048e+01 2.235819e+00 3.025095e-04 7.301670e-02 1.434878e+01 2.335250e+00
           24          23          22
2.110050e+00 1.552251e+00 2.440110e-03

$condv1
  3.992947e-01 -1.512630e-01 -0.2302951722 -1.683236e-02 -1.354645e-02
-1.512630e-01 1.285627e+00 -1.1337928058 -9.767044e-04 -2.392629e-03
-2.302952e-01 -1.133793e+00 1.5130688567 -1.460797e-01 1.802070e-02
-1.683236e-02 -9.767044e-04 -0.1460797229 1.643946e-01 -1.958202e-03
-1.354645e-02 -2.392629e-03 0.0180207042 -1.958202e-03 2.886289e-02
-8.111453e-02 -5.988614e-01 0.6966776416 -1.548698e-02 -1.038945e-02
  1.894272e-01 4.925053e-01 -0.8031364378 1.162690e-01 -2.453056e-03
-5.915681e-02 7.589214e-02 0.0632142608 -7.761053e-02 -1.042780e-02
-1.685691e-04 -3.183465e-06 0.0002077854 -3.388633e-05 -1.587280e-05
-9.327963e-03 -3.675231e-02 0.0488399809 -2.572783e-03 -1.225006e-03
-2.138232e-03 6.014399e-02 -0.1636048047 1.032278e-01 -1.557045e-03
-3.855792e-01 1.536587e-01 0.2120661394 1.882458e-02 -1.530052e-02
  2.419696e-01 -6.495954e-01 0.3874878075 1.913509e-02 1.404431e-02
  1.437071e-01 4.949123e-01 -0.5989177210 -3.768255e-02 1.302339e-03
-9.565519e-05 1.019615e-03 -0.0006350826 -2.754771e-04 -4.573679e-05

-0.0811145281 0.1894272278 -0.0591568137 -1.685691e-04 -9.327963e-03
-0.5988613532 0.4925052899 0.0758921360 -3.183465e-06 -3.675231e-02
  0.6966776416 -0.8031364378 0.0632142608 2.077854e-04 4.883998e-02
-0.0154869817 0.1162689632 -0.0776105282 -3.388633e-05 -2.572783e-03
-0.0103894478 -0.0024530562 -0.0104277955 -1.587280e-05 -1.225006e-03
  0.7869316765 -0.5710434774 -0.1405318761 -1.493944e-04 -2.672783e-02
-0.5710434774 1.7623815394 -1.1342630814 3.904828e-04 4.405264e-02
-0.1405318761 -1.1342630814 1.4174614975 -1.347161e-04 -8.302405e-03
-0.0001493944 0.0003904828 -0.0001347161 3.022609e-04 -2.146740e-05
-0.0267278342 0.0440526416 -0.0083024047 -2.146740e-05 6.998117e-02
-0.0268356441 -1.4105516405 1.2509438439 -2.596956e-04 -6.002243e-02
  0.0916538934 -0.1873660854 0.0697198468 -1.178181e-04 1.057451e-02
-0.1607465057 0.0332474968 0.0732946813 1.746923e-04 -6.426580e-03
  0.0694956953 0.1515129370 -0.1414406076 -5.596201e-05 -4.068555e-03
-0.0003991607 0.0025894889 -0.0015662853 -9.049401e-07 -7.872439e-05

-0.0021382316 -0.3855791564 0.2419696249 1.437071e-01 -9.565519e-05
  0.0601439882 0.1536587142 -0.6495953877 4.949123e-01 1.019615e-03
-0.1636048047 0.2120661394 0.3874878075 -5.989177e-01 -6.350826e-04
  0.1032278276 0.0188245778 0.0191350909 -3.768255e-02 -2.754771e-04
-0.0015570454 -0.0153005192 0.0140443088 1.302339e-03 -4.573679e-05
-0.0268356441 0.0916538934 -0.1607465057 6.949570e-02 -3.991607e-04
-1.4105516405 -0.1873660854 0.0332474968 1.515129e-01 2.589489e-03
  1.2509438439 0.0697198468 0.0732946813 -1.414406e-01 -1.566285e-03
-0.0002596956 -0.0001178181 0.0001746923 -5.596201e-05 -9.049401e-07
-0.0600224324 0.0105745120 -0.0064265799 -4.068555e-03 -7.872439e-05
  2.4262895610 0.0039554188 0.0273610511 -3.269460e-02 1.373295e-03

```

```

0.0039554188 0.4009976184 -0.2561891403 -1.449531e-01 1.423006e-04
0.0273610511 -0.2561891403 0.8167173280 -5.599893e-01 -5.387153e-04
-0.0326945978 -0.1449530621 -0.5599893053 7.069878e-01 -2.034924e-03
0.0013732947 0.0001423006 -0.0005387153 -2.034924e-03 2.431391e-03

$dens
function (y)
sum(-lgamma(y + 1))
<environment: namespace:exactLoglinTest>

$dobs
[1] 16.21453 14.72928

$mu.hat
      20          19          18          17          15          14
6.344616e-01 3.692094e+00 1.749242e+01 1.770945e-01 2.998565e-02 1.123799e+00
      13          12          10          9           8          25
3.429048e+01 2.235819e+00 3.025095e-04 7.301670e-02 1.434878e+01 2.335250e+00
      24          23          22          21          16          11
2.110050e+00 1.552251e+00 2.440110e-03 8.417609e-06 3.934524e-03 3.199129e-01
      7           6           5           4           3           2
6.025400e+00 5.552502e+00 6.689408e-07 1.039869e-03 1.316071e+00 3.559247e+00
      1
2.112364e+01

$n
[1] 25

$n1
[1] 15

$nosim
[1] 10000

$s
[,1]
(Intercept) 118
factor(A)2   12
factor(A)3   69
factor(A)4    7
factor(A)5    3
factor(B)2   26
factor(B)3   38
factor(B)4   22
factor(B)5    6
I(A * B)  898

$stat
function (y = NULL, mu = NULL, rowlabels = FALSE)
{
  if (rowlabels)
    c("deviance", "Pearson")
  else {
    temp <- y != 0
    c(2 * sum(y[temp] * log(y[temp]/mu[temp])), sum((y -
      mu)^2/mu))
  }
}

```

```
<environment: namespace:exactLoglinTest>
```

```
$tdf  
[1] 3
```

```
$x
```

	(Intercept)	factor(A)2	factor(A)3	factor(A)4	factor(A)5	factor(B)2
20	1	0	0	0	1	0
19	1	0	0	1	0	0
18	1	0	1	0	0	0
17	1	1	0	0	0	0
15	1	0	0	0	1	0
14	1	0	0	1	0	0
13	1	0	1	0	0	0
12	1	1	0	0	0	0
10	1	0	0	0	1	1
9	1	0	0	1	0	1
8	1	0	1	0	0	1
25	1	0	0	0	1	0
24	1	0	0	1	0	0
23	1	0	1	0	0	0
22	1	1	0	0	0	0
21	1	0	0	0	0	0
16	1	0	0	0	0	0
11	1	0	0	0	0	0
7	1	1	0	0	0	1
6	1	0	0	0	0	1
5	1	0	0	0	1	0
4	1	0	0	1	0	0
3	1	0	1	0	0	0
2	1	1	0	0	0	0
1	1	0	0	0	0	0
	factor(B)3	factor(B)4	factor(B)5	I(A * B)		
20	0	1	0	20		
19	0	1	0	16		
18	0	1	0	12		
17	0	1	0	8		
15	1	0	0	15		
14	1	0	0	12		
13	1	0	0	9		
12	1	0	0	6		
10	0	0	0	10		
9	0	0	0	8		
8	0	0	0	6		
25	0	0	1	25		
24	0	0	1	20		
23	0	0	1	15		
22	0	0	1	10		
21	0	0	1	5		
16	0	1	0	4		
11	1	0	0	3		
7	0	0	0	4		
6	0	0	0	2		
5	0	0	0	5		
4	0	0	0	4		
3	0	0	0	3		
2	0	0	0	2		
1	0	0	0	1		

```

$x1
  (Intercept) factor(A)2 factor(A)3 factor(A)4 factor(A)5 factor(B)2
20          1         0         0         0         1         0
19          1         0         0         1         0         0
18          1         0         1         0         0         0
17          1         1         0         0         0         0
15          1         0         0         0         1         0
14          1         0         0         1         0         0
13          1         0         1         0         0         0
12          1         1         0         0         0         0
10          1         0         0         0         1         1
9           1         0         0         1         0         1
8            1         0         1         0         0         1
25          1         0         0         0         1         0
24          1         0         0         1         0         0
23          1         0         1         0         0         0
22          1         1         0         0         0         0

  factor(B)3 factor(B)4 factor(B)5 I(A * B)
20          0         1         0        20
19          0         1         0        16
18          0         1         0        12
17          0         1         0         8
15          1         0         0        15
14          1         0         0        12
13          1         0         0         9
12          1         0         0         6
10          0         0         0        10
9           0         0         0         8
8            0         0         0         6
25          0         0         1        25
24          0         0         1        20
23          0         0         1        15
22          0         0         1        10

$x2invt
  (Intercept) factor(A)2 factor(A)3 factor(A)4 factor(A)5 factor(B)2
21          0         0         0         0         0         0
16          0         0         0         0         0         0
11          0         0         0         0         0         0
7           -1        -1        -2        -3        -4        -1
6            1         1         2         3         4         2
5            0         0         0         0         1         0
4            0         0         0         1         0         0
3            0         0         1         0         0         0
2            1         2         2         3         4         1
1            0        -2        -3        -4        -5        -2

  factor(B)3 factor(B)4 factor(B)5 I(A * B)
21          0         0         1         0
16          0         1         0         0
11          1         0         0         0
7           -2        -3        -4         1
6            2         3         4        -1
5            0         0         0         0
4            0         0         0         0
3            0         0         0         0
2            2         3         4        -1
1           -3        -4        -5         1

```

```

$y
20 19 18 17 15 14 13 12 10 9 8 25 24 23 22 21 16 11 7 6 5 4 3 2 1
 0 7 14 1 0 0 36 2 0 0 14 3 0 3 0 0 0 0 7 5 0 0 2 2 22

$ord
[1] 20 19 18 17 15 14 13 12 10 9 8 25 24 23 22 21 16 11 7 6 5 4 3 2 1

$glm.fit

Call: glm(formula = formula, family = poisson, data = data, x = TRUE,
y = TRUE)

Coefficients:
(Intercept) factor(A)2 factor(A)3 factor(A)4 factor(A)5 factor(B)2
      1.188     -3.643     -6.501    -15.507    -24.718     -3.199
factor(B)3 factor(B)4 factor(B)5 I(A * B)
      -7.915    -14.176   -22.186     1.863

Degrees of Freedom: 24 Total (i.e. Null); 15 Residual
Null Deviance: 267.7
Residual Deviance: 16.21      AIC: 82.48

$maxiter
[1] 10000

$startiter
[1] 1

$sumdw
[1] 0

$sumdwsq
[1] 0

$sumw
[1] 0

$sumwsq
[1] 0

$phat
[1] NaN

$mcse
[1] NaN

$perpos
[1] 0

attr(,"class")
[1] "babSummary"

```

The previous code chunk takes about 1 minute on my laptop. It is worth comparing these results to the asymptotic Chi-squared results

```

> pchisq(c(16.214, 14.729), 15, lower.tail = FALSE)
[1] 0.3679734 0.4711083

```

### 3.3 Alligator Food Choice Data Using MCMC

In this example we illustrate the algorithm from[3] using the data and Poisson log-linear model from Table 3. The alligator data is a good choice for MCMC as the percent of valid tables generated using `method = "bab"` is very small, less than 1% of the tables simulated. It is often the case that the MCMC algorithm will be preferable when the table is large and/or sparse. Of course, using MCMC introduces further complications in reliably running and using the output of the algorithm.

The algorithm from [3] uses local moves to reduce the number of tables with negative entries that the chain produces. You can specify this method by using `method = "cab"`. The parameter `p` represents the average proportion of table entries left fixed. So a chain with `p=.9` will leave most of the table entries fixed from one iteration to the next. A high value of `p` will result in a high proportion of valid (non-negative) simulated tables. Too large of a value of `p` causes the chain to mix slowly because the tables will be very similar from one iteration to the next. However, it is sometimes the case that a small value of `p` will produce too many tables with negative entries. Hence the Metropolis/Hastings/Green algorithm will stay at the current table for long periods and again result in a slowly mixing chain. It is also worth mentioning that for large values of `p` the algorithm is theoretically irreducible, but may not be practically irreducible. Therefore, it is advisable to both tinker with the chain some and make final runs using multiple values of `p`.

The program allows for the option to save the chain goodness of fit statistics, so that some initial tinkering can be performed. This is specified with the `savechain = TRUE` option. If using importance sampling, `method = "bab"`, then `savechain` saves both the statistic values and the importance weights on the log scale.

```
> data(alligator.dat)
> alligator.mcx <- mcexact(y ~ (lake + gender + size) * food + lake * gender * size,
+                               data = alligator.dat,
+                               nosim = 10 ^ 3,
+                               method = "cab",
+                               savechain = TRUE,
+                               batchsize = 100,
+                               p = .4)
> summary(alligator.mcx)

$conde1
    75      74      73      72      70      69      68
1.31600087 0.48346172 0.18073692 6.51660315 1.13800295 0.81453108 0.25072319
       67      60      59      58      57      55      54
1.60473559 0.18105409 0.13394981 0.26096632 0.21080481 1.97444067 0.52630855
       53      52      50      49      48      47      40
1.21928164 6.54106633 5.63440188 2.92618991 5.58172191 5.31553870 0.13185304
       39      38      37      35      34      33      32
0.07554443 0.51708045 0.55718074 0.79011836 0.16310491 1.32752883 9.50014868
       30      29      28      27      20      19      18
1.78879234 0.71943767 4.82138891 6.12481782 1.78671996 1.50458067 0.82331031
       17      80      79      78      77
0.24350239 1.03386967 1.05416634 0.33141537 1.79927933

$condv1
  0.8158428899 -4.024685e-02 -1.553110e-02 -0.349190606 -0.1432926821
-0.0402468520  3.425437e-01 -6.423501e-03 -0.132000575  0.0112669026
-0.0155310983 -6.423501e-03  1.418543e-01 -0.056732328  0.0054324960
-0.3491906063 -1.320006e-01 -5.673233e-02  1.944240192  0.0541580685
-0.1432926821  1.126690e-02  5.432496e-03  0.054158069  0.7401576216
  0.0126479801 -6.698040e-02  2.194671e-03  0.021894398 -0.0553905322
  0.0051999933  1.668882e-03 -4.001101e-02  0.018815577 -0.0196291578
  0.0427174386  1.701258e-02  1.118021e-02 -0.206501050 -0.1424549232
-0.0107478602  9.515460e-04  3.247559e-04  0.007024218 -0.0004989307
  0.0009304963 -5.024699e-03  2.000605e-04  0.004639496 -0.0013730257
```

0.0020305479	1.354304e-03	-1.518614e-03	-0.002545615	-0.0007124931
0.0045797255	1.497876e-03	5.267360e-04	-0.023797868	0.0028035524
-0.1980993866	6.075710e-03	5.407843e-03	0.184127587	0.1496365772
0.0078073066	-6.873110e-02	1.977967e-03	0.056534616	-0.0136143474
0.0102063142	2.962669e-03	-3.255049e-02	0.042264127	-0.0142522175
0.1366844470	4.568478e-02	1.659121e-02	-0.517973431	-0.0627665744
0.1993899950	-1.367119e-02	-9.238751e-03	-0.110748159	-0.2337196537
-0.0140866155	9.559156e-02	-3.555370e-03	-0.054177923	0.0183523013
-0.0188685469	-7.591748e-03	4.410161e-02	-0.012509049	0.0190353775
-0.0920784386	-4.329516e-02	-1.459001e-02	0.361106082	0.0891353606
-0.0080752925	1.324869e-04	2.071072e-04	0.004468277	-0.0004131863
-0.0003415250	-3.020569e-03	9.053576e-05	0.002609869	-0.0006105333
-0.0016771963	2.878589e-05	-2.867681e-03	-0.003494169	-0.0009174062
0.0074260713	2.258904e-03	1.114944e-03	-0.050775447	0.0030639985
-0.0849167457	-2.050967e-03	1.872812e-03	0.068924106	0.0719471826
-0.0003087532	-2.193521e-02	5.410853e-04	0.017323964	-0.0013128616
-0.0105051563	-5.477681e-03	-3.527090e-02	0.048514814	0.0065273111
0.0687785132	2.385286e-02	1.798516e-02	-0.556154021	-0.0165875622
0.0895235521	1.612037e-03	-2.541660e-03	-0.056763707	-0.0857398927
0.0001866741	2.717585e-02	-7.686077e-04	-0.018541918	0.0017031657
0.0102985658	5.228012e-03	4.154175e-02	-0.030921208	-0.0082281417
-0.0562173667	-2.215968e-02	-1.715349e-02	0.505456857	0.0177359687
-0.0052008245	-7.118337e-03	-2.684526e-04	0.004642330	-0.0863596513
-0.0037068574	3.700360e-02	-1.540702e-03	-0.015858387	0.0046324516
0.0008862818	-2.389580e-03	6.526212e-03	-0.009244601	0.0021926126
0.0022527803	-1.239194e-03	2.709523e-04	-0.010948376	0.0042210349
-0.2410652748	1.935201e-02	6.659537e-03	0.082691382	-0.2126596733
0.0155880999	-1.594698e-01	3.834239e-03	0.056894076	0.0217753875
0.0064294250	4.752970e-03	-5.802036e-02	0.013744369	0.0068771464
0.0956599413	4.855803e-02	1.879302e-02	-0.603778526	0.0232833502
0.0126479801	0.0051999933	0.0427174386	-0.0107478602	9.304963e-04
-0.0669804029	0.0016688823	0.0170125805	0.0009515460	-5.024699e-03
0.0021946710	-0.0400110088	0.0111802099	0.0003247559	2.000605e-04
0.0218943983	0.0188155772	-0.2065010499	0.0070242177	4.639496e-03
-0.0553905322	-0.0196291578	-0.1424549232	-0.0004989307	-1.373026e-03
0.4699468498	-0.0123104240	-0.0821830095	-0.0022970012	1.151175e-02
-0.0123104240	0.1777975938	-0.0324663406	-0.001022218	-1.121173e-03
-0.0821830095	-0.0324663406	1.0664840652	0.0033920589	-2.549591e-04
-0.0022970012	-0.0010022218	0.0033920589	0.1407906696	-2.286272e-02
0.0115117504	-0.0011211725	-0.0002549591	-0.0228627205	1.069917e-01
-0.0034299062	0.0045169851	0.0030080740	-0.0420030278	-3.002572e-02
-0.0020880710	-0.0008521845	-0.0088988247	-0.0374788962	-2.663943e-02
-0.0133854403	-0.0085222713	-0.0618389683	-0.0462481557	5.159438e-03
0.0922495421	-0.0037306178	-0.0296581971	0.0056789335	-2.767602e-02
-0.0064150666	0.0406810936	-0.0145578408	0.0147496924	9.484085e-03
-0.0410168313	-0.0138090712	0.2110348280	0.0191931125	1.080015e-02
0.0189441710	0.0105416530	0.0975417670	-0.0913671295	1.576411e-02
-0.1193893942	0.0050729944	0.0404832621	0.0160377018	-7.596599e-02
0.0107283400	-0.0487382052	0.0166439096	0.0322719142	2.399055e-02
0.0403061795	0.0114673746	-0.3465284760	0.0183331781	1.530134e-02
-0.0003138193	-0.0006671666	0.0027339907	-0.0032659214	-1.864083e-05
0.0067659440	-0.0005726100	0.0000333626	0.0001957909	-2.969134e-03
-0.0009585807	0.0081423905	0.0068915377	0.0059071292	4.404260e-03
-0.0011963837	-0.0020195148	-0.0188973131	-0.0003265022	8.651739e-05
0.0010770017	-0.0028448799	-0.0308240999	-0.0048706854	3.978516e-04
0.0288261683	-0.0009880553	-0.0103895660	0.0006047980	-3.078922e-03
0.0051290539	0.0425381838	-0.0263261141	0.0054666140	4.126056e-03

-0.0064310939	-0.0138033770	0.2932539021	-0.0020637710	-6.395668e-04	
-0.0010315134	0.0035525044	0.0344151709	0.0029796051	-3.912278e-04	
-0.0369965501	0.0015564646	0.0115881677	-0.0007040545	4.921347e-03	
-0.0049868857	-0.0513676031	0.0227106812	-0.0075922700	-6.167792e-03	
0.0067072418	0.0135653298	-0.3489096838	0.0056361985	1.550741e-03	
0.0007924853	-0.0005548973	-0.0040734208	-0.0302563131	7.942514e-03	
-0.0072037068	-0.0015637203	-0.0052136601	0.0075861027	-3.075352e-02	
-0.0007833930	0.0003018796	-0.0123086040	0.0104799047	8.203715e-03	
0.0008049234	-0.0001603018	-0.0268160003	0.0014269821	1.287728e-03	
0.0244478758	0.0079935766	0.0250158238	-0.0233704312	4.201409e-03	
-0.2191987175	0.00755580068	0.0330149286	0.0052909104	-2.827038e-02	
0.0080217961	-0.0770320848	0.0089504876	0.0043979191	3.485831e-03	
0.0353895251	0.0107155495	-0.2959519775	0.0087738144	8.881541e-03	
0.0020305479	0.0045797255	-1.980994e-01	0.0078073066	0.0102063142	
0.0013543036	0.0014978761	6.075710e-03	-0.0687311011	0.0029626691	
-0.0015186139	0.0005267360	5.407843e-03	0.0019779671	-0.0325504915	
-0.0025456149	-0.0237978676	1.841276e-01	0.0565346157	0.0422641267	
-0.0007124931	0.0028035524	1.496366e-01	-0.0136143474	-0.0142522175	
-0.0034299062	-0.0020880710	-1.338544e-02	0.0922495421	-0.0064150666	
0.0045169851	-0.0008521845	-8.522271e-03	-0.0037306178	0.0406810936	
0.0030080740	-0.0088988247	-6.183897e-02	-0.0296581971	-0.0145578408	
-0.0420030278	-0.0374788962	-4.624816e-02	0.0056789335	0.0147496924	
-0.0300257241	-0.0266394265	5.159438e-03	-0.0276760239	0.0094840853	
0.1718084526	-0.0494526993	1.537225e-02	0.0077831025	-0.0607035817	
-0.0494526993	0.1585909826	1.904074e-02	0.0088418845	0.0215914319	
0.0153722508	0.0190407350	9.145374e-01	-0.0668014199	-0.1176860809	
0.0077831025	0.0088418845	-6.680142e-02	0.3215796804	-0.0370742254	
-0.0607035817	0.0215914319	-1.176861e-01	-0.0370742254	0.6085968528	
0.0278206701	-0.0663303568	-4.807257e-01	-0.1381671907	-0.3107271639	
0.0312802546	0.0191538978	-4.635803e-01	0.0495094373	0.0711436767	
0.0225639360	0.0172948393	4.854106e-02	-0.2137723814	0.0235998902	
-0.1307969846	0.0344243907	6.743091e-02	0.0239238152	-0.3683467327	
0.0343035956	-0.0917555929	1.713166e-01	0.0650401894	0.1565394565	
0.0026361368	0.0005520898	-1.233563e-02	0.0005286044	0.0050599043	
0.0018306898	0.0005905866	8.828207e-05	-0.0068328922	0.0029809887	
-0.0269601665	0.0085506529	8.740781e-03	0.0027425457	-0.0521044107	
0.0100231951	-0.0099735877	7.719214e-03	0.0028308240	0.0176508644	
0.0029767060	0.0003022203	-1.638771e-01	0.0012566405	0.0285369530	
0.0011702958	0.0004960990	5.296996e-04	-0.0342591332	0.0060393209	
-0.0216164891	0.0043688967	3.849739e-02	0.0104258340	-0.3055965349	
0.0078809809	-0.0076458349	1.668007e-01	0.0455489802	0.1953557053	
-0.0041195445	0.0022932975	1.764678e-01	-0.0027174578	-0.0373721063	
-0.0026895340	-0.0005066030	-1.233410e-03	0.0432829004	-0.0098612167	
0.0300545227	-0.0053338500	-5.242853e-02	-0.0153484186	0.3636482428	
-0.0049405014	-0.0047913569	-1.543108e-01	-0.0464030121	-0.1943050371	
0.0110257996	0.0031221958	2.323909e-02	-0.0095204502	-0.0065092455	
0.0104701647	0.0049723134	-7.438347e-03	0.0245082784	-0.0046016531	
-0.0395963274	0.0089755435	-4.592797e-03	-0.0046054720	0.0056462534	
0.0015435686	-0.0054937043	-1.777478e-03	-0.0020498769	0.0005614384	
0.0040343291	0.0075599150	-4.487586e-02	0.0031110794	0.0013684638	
0.0063176806	0.0083299532	3.964997e-03	-0.0294235374	-0.0001360425	
-0.0192634126	0.0053647356	3.678396e-03	0.0010115479	-0.0196713847	
0.0052224958	-0.0372803569	3.207155e-02	0.0065124972	0.0160335874	
0.136684447	0.199389995	-0.014086615	-0.018868547	-0.092078439	-8.075292e-03
0.045684776	-0.013671191	0.095591557	-0.007591748	-0.043295161	1.324869e-04
0.016591212	-0.009238751	-0.003555370	0.044101605	-0.014590006	2.071072e-04

-0.517973431	-0.110748159	-0.054177923	-0.012509049	0.361106082	4.468277e-03
-0.062766574	-0.233719654	0.018352301	0.019035378	0.089135361	-4.131863e-04
-0.041016831	0.018944171	-0.119389394	0.010728340	0.040306179	-3.138193e-04
-0.013809071	0.010541653	0.005072994	-0.048738205	0.011467375	-6.671666e-04
0.211034828	0.097541767	0.040483262	0.016643910	-0.346528476	2.733991e-03
0.019193113	-0.091367130	0.016037702	0.032271914	0.018333178	-3.265921e-03
0.010800152	0.015764113	-0.075965988	0.023990547	0.015301337	-1.864083e-05
0.027820670	0.031280255	0.022563936	-0.130796985	0.034303596	2.636137e-03
-0.066330357	0.019153898	0.017294839	0.034424391	-0.091755593	5.520898e-04
-0.480725741	-0.463580280	0.048541056	0.067430908	0.171316639	-1.233563e-02
-0.138167191	0.049509437	-0.213772381	0.023923815	0.065040189	5.286044e-04
-0.310727164	0.071143677	0.023599890	-0.368346733	0.156539457	5.059904e-03
1.503918926	0.164600551	0.071204797	0.167381313	-0.677100460	4.695245e-03
0.164600551	1.252463499	-0.118296805	-0.192684682	-0.441662591	-5.307306e-03
0.071204797	-0.118296805	0.518281932	-0.073402417	-0.148750150	-3.581620e-04
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```

```

$dens
function (y)
sum(-lgamma(y + 1))
<environment: namespace:exactLoglinTest>

$dobs
[1] 50.26369 52.56769

$mu.hat
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       68        67        60        59        58        57
0.25072319 1.60473559 0.18105409 0.13394981 0.26096632 0.21080481
       55        54        53        52        50        49
1.97444067 0.52630855 1.21928164 6.54106633 5.63440188 2.92618991
       48        47        40        39        38        37
5.58172191 5.31553870 0.13185304 0.07554443 0.51708045 0.55718074
       35        34        33        32        30        29
0.79011836 0.16310491 1.32752883 9.50014868 1.78879234 0.71943767
       28        27        20        19        18        17
4.82138891 6.12481782 1.78671996 1.50458067 0.82331031 0.24350239
       80        79        78        77        76        71
1.03386967 1.05416634 0.33141537 1.79927933 5.78126929 5.50319734
       66        65        64        63        62        61
8.19200719 2.51212650 0.64784087 0.23712452 10.07938194 13.52352617
       56        51        46        45        44        43
0.21322497 1.73890282 8.54214760 2.21010335 0.41355173 0.93803014
       42        41        36        31        26        25
5.93259017 2.50572461 0.71834133 3.21909922 12.54556326 0.28923627
       24        23        22        21        16        15

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     8          7          6          5          4          3
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     2          1
0.98094241 7.80847529

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\$n  
[1] 80

\$n1  
[1] 40

\$nosim  
[1] 1000

\$s

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lake3	53
lake4	63
gender2	89
size2	95
food2	61
food3	19
food4	13
food5	32
lake2:food2	19
lake3:food2	18
lake4:food2	20
lake2:food3	7
lake3:food3	8
lake4:food3	1
lake2:food4	1
lake3:food4	4
lake4:food4	3
lake2:food5	3
lake3:food5	10
lake4:food5	6
gender2:food2	28
gender2:food3	6
gender2:food4	6
gender2:food5	14
size2:food2	16
size2:food3	13
size2:food4	8
size2:food5	13
lake2:gender2	17
lake3:gender2	13
lake4:gender2	24
lake2:size2	28
lake3:size2	29
lake4:size2	22
gender2:size2	22
lake2:gender2:size2	2
lake3:gender2:size2	1

```

lake4:gender2:size2    10

$stat
function (y = NULL, mu = NULL, rowlabels = FALSE)
{
  if (rowlabels)
    c("deviance", "Pearson")
  else {
    temp <- y != 0
    c(2 * sum(y[temp] * log(y[temp]/mu[temp])), sum((y -
      mu)^2/mu))
  }
}
<environment: namespace:exactLoglinTest>

$tdf
[1] 3

$x
  (Intercept) lake2 lake3 lake4 gender2 size2 food2 food3 food4 food5
75          1     0     0     1     1     0     0     0     0     1
74          1     0     0     1     1     0     0     0     0     0
73          1     0     0     1     1     0     0     0     1     0
72          1     0     0     1     1     0     1     0     0     0
70          1     0     0     1     0     1     0     0     0     1
69          1     0     0     1     0     1     0     0     0     1
68          1     0     0     1     0     1     0     1     0     0
67          1     0     0     1     0     1     1     0     0     0
60          1     0     1     0     1     1     0     0     0     1
59          1     0     1     0     1     1     0     0     0     1
58          1     0     1     0     1     1     0     1     0     0
57          1     0     1     0     1     1     1     0     0     0
55          1     0     1     0     1     0     0     0     0     1
54          1     0     1     0     1     0     0     0     0     0
53          1     0     1     0     1     0     0     0     1     0
52          1     0     1     0     1     0     1     0     0     0
50          1     0     1     0     0     1     0     0     0     1
49          1     0     1     0     0     1     0     0     0     1
48          1     0     1     0     0     1     0     1     0     0
47          1     0     1     0     0     1     1     0     0     0
40          1     1     0     0     1     1     0     0     0     1
39          1     1     0     0     1     1     0     0     0     1
38          1     1     0     0     1     1     0     1     0     0
37          1     1     0     0     1     1     1     0     0     0
35          1     1     0     0     1     0     0     0     0     1
34          1     1     0     0     1     0     0     0     0     0
33          1     1     0     0     1     0     0     0     1     0
32          1     1     0     0     1     0     1     0     0     0
30          1     1     0     0     0     1     0     0     0     1
29          1     1     0     0     0     1     0     0     0     1
28          1     1     0     0     0     1     0     1     0     0
27          1     1     0     0     0     1     1     1     0     0
20          1     0     0     0     1     1     0     0     0     1
19          1     0     0     0     1     1     0     0     0     1
18          1     0     0     0     1     1     0     1     0     0
17          1     0     0     0     1     1     1     0     0     0
80          1     0     0     1     1     1     0     0     0     1
79          1     0     0     1     1     1     0     0     1     0

```



52	0	1	0	0	0	0
50	0	0	0	0	0	0
49	0	0	0	0	0	0
48	0	0	0	0	1	0
47	0	1	0	0	0	0
40	0	0	0	0	0	0
39	0	0	0	0	0	0
38	0	0	0	1	0	0
37	1	0	0	0	0	0
35	0	0	0	0	0	0
34	0	0	0	0	0	0
33	0	0	0	1	0	0
32	1	0	0	0	0	0
30	0	0	0	0	0	0
29	0	0	0	0	0	0
28	0	0	0	1	0	0
27	1	0	0	0	0	0
20	0	0	0	0	0	0
19	0	0	0	0	0	0
18	0	0	0	0	0	0
17	0	0	0	0	0	0
80	0	0	0	0	0	0
79	0	0	0	0	0	0
78	0	0	0	0	0	1
77	0	0	1	0	0	0
76	0	0	0	0	0	0
71	0	0	0	0	0	0
66	0	0	0	0	0	0
65	0	0	0	0	0	0
64	0	0	0	0	0	0
63	0	0	0	0	0	1
62	0	0	1	0	0	0
61	0	0	0	0	0	0
56	0	0	0	0	0	0
51	0	0	0	0	0	0
46	0	0	0	0	0	0
45	0	0	0	0	0	0
44	0	0	0	0	0	0
43	0	0	0	0	1	0
42	0	1	0	0	0	0
41	0	0	0	0	0	0
36	0	0	0	0	0	0
31	0	0	0	0	0	0
26	0	0	0	0	0	0
25	0	0	0	0	0	0
24	0	0	0	0	0	0
23	0	0	0	1	0	0
22	1	0	0	0	0	0
21	0	0	0	0	0	0
16	0	0	0	0	0	0
15	0	0	0	0	0	0
14	0	0	0	0	0	0
13	0	0	0	0	0	0
12	0	0	0	0	0	0
11	0	0	0	0	0	0
10	0	0	0	0	0	0
9	0	0	0	0	0	0
8	0	0	0	0	0	0

	0	0	0	0	0	0
7	0	0	0	0	0	0
6	0	0	0	0	0	0
5	0	0	0	0	0	0
4	0	0	0	0	0	0
3	0	0	0	0	0	0
2	0	0	0	0	0	0
1	0	0	0	0	0	0
	lake2:food4 lake3:food4 lake4:food4 lake2:food5 lake3:food5 lake4:food5					
75	0	0	0	0	0	1
74	0	0	1	0	0	0
73	0	0	0	0	0	0
72	0	0	0	0	0	0
70	0	0	0	0	0	1
69	0	0	1	0	0	0
68	0	0	0	0	0	0
67	0	0	0	0	0	0
60	0	0	0	0	1	0
59	0	1	0	0	0	0
58	0	0	0	0	0	0
57	0	0	0	0	0	0
55	0	0	0	0	1	0
54	0	1	0	0	0	0
53	0	0	0	0	0	0
52	0	0	0	0	0	0
50	0	0	0	0	1	0
49	0	1	0	0	0	0
48	0	0	0	0	0	0
47	0	0	0	0	0	0
40	0	0	0	1	0	0
39	1	0	0	0	0	0
38	0	0	0	0	0	0
37	0	0	0	0	0	0
35	0	0	0	1	0	0
34	1	0	0	0	0	0
33	0	0	0	0	0	0
32	0	0	0	0	0	0
30	0	0	0	1	0	0
29	1	0	0	0	0	0
28	0	0	0	0	0	0
27	0	0	0	0	0	0
20	0	0	0	0	0	0
19	0	0	0	0	0	0
18	0	0	0	0	0	0
17	0	0	0	0	0	0
80	0	0	0	0	0	1
79	0	0	1	0	0	0
78	0	0	0	0	0	0
77	0	0	0	0	0	0
76	0	0	0	0	0	0
71	0	0	0	0	0	0
66	0	0	0	0	0	0
65	0	0	0	0	0	1
64	0	0	1	0	0	0
63	0	0	0	0	0	0
62	0	0	0	0	0	0
61	0	0	0	0	0	0
56	0	0	0	0	0	0
51	0	0	0	0	0	0

46	0	0	0	0	0	0
45	0	0	0	0	1	0
44	0	1	0	0	0	0
43	0	0	0	0	0	0
42	0	0	0	0	0	0
41	0	0	0	0	0	0
36	0	0	0	0	0	0
31	0	0	0	0	0	0
26	0	0	0	0	0	0
25	0	0	0	1	0	0
24	1	0	0	0	0	0
23	0	0	0	0	0	0
22	0	0	0	0	0	0
21	0	0	0	0	0	0
16	0	0	0	0	0	0
15	0	0	0	0	0	0
14	0	0	0	0	0	0
13	0	0	0	0	0	0
12	0	0	0	0	0	0
11	0	0	0	0	0	0
10	0	0	0	0	0	0
9	0	0	0	0	0	0
8	0	0	0	0	0	0
7	0	0	0	0	0	0
6	0	0	0	0	0	0
5	0	0	0	0	0	0
4	0	0	0	0	0	0
3	0	0	0	0	0	0
2	0	0	0	0	0	0
1	0	0	0	0	0	0
	gender2:food2	gender2:food3	gender2:food4	gender2:food5	size2:food2	
75	0	0	0	1	0	
74	0	0	1	0	0	
73	0	1	0	0	0	
72	1	0	0	0	0	
70	0	0	0	0	0	
69	0	0	0	0	0	
68	0	0	0	0	0	
67	0	0	0	0	1	
60	0	0	0	1	0	
59	0	0	1	0	0	
58	0	1	0	0	0	
57	1	0	0	0	1	
55	0	0	0	1	0	
54	0	0	1	0	0	
53	0	1	0	0	0	
52	1	0	0	0	0	
50	0	0	0	0	0	
49	0	0	0	0	0	
48	0	0	0	0	0	
47	0	0	0	0	1	
40	0	0	0	1	0	
39	0	0	1	0	0	
38	0	1	0	0	0	
37	1	0	0	0	1	
35	0	0	0	1	0	
34	0	0	1	0	0	
33	0	1	0	0	0	

	size2:food3	size2:food4	size2:food5	lake2:gender2	lake3:gender2
32	1	0	0	0	0
30	0	0	0	0	0
29	0	0	0	0	0
28	0	0	0	0	0
27	0	0	0	0	1
20	0	0	0	1	0
19	0	0	1	0	0
18	0	1	0	0	0
17	1	0	0	0	1
80	0	0	0	1	0
79	0	0	1	0	0
78	0	1	0	0	0
77	1	0	0	0	1
76	0	0	0	0	0
71	0	0	0	0	0
66	0	0	0	0	0
65	0	0	0	0	0
64	0	0	0	0	0
63	0	0	0	0	0
62	0	0	0	0	0
61	0	0	0	0	0
56	0	0	0	0	0
51	0	0	0	0	0
46	0	0	0	0	0
45	0	0	0	0	0
44	0	0	0	0	0
43	0	0	0	0	0
42	0	0	0	0	0
41	0	0	0	0	0
36	0	0	0	0	0
31	0	0	0	0	0
26	0	0	0	0	0
25	0	0	0	0	0
24	0	0	0	0	0
23	0	0	0	0	0
22	0	0	0	0	0
21	0	0	0	0	0
16	0	0	0	0	0
15	0	0	0	1	0
14	0	0	1	0	0
13	0	1	0	0	0
12	1	0	0	0	0
11	0	0	0	0	0
10	0	0	0	0	0
9	0	0	0	0	0
8	0	0	0	0	0
7	0	0	0	0	1
6	0	0	0	0	0
5	0	0	0	0	0
4	0	0	0	0	0
3	0	0	0	0	0
2	0	0	0	0	0
1	0	0	0	0	0

70	0	0	1	0	0
69	0	1	0	0	0
68	1	0	0	0	0
67	0	0	0	0	0
60	0	0	1	0	1
59	0	1	0	0	1
58	1	0	0	0	1
57	0	0	0	0	1
55	0	0	0	0	1
54	0	0	0	0	1
53	0	0	0	0	1
52	0	0	0	0	1
50	0	0	1	0	0
49	0	1	0	0	0
48	1	0	0	0	0
47	0	0	0	0	0
40	0	0	1	1	0
39	0	1	0	1	0
38	1	0	0	1	0
37	0	0	0	1	0
35	0	0	0	1	0
34	0	0	0	1	0
33	0	0	0	1	0
32	0	0	0	1	0
30	0	0	1	0	0
29	0	1	0	0	0
28	1	0	0	0	0
27	0	0	0	0	0
20	0	0	1	0	0
19	0	1	0	0	0
18	1	0	0	0	0
17	0	0	0	0	0
80	0	0	1	0	0
79	0	1	0	0	0
78	1	0	0	0	0
77	0	0	0	0	0
76	0	0	0	0	0
71	0	0	0	0	0
66	0	0	0	0	0
65	0	0	0	0	0
64	0	0	0	0	0
63	0	0	0	0	0
62	0	0	0	0	0
61	0	0	0	0	0
56	0	0	0	0	1
51	0	0	0	0	1
46	0	0	0	0	0
45	0	0	0	0	0
44	0	0	0	0	0
43	0	0	0	0	0
42	0	0	0	0	0
41	0	0	0	0	0
36	0	0	0	1	0
31	0	0	0	1	0
26	0	0	0	0	0
25	0	0	0	0	0
24	0	0	0	0	0
23	0	0	0	0	0

22	0	0	0	0	0
21	0	0	0	0	0
16	0	0	0	0	0
15	0	0	0	0	0
14	0	0	0	0	0
13	0	0	0	0	0
12	0	0	0	0	0
11	0	0	0	0	0
10	0	0	1	0	0
9	0	1	0	0	0
8	1	0	0	0	0
7	0	0	0	0	0
6	0	0	0	0	0
5	0	0	0	0	0
4	0	0	0	0	0
3	0	0	0	0	0
2	0	0	0	0	0
1	0	0	0	0	0
		lake4:gender2	lake2:size2	lake3:size2	lake4:size2
75	1	0	0	0	0
74	1	0	0	0	0
73	1	0	0	0	0
72	1	0	0	0	0
70	0	0	0	1	0
69	0	0	0	1	0
68	0	0	0	1	0
67	0	0	0	1	0
60	0	0	1	0	1
59	0	0	1	0	1
58	0	0	1	0	1
57	0	0	1	0	1
55	0	0	0	0	0
54	0	0	0	0	0
53	0	0	0	0	0
52	0	0	0	0	0
50	0	0	1	0	0
49	0	0	1	0	0
48	0	0	1	0	0
47	0	0	1	0	0
40	0	1	0	0	1
39	0	1	0	0	1
38	0	1	0	0	1
37	0	1	0	0	1
35	0	0	0	0	0
34	0	0	0	0	0
33	0	0	0	0	0
32	0	0	0	0	0
30	0	1	0	0	0
29	0	1	0	0	0
28	0	1	0	0	0
27	0	1	0	0	0
20	0	0	0	0	1
19	0	0	0	0	1
18	0	0	0	0	1
17	0	0	0	0	1
80	1	0	0	1	1
79	1	0	0	1	1
78	1	0	0	1	1

77	1	0	0	1	1
76	1	0	0	1	1
71	1	0	0	0	0
66	0	0	0	1	0
65	0	0	0	0	0
64	0	0	0	0	0
63	0	0	0	0	0
62	0	0	0	0	0
61	0	0	0	0	0
56	0	0	1	0	1
51	0	0	0	0	0
46	0	0	1	0	0
45	0	0	0	0	0
44	0	0	0	0	0
43	0	0	0	0	0
42	0	0	0	0	0
41	0	0	0	0	0
36	0	1	0	0	1
31	0	0	0	0	0
26	0	1	0	0	0
25	0	0	0	0	0
24	0	0	0	0	0
23	0	0	0	0	0
22	0	0	0	0	0
21	0	0	0	0	0
16	0	0	0	0	1
15	0	0	0	0	0
14	0	0	0	0	0
13	0	0	0	0	0
12	0	0	0	0	0
11	0	0	0	0	0
10	0	0	0	0	0
9	0	0	0	0	0
8	0	0	0	0	0
7	0	0	0	0	0
6	0	0	0	0	0
5	0	0	0	0	0
4	0	0	0	0	0
3	0	0	0	0	0
2	0	0	0	0	0
1	0	0	0	0	0
		lake2:gender2:size2	lake3:gender2:size2	lake4:gender2:size2	
75		0	0	0	
74		0	0	0	
73		0	0	0	
72		0	0	0	
70		0	0	0	
69		0	0	0	
68		0	0	0	
67		0	0	0	
60		0	1	0	
59		0	1	0	
58		0	1	0	
57		0	1	0	
55		0	0	0	
54		0	0	0	
53		0	0	0	
52		0	0	0	

50	0	0	0
49	0	0	0
48	0	0	0
47	0	0	0
40	1	0	0
39	1	0	0
38	1	0	0
37	1	0	0
35	0	0	0
34	0	0	0
33	0	0	0
32	0	0	0
30	0	0	0
29	0	0	0
28	0	0	0
27	0	0	0
20	0	0	0
19	0	0	0
18	0	0	0
17	0	0	0
80	0	0	1
79	0	0	1
78	0	0	1
77	0	0	1
76	0	0	1
71	0	0	0
66	0	0	0
65	0	0	0
64	0	0	0
63	0	0	0
62	0	0	0
61	0	0	0
56	0	1	0
51	0	0	0
46	0	0	0
45	0	0	0
44	0	0	0
43	0	0	0
42	0	0	0
41	0	0	0
36	1	0	0
31	0	0	0
26	0	0	0
25	0	0	0
24	0	0	0
23	0	0	0
22	0	0	0
21	0	0	0
16	0	0	0
15	0	0	0
14	0	0	0
13	0	0	0
12	0	0	0
11	0	0	0
10	0	0	0
9	0	0	0
8	0	0	0
7	0	0	0

6	0	0	0	0	0	0	0	0	0
5	0	0	0	0	0	0	0	0	0
4	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0
1	0	0	0	0	0	0	0	0	0
 \$x1									
(Intercept) lake2 lake3 lake4 gender2 size2 food2 food3 food4 food5									
75	1	0	0	1	1	0	0	0	0
74	1	0	0	1	1	0	0	0	1
73	1	0	0	1	1	0	0	1	0
72	1	0	0	1	1	0	1	0	0
70	1	0	0	1	0	1	0	0	0
69	1	0	0	1	0	1	0	0	1
68	1	0	0	1	0	1	0	1	0
67	1	0	0	1	0	1	1	0	0
60	1	0	1	0	1	1	0	0	0
59	1	0	1	0	1	1	0	0	1
58	1	0	1	0	1	1	0	1	0
57	1	0	1	0	1	1	1	0	0
55	1	0	1	0	1	0	0	0	0
54	1	0	1	0	1	0	0	0	1
53	1	0	1	0	1	0	0	1	0
52	1	0	1	0	1	0	1	0	0
50	1	0	1	0	0	1	0	0	0
49	1	0	1	0	0	1	0	0	1
48	1	0	1	0	0	1	0	1	0
47	1	0	1	0	0	1	1	0	0
40	1	1	0	0	1	1	0	0	0
39	1	1	0	0	1	1	0	0	1
38	1	1	0	0	1	1	0	1	0
37	1	1	0	0	1	1	1	0	0
35	1	1	0	0	1	0	0	0	0
34	1	1	0	0	1	0	0	0	1
33	1	1	0	0	1	0	0	1	0
32	1	1	0	0	1	0	1	0	0
30	1	1	0	0	0	1	0	0	0
29	1	1	0	0	0	1	0	0	1
28	1	1	0	0	0	1	0	1	0
27	1	1	0	0	0	1	1	0	0
20	1	0	0	0	1	1	0	0	0
19	1	0	0	0	1	1	0	0	1
18	1	0	0	0	1	1	0	1	0
17	1	0	0	0	1	1	1	0	0
80	1	0	0	1	1	1	0	0	0
79	1	0	0	1	1	1	0	0	1
78	1	0	0	1	1	1	0	1	0
77	1	0	0	1	1	1	1	0	0
lake2:food2 lake3:food2 lake4:food2 lake2:food3 lake3:food3 lake4:food3									
75	0	0	0	0	0	0	0	0	0
74	0	0	0	0	0	0	0	0	0
73	0	0	0	0	0	0	0	0	1
72	0	0	1	0	0	0	0	0	0
70	0	0	0	0	0	0	0	0	0
69	0	0	0	0	0	0	0	0	0
68	0	0	0	0	0	0	0	0	1
67	0	0	1	0	0	0	0	0	0

	0	0	0	0	0	0
60	0	0	0	0	0	0
59	0	0	0	0	0	0
58	0	0	0	0	1	0
57	0	1	0	0	0	0
55	0	0	0	0	0	0
54	0	0	0	0	0	0
53	0	0	0	0	1	0
52	0	1	0	0	0	0
50	0	0	0	0	0	0
49	0	0	0	0	0	0
48	0	0	0	0	1	0
47	0	1	0	0	0	0
40	0	0	0	0	0	0
39	0	0	0	0	0	0
38	0	0	0	1	0	0
37	1	0	0	0	0	0
35	0	0	0	0	0	0
34	0	0	0	0	0	0
33	0	0	0	1	0	0
32	1	0	0	0	0	0
30	0	0	0	0	0	0
29	0	0	0	0	0	0
28	0	0	0	1	0	0
27	1	0	0	0	0	0
20	0	0	0	0	0	0
19	0	0	0	0	0	0
18	0	0	0	0	0	0
17	0	0	0	0	0	0
80	0	0	0	0	0	0
79	0	0	0	0	0	0
78	0	0	0	0	0	1
77	0	0	1	0	0	0
	lake2:food4 lake3:food4 lake4:food4 lake2:food5 lake3:food5 lake4:food5					
75	0	0	0	0	0	1
74	0	0	1	0	0	0
73	0	0	0	0	0	0
72	0	0	0	0	0	0
70	0	0	0	0	0	1
69	0	0	1	0	0	0
68	0	0	0	0	0	0
67	0	0	0	0	0	0
60	0	0	0	0	1	0
59	0	1	0	0	0	0
58	0	0	0	0	0	0
57	0	0	0	0	0	0
55	0	0	0	0	1	0
54	0	1	0	0	0	0
53	0	0	0	0	0	0
52	0	0	0	0	0	0
50	0	0	0	0	1	0
49	0	1	0	0	0	0
48	0	0	0	0	0	0
47	0	0	0	0	0	0
40	0	0	0	1	0	0
39	1	0	0	0	0	0
38	0	0	0	0	0	0
37	0	0	0	0	0	0
35	0	0	0	1	0	0

34	1	0	0	0	0	0
33	0	0	0	0	0	0
32	0	0	0	0	0	0
30	0	0	0	1	0	0
29	1	0	0	0	0	0
28	0	0	0	0	0	0
27	0	0	0	0	0	0
20	0	0	0	0	0	0
19	0	0	0	0	0	0
18	0	0	0	0	0	0
17	0	0	0	0	0	0
80	0	0	0	0	0	1
79	0	0	1	0	0	0
78	0	0	0	0	0	0
77	0	0	0	0	0	0
	gender2:food2	gender2:food3	gender2:food4	gender2:food5	size2:food2	
75	0	0	0	1	0	
74	0	0	1	0	0	
73	0	1	0	0	0	
72	1	0	0	0	0	
70	0	0	0	0	0	
69	0	0	0	0	0	
68	0	0	0	0	0	
67	0	0	0	0	0	1
60	0	0	0	1	0	
59	0	0	1	0	0	
58	0	1	0	0	0	
57	1	0	0	0	0	1
55	0	0	0	1	0	
54	0	0	1	0	0	
53	0	1	0	0	0	
52	1	0	0	0	0	
50	0	0	0	0	0	
49	0	0	0	0	0	
48	0	0	0	0	0	
47	0	0	0	0	0	1
40	0	0	0	1	0	
39	0	0	1	0	0	
38	0	1	0	0	0	
37	1	0	0	0	0	1
35	0	0	0	1	0	
34	0	0	1	0	0	
33	0	1	0	0	0	
32	1	0	0	0	0	
30	0	0	0	0	0	
29	0	0	0	0	0	
28	0	0	0	0	0	
27	0	0	0	0	0	1
20	0	0	0	1	0	
19	0	0	1	0	0	
18	0	1	0	0	0	
17	1	0	0	0	0	1
80	0	0	0	1	0	
79	0	0	1	0	0	
78	0	1	0	0	0	
77	1	0	0	0	0	1
	size2:food3	size2:food4	size2:food5	lake2:gender2	lake3:gender2	
75	0	0	0	0	0	

74	0	0	0	0	0
73	0	0	0	0	0
72	0	0	0	0	0
70	0	0	1	0	0
69	0	1	0	0	0
68	1	0	0	0	0
67	0	0	0	0	0
60	0	0	1	0	1
59	0	1	0	0	1
58	1	0	0	0	1
57	0	0	0	0	1
55	0	0	0	0	1
54	0	0	0	0	1
53	0	0	0	0	1
52	0	0	0	0	1
50	0	0	1	0	0
49	0	1	0	0	0
48	1	0	0	0	0
47	0	0	0	0	0
40	0	0	1	1	0
39	0	1	0	1	0
38	1	0	0	1	0
37	0	0	0	1	0
35	0	0	0	1	0
34	0	0	0	1	0
33	0	0	0	1	0
32	0	0	0	1	0
30	0	0	1	0	0
29	0	1	0	0	0
28	1	0	0	0	0
27	0	0	0	0	0
20	0	0	1	0	0
19	0	1	0	0	0
18	1	0	0	0	0
17	0	0	0	0	0
80	0	0	1	0	0
79	0	1	0	0	0
78	1	0	0	0	0
77	0	0	0	0	0
lake4:gender2 lake2:size2 lake3:size2 lake4:size2 gender2:size2					
75	1	0	0	0	0
74	1	0	0	0	0
73	1	0	0	0	0
72	1	0	0	0	0
70	0	0	0	1	0
69	0	0	0	1	0
68	0	0	0	1	0
67	0	0	0	1	0
60	0	0	1	0	1
59	0	0	1	0	1
58	0	0	1	0	1
57	0	0	1	0	1
55	0	0	0	0	0
54	0	0	0	0	0
53	0	0	0	0	0
52	0	0	0	0	0
50	0	0	1	0	0
49	0	0	1	0	0

48	0	0	1	0	0
47	0	0	1	0	0
40	0	1	0	0	1
39	0	1	0	0	1
38	0	1	0	0	1
37	0	1	0	0	1
35	0	0	0	0	0
34	0	0	0	0	0
33	0	0	0	0	0
32	0	0	0	0	0
30	0	1	0	0	0
29	0	1	0	0	0
28	0	1	0	0	0
27	0	1	0	0	0
20	0	0	0	0	1
19	0	0	0	0	1
18	0	0	0	0	1
17	0	0	0	0	1
80	1	0	0	1	1
79	1	0	0	1	1
78	1	0	0	1	1
77	1	0	0	1	1
lake2:gender2:size2 lake3:gender2:size2 lake4:gender2:size2					
75	0	0	0	0	0
74	0	0	0	0	0
73	0	0	0	0	0
72	0	0	0	0	0
70	0	0	0	0	0
69	0	0	0	0	0
68	0	0	0	0	0
67	0	0	0	0	0
60	0	1	0	0	0
59	0	1	0	0	0
58	0	1	0	0	0
57	0	1	0	0	0
55	0	0	0	0	0
54	0	0	0	0	0
53	0	0	0	0	0
52	0	0	0	0	0
50	0	0	0	0	0
49	0	0	0	0	0
48	0	0	0	0	0
47	0	0	0	0	0
40	1	0	0	0	0
39	1	0	0	0	0
38	1	0	0	0	0
37	1	0	0	0	0
35	0	0	0	0	0
34	0	0	0	0	0
33	0	0	0	0	0
32	0	0	0	0	0
30	0	0	0	0	0
29	0	0	0	0	0
28	0	0	0	0	0
27	0	0	0	0	0
20	0	0	0	0	0
19	0	0	0	0	0
18	0	0	0	0	0

17	0	0	0	0
80	0	0	0	1
79	0	0	0	1
78	0	0	0	1
77	0	0	0	1

\$x2invt

	(Intercept)	lake2	lake3	lake4	gender2	size2	food2	food3	food4	food5
76	0	0	0	0	0	0	0	0	0	0
71	0	0	0	0	0	0	0	0	0	0
66	0	0	0	0	0	0	0	0	0	0
65	0	0	0	0	0	0	0	0	0	0
64	0	0	0	0	0	0	0	0	0	0
63	0	0	0	0	0	0	0	0	0	0
62	0	0	0	0	0	0	0	0	0	0
61	0	0	0	1	0	0	0	0	0	0
56	0	0	0	0	0	0	0	0	0	0
51	0	0	0	0	0	0	0	0	0	0
46	0	0	0	0	0	0	0	0	0	0
45	0	0	0	0	0	0	0	0	0	0
44	0	0	0	0	0	0	0	0	0	0
43	0	0	0	0	0	0	0	0	0	0
42	0	0	0	0	0	0	0	0	0	0
41	0	0	1	0	0	0	0	0	0	0
36	0	0	0	0	0	0	0	0	0	0
31	0	0	0	0	0	0	0	0	0	0
26	0	0	0	0	0	0	0	0	0	0
25	0	0	0	0	0	0	0	0	0	0
24	0	0	0	0	0	0	0	0	0	0
23	0	0	0	0	0	0	0	0	0	0
22	0	0	0	0	0	0	0	0	0	0
21	0	1	0	0	0	0	0	0	0	0
16	0	0	0	0	0	0	0	0	0	0
15	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	0	0	0	0	0	0
13	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0
11	0	0	0	0	1	0	0	0	0	0
10	0	0	0	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0
8	0	0	0	0	0	0	0	0	0	0
7	0	0	0	0	0	0	0	0	0	0
6	0	0	0	0	0	1	0	0	0	0
5	0	0	0	0	0	0	0	0	0	1
4	0	0	0	0	0	0	0	0	1	0
3	0	0	0	0	0	0	0	1	0	0
2	0	0	0	0	0	0	1	0	0	0
1	1	-1	-1	-1	-1	-1	-1	-1	-1	-1
	lake2:food2	lake3:food2	lake4:food2	lake2:food3	lake3:food3	lake4:food3				
76	0	0	0	0	0	0	0	0	0	0
71	0	0	0	0	0	0	0	0	0	0
66	0	0	0	0	0	0	0	0	0	0
65	0	0	0	0	0	0	0	0	0	0
64	0	0	0	0	0	0	0	0	0	0
63	0	0	0	0	0	0	0	0	0	1
62	0	0	0	1	0	0	0	0	0	0
61	0	0	-1	0	0	0	0	0	-1	0
56	0	0	0	0	0	0	0	0	0	0

51	0	0	0	0	0	0
46	0	0	0	0	0	0
45	0	0	0	0	0	0
44	0	0	0	0	0	0
43	0	0	0	0	1	0
42	0	1	0	0	0	0
41	0	-1	0	0	-1	0
36	0	0	0	0	0	0
31	0	0	0	0	0	0
26	0	0	0	0	0	0
25	0	0	0	0	0	0
24	0	0	0	0	0	0
23	0	0	0	1	0	0
22	1	0	0	0	0	0
21	-1	0	0	-1	0	0
16	0	0	0	0	0	0
15	0	0	0	0	0	0
14	0	0	0	0	0	0
13	0	0	0	0	0	0
12	0	0	0	0	0	0
11	0	0	0	0	0	0
10	0	0	0	0	0	0
9	0	0	0	0	0	0
8	0	0	0	0	0	0
7	0	0	0	0	0	0
6	0	0	0	0	0	0
5	0	0	0	0	0	0
4	0	0	0	0	0	0
3	0	0	0	-1	-1	-1
2	-1	-1	-1	0	0	0
1	1	1	1	1	1	1
	lake2:food4	lake3:food4	lake4:food4	lake2:food5	lake3:food5	lake4:food5
76	0	0	0	0	0	0
71	0	0	0	0	0	0
66	0	0	0	0	0	0
65	0	0	0	0	0	1
64	0	0	1	0	0	0
63	0	0	0	0	0	0
62	0	0	0	0	0	0
61	0	0	-1	0	0	-1
56	0	0	0	0	0	0
51	0	0	0	0	0	0
46	0	0	0	0	0	0
45	0	0	0	0	1	0
44	0	1	0	0	0	0
43	0	0	0	0	0	0
42	0	0	0	0	0	0
41	0	-1	0	0	-1	0
36	0	0	0	0	0	0
31	0	0	0	0	0	0
26	0	0	0	0	0	0
25	0	0	0	1	0	0
24	1	0	0	0	0	0
23	0	0	0	0	0	0
22	0	0	0	0	0	0
21	-1	0	0	-1	0	0
16	0	0	0	0	0	0
15	0	0	0	0	0	0

14	0	0	0	0	0	0
13	0	0	0	0	0	0
12	0	0	0	0	0	0
11	0	0	0	0	0	0
10	0	0	0	0	0	0
9	0	0	0	0	0	0
8	0	0	0	0	0	0
7	0	0	0	0	0	0
6	0	0	0	0	0	0
5	0	0	0	-1	-1	-1
4	-1	-1	-1	0	0	0
3	0	0	0	0	0	0
2	0	0	0	0	0	0
1	1	1	1	1	1	1
	gender2:food2	gender2:food3	gender2:food4	gender2:food5	size2:food2	
76	0	0	0	0	0	0
71	0	0	0	0	0	0
66	0	0	0	0	0	0
65	0	0	0	0	0	0
64	0	0	0	0	0	0
63	0	0	0	0	0	0
62	0	0	0	0	0	0
61	0	0	0	0	0	0
56	0	0	0	0	0	0
51	0	0	0	0	0	0
46	0	0	0	0	0	0
45	0	0	0	0	0	0
44	0	0	0	0	0	0
43	0	0	0	0	0	0
42	0	0	0	0	0	0
41	0	0	0	0	0	0
36	0	0	0	0	0	0
31	0	0	0	0	0	0
26	0	0	0	0	0	0
25	0	0	0	0	0	0
24	0	0	0	0	0	0
23	0	0	0	0	0	0
22	0	0	0	0	0	0
21	0	0	0	0	0	0
16	0	0	0	0	0	0
15	0	0	0	1	0	0
14	0	0	1	0	0	0
13	0	1	0	0	0	0
12	1	0	0	0	0	0
11	-1	-1	-1	-1	-1	0
10	0	0	0	0	0	0
9	0	0	0	0	0	0
8	0	0	0	0	0	0
7	0	0	0	0	0	1
6	0	0	0	0	0	-1
5	0	0	0	-1	0	0
4	0	0	-1	0	0	0
3	0	-1	0	0	0	0
2	-1	0	0	0	0	-1
1	1	1	1	1	1	1
	size2:food3	size2:food4	size2:food5	lake2:gender2	lake3:gender2	
76	0	0	0	0	0	0
71	0	0	0	0	0	0

66	0	0	0	0	0
65	0	0	0	0	0
64	0	0	0	0	0
63	0	0	0	0	0
62	0	0	0	0	0
61	0	0	0	0	0
56	0	0	0	0	0
51	0	0	0	0	1
46	0	0	0	0	0
45	0	0	0	0	0
44	0	0	0	0	0
43	0	0	0	0	0
42	0	0	0	0	0
41	0	0	0	0	-1
36	0	0	0	0	0
31	0	0	0	1	0
26	0	0	0	0	0
25	0	0	0	0	0
24	0	0	0	0	0
23	0	0	0	0	0
22	0	0	0	0	0
21	0	0	0	-1	0
16	0	0	0	0	0
15	0	0	0	0	0
14	0	0	0	0	0
13	0	0	0	0	0
12	0	0	0	0	0
11	0	0	0	-1	-1
10	0	0	1	0	0
9	0	1	0	0	0
8	1	0	0	0	0
7	0	0	0	0	0
6	-1	-1	-1	0	0
5	0	0	-1	0	0
4	0	-1	0	0	0
3	-1	0	0	0	0
2	0	0	0	0	0
1	1	1	1	1	1
				lake4:gender2	lake2:size2
76	0	0	0	0	0
71	1	0	0	0	0
66	0	0	0	1	0
65	0	0	0	0	0
64	0	0	0	0	0
63	0	0	0	0	0
62	0	0	0	0	0
61	-1	0	0	-1	0
56	0	0	0	0	0
51	0	0	0	0	0
46	0	0	1	0	0
45	0	0	0	0	0
44	0	0	0	0	0
43	0	0	0	0	0
42	0	0	0	0	0
41	0	0	-1	0	0
36	0	0	0	0	0
31	0	0	0	0	0
26	0	1	0	0	0

25	0	0	0	0	0
24	0	0	0	0	0
23	0	0	0	0	0
22	0	0	0	0	0
21	0	-1	0	0	0
16	0	0	0	0	1
15	0	0	0	0	0
14	0	0	0	0	0
13	0	0	0	0	0
12	0	0	0	0	0
11	-1	0	0	0	-1
10	0	0	0	0	0
9	0	0	0	0	0
8	0	0	0	0	0
7	0	0	0	0	0
6	0	-1	-1	-1	-1
5	0	0	0	0	0
4	0	0	0	0	0
3	0	0	0	0	0
2	0	0	0	0	0
1	1	1	1	1	1
		lake2:gender2:size2	lake3:gender2:size2	lake4:gender2:size2	
76	0	0	0	1	
71	0	0	0	-1	
66	0	0	0	-1	
65	0	0	0	0	
64	0	0	0	0	
63	0	0	0	0	
62	0	0	0	0	
61	0	0	0	1	
56	0	1	0	0	
51	0	-1	0	0	
46	0	-1	0	0	
45	0	0	0	0	
44	0	0	0	0	
43	0	0	0	0	
42	0	0	0	0	
41	0	1	0	0	
36	1	0	0	0	
31	-1	0	0	0	
26	-1	0	0	0	
25	0	0	0	0	
24	0	0	0	0	
23	0	0	0	0	
22	0	0	0	0	
21	1	0	0	0	
16	-1	-1	-1	-1	
15	0	0	0	0	
14	0	0	0	0	
13	0	0	0	0	
12	0	0	0	0	
11	1	1	1	1	
10	0	0	0	0	
9	0	0	0	0	
8	0	0	0	0	
7	0	0	0	0	
6	1	1	1	1	
5	0	0	0	0	

```

4          0          0          0
3          0          0          0
2          0          0          0
1         -1         -1         -1

$y
75 74 73 72 70 69 68 67 60 59 58 57 55 54 53 52 50 49 48 47 40 39 38 37 35 34
 1  0  1  9  2  1  0  0  0  0  0  1  4  1  1  4  5  3  6  6  0  1  0  1  2  0
33 32 30 29 28 27 20 19 18 17 80 79 78 77 76 71 66 65 64 63 62 61 56 51 46 45
 1  9  0  0  6  7  3  2  1  0  1  0  0  1  8  3  9  2  2  0 10 13  0  2  8  1
44 43 42 41 36 31 26 25 24 23 22 21 16 15 14 13 12 11 10  9  8  7  6  5  4  3
 0  1  7  3  0  3 13  1  0  0  2  2  3  3  2  2  3 16  2  1  0  0  4  5  0  0
 2  1
 1  7

$ord
 [1] 75 74 73 72 70 69 68 67 60 59 58 57 55 54 53 52 50 49 48 47 40 39 38 37 35
[26] 34 33 32 30 29 28 27 20 19 18 17 80 79 78 77 76 71 66 65 64 63 62 61 56 51
[51] 46 45 44 43 42 41 36 31 26 25 24 23 22 21 16 15 14 13 12 11 10  9  8  7  6
[76]  5  4  3  2  1

$glm.fit

Call: glm(formula = formula, family = poisson, data = data, x = TRUE,
          y = TRUE)

Coefficients:
(Intercept)      lake2       lake3
 2.05521     -1.63848    -1.13663
  lake4       gender2      size2
 0.54922      0.52380    -0.58146
 food2        food3       food4
-2.07445     -2.91414    -2.46327
 food5       lake2:food2  lake3:food2
-0.91673      2.69369     2.93633
 lake4:food2   lake2:food3  lake3:food3
 1.78051      1.40080     1.93159
 lake4:food3   lake2:food4  lake3:food4
 -1.12946     -1.12562     0.66172
 lake4:food4   lake2:food5  lake3:food5
 -0.57527     -0.74052     0.79119
 lake4:food5   gender2:food2 gender2:food3
 -0.76658      0.46296     0.62756
 gender2:food4  gender2:food5 size2:food2
  0.60643      0.25257    -1.33626
 size2:food3   size2:food4  size2:food5
  0.55704      0.73024    -0.29058
 lake2:gender2  lake3:gender2  lake4:gender2
  0.22857     -0.88912    -1.42290
 lake2:size2    lake3:size2  lake4:size2
  2.69410      1.80790     0.08019
 gender2:size2 lake2:gender2:size2 lake3:gender2:size2
 -0.46243     -3.15012    -2.86267
 lake4:gender2:size2
  1.01299

Degrees of Freedom: 79 Total (i.e. Null);  40 Residual
Null Deviance:      307.2

```

```

Residual Deviance: 50.26          AIC: 293.7

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[1] 100

$startiter
[1] 1001

$mhap
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$chain
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[982,] 38.35763 37.72696
[983,] 38.35763 37.72696
[984,] 38.35763 37.72696
[985,] 38.35763 37.72696
[986,] 38.35763 37.72696
[987,] 38.35763 37.72696
[988,] 38.35763 37.72696
[989,] 38.35763 37.72696
[990,] 38.35763 37.72696
[991,] 38.35763 37.72696
[992,] 38.35763 37.72696
[993,] 38.35763 37.72696
[994,] 38.35763 37.72696
[995,] 38.35763 37.72696
[996,] 38.35763 37.72696
[997,] 38.35763 37.72696
[998,] 38.35763 37.72696
[999,] 38.35763 37.72696
[1000,] 38.35763 37.72696

$current.batchmean
[1] 0 0

$bmsq
[1] 2.1117 2.1117

$nobatches
[1] 10

$phat
[1] 0.251 0.251

$mcse
[1] 0.1217247 0.1217247

$y1.start
[1] 0 0 0 8 2 1 0 1 0 0 0 0 2 0 1 7 5 4 6 4 0 0 1 1 1 0 1 9 1 1 5 6 3 0 2 0 1 2
[39] 0 3

$perpos
[1] 0.02

attr(,"class")
[1] "cabSummary"

```

The chain of goodness of fit statistics are saved in `alligator.mcx$chain`. The saved chain is discarded if the simulations are resumed with `update`, even if `savechain = T` when the simulation is resumed.

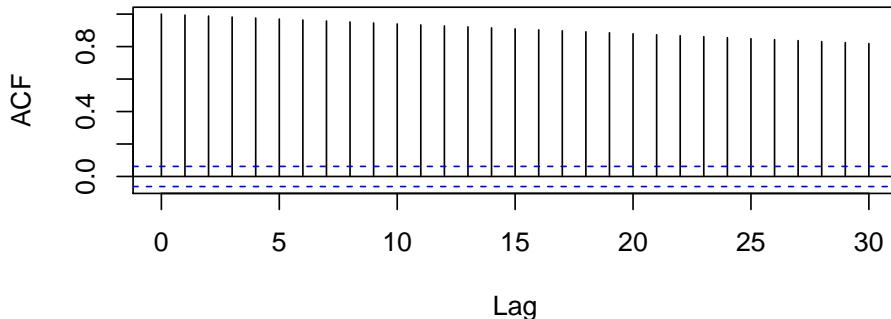
We would want to look at the autocorrelation function of the goodness of fit statistics.

```

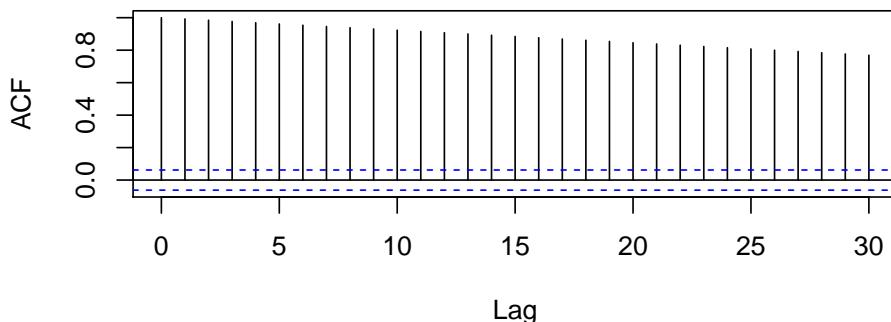
> par(mfrow = c(2, 1))
> acf(alligator.mcx$chain[, 1])
> acf(alligator.mcx$chain[, 2])

```

**Series alligator.mcx\$chain[, 1]**



**Series alligator.mcx\$chain[, 2]**

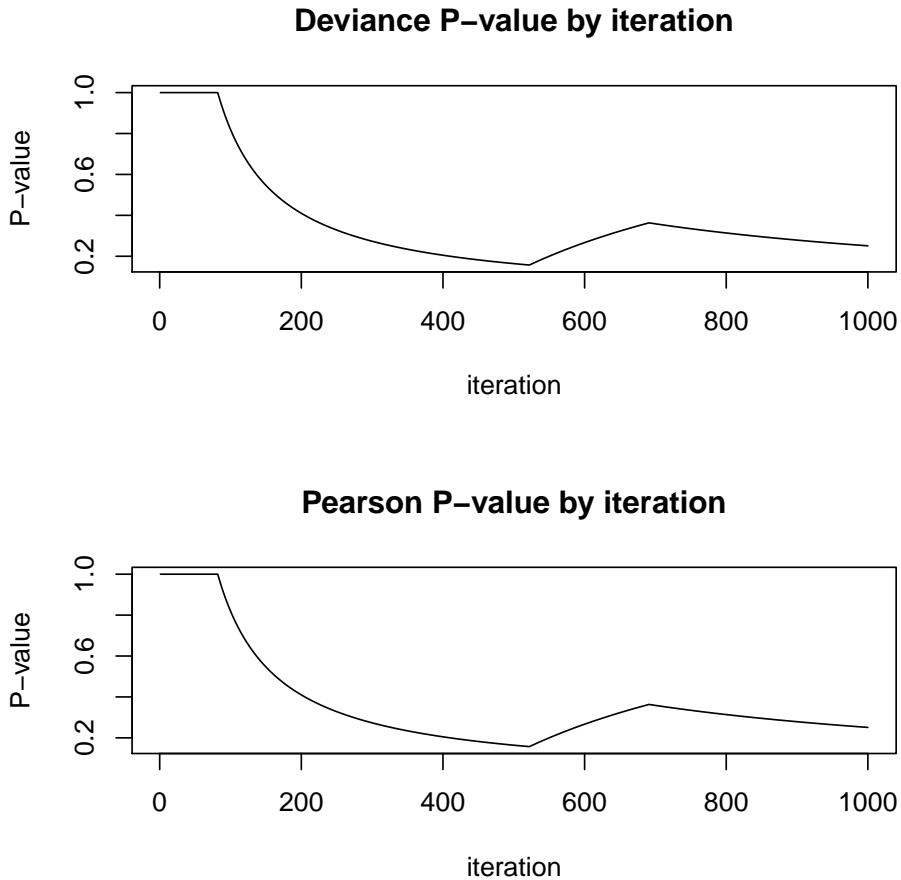


We would also want to look at the chain of P-values.

```

> dev.p <- cumsum(alligator.mcx$chain[, 1] >= alligator.mcx$dobs[1]) / (1 : alligator.mcx$nosim)
> pearson.p <- cumsum(alligator.mcx$chain[, 1] >= alligator.mcx$dobs[1]) / (1 : alligator.mcx$nosim)
> par(mfrow = c(2, 1))
> plot(dev.p, type = "l", ylab = "P-value", xlab = "iteration")
> title("Deviance P-value by iteration")
> plot(pearson.p, type = "l", ylab = "P-value", xlab = "iteration")
> title("Pearson P-value by iteration")

```



The P-values have apparently not stabilized. Also, there is an extremely slow decay in the autocorrelations of the chain of goodness of fit statistics. Therefore, we should execute a longer run using large batch sizes. While on the subject of batch sizes, note that `mctest` does not require the total number of simulations to be a multiple of the batch size. If the algorithm terminates in the middle of completing a batch, it is not used in the P-value calculations. However, the simulations are not wasted if the algorithm is resumed with `update`.

One large final run of this data discarding all of the initial tinkering could be performed by setting `flush = TRUE` as an argument to `update`. Here, `flush = TRUE`, tells `update` to throw out all of the data used in the initial tinkering, except that it starts the new chain from the final table from the initial runs. This is a harmless way to burn the chain in while you are tinkering with it. Of course, the chain can be restarted at the default starting value, the observed data, by simply rerunning `mctest`.

## 4 Application to Disclosure Limitation

Though there are certainly more rigorous procedures available [see 4], `exactLoglinTest` is a useful tool for exploring disclosure limitation in contingency tables. Consider the Czech Auto Worker's data given in Table 4. Suppose a researcher is concerned about the potential disclosure risk of releasing all two-way marginals from this table. The following code will load the Czech auto worker data into a data frame:

```
> data(czech.dat)
```

We will explore disclosure limitation by simulating tables from the hypergeometric distribution obtained by conditioning on all two way margins. However, we would like to save all of the simulated table entries, not just the deviance and Pearson statistics. This could be accomplished by changing the argument `stat` of `mctest` to an appropriate statistic. However, the function `simulateConditional` performs this simulation for us. It returns the simulated tables in a matrix with each row being a complete simulated table.

Now we run the chain. Notice the `stat = cell.stat` option to load the newly defined statistic.

```

> chain <- simulateConditional(y ~ (A + B + C + D + E + F) ^ 2,
+                               data = czech.dat,
+                               method = "cab",
+                               nosim = 10 ^ 3,
+                               p = .4)

```

Now, `chain` is a matrix where each row is a simulated table. We were particularly concerned with cells 39, 48, and 55 which contained only one, two and two individuals respectively. Consider the proportion of tables which have greater than 0 but fewer than three individuals

```
> mean(chain[,39] > 0 & chain[,39] < 3)
```

```
[1] 0.389
```

```
> mean(chain[,48] > 0 & chain[,58] < 3)
```

```
[1] 0.11
```

```
> mean(chain[,55] > 0 & chain[,55] < 3)
```

```
[1] 0.896
```

We used the model in question because this model fixes all two-way margins. However, that model need not fit the data well (in fact, it doesn't). Therefore, in addition to simulating from the hypergeometric density, a user would likely also want to simulate from other densities, such as a uniform distribution on tables with these margins. Though the normal approximations for `exactLoglinTest` were tailored specifically to the hypergeometric density, it allows for other target distributions. Here the density must be specified on the log scale up to a constant. Since a uniform density is simply a constant we use a density that always returns 0.

```

> chain2 <- simulateConditional(y ~ (A + B + C + D + E + F) ^ 2,
+                                 data = czech.dat,
+                                 method = "cab",
+                                 nosim = 10 ^ 3,
+                                 p = .4,
+                                 dens = function(y) 0)
> mean(chain2[,39] > 0 & chain2[,39] < 3)

```

```
[1] 0.363
```

```
> mean(chain2[,48] > 0 & chain2[,58] < 3)
```

```
[1] 0.59
```

```
> mean(chain2[,55] > 0 & chain2[,55] < 3)
```

```
[1] 1
```

Both simulations suggest that there are plenty of tables with higher counts than the observed counts for cells 39, 48 and 55. Hence the disclosure risk in releasing the two-way marginals seems minimal. However, it should be reiterated that this example is given only to illustrate how to obtain simulated tables from `exactLoglinTest`, further investigation of the chain and the data would be necessary for a thorough analysis of the disclosure risk.

## 4.1 Exact Score Test for Binomial Counts

The data given in A are obtained from the Cytel web site<sup>1</sup>. The data cross classify the survival of the Titanic passengers by class, gender and age. You can obtain the data with

```
> data(titanic.dat)
```

---

<sup>1</sup><http://www.cytel.com/>

Following the analysis done at the Cytel web site, we view each person's survival as a binary outcome. We use a model where a person's age, sex and class are additive effects on the logit scale. In the light of the discussion from Subsection 1.1, this model is equivalent to the following:

```

> titanic.dat$alpha <- rep(1 : 16, 2)
> fit <- glm(y ~ (factor(class) + factor(age) + factor(sex)) : factor(surv) +
+             factor(surv) + factor(alpha),
+             family = poisson,
+             data = titanic.dat)
> summary(fit)

Call:
glm(formula = y ~ (factor(class) + factor(age) + factor(sex)):factor(surv) +
    factor(surv) + factor(alpha), family = poisson, data = titanic.dat)

Deviance Residuals:
    Min      1Q  Median      3Q      Max 
-3.7995 -1.7072 -0.0003  0.9135  3.5931 

Coefficients: (5 not defined because of singularities)
              Estimate Std. Error z value Pr(>|z|)    
(Intercept) -18.7133   2170.2682 -0.009   0.993    
factor(surv)1  2.2477    0.2988   7.522 5.40e-14 ***  
factor(alpha)2 16.4218   2170.2684  0.008   0.994    
factor(alpha)3 18.9137   2170.2682  0.009   0.993    
factor(alpha)4 19.6645   2170.2682  0.009   0.993    
factor(alpha)5 19.3346   2170.2682  0.009   0.993    
factor(alpha)6 21.3136   2170.2682  0.010   0.992    
factor(alpha)7 20.6918   2170.2682  0.010   0.992    
factor(alpha)8 21.0027   2170.2682  0.010   0.992    
factor(alpha)9 -0.8226   3182.4092  0.000   1.000    
factor(alpha)10 17.6670   2170.2683  0.008   0.994    
factor(alpha)11 17.9902   2170.2682  0.008   0.993    
factor(alpha)12 18.9552   2170.2682  0.009   0.993    
factor(alpha)13 21.7355   2170.2682  0.010   0.992    
factor(alpha)14 20.7316   2170.2682  0.010   0.992    
factor(alpha)15 19.9737   2170.2682  0.009   0.993    
factor(alpha)16 20.3374   2170.2682  0.009   0.993    
factor(class)1:factor(surv)0 -0.8577    0.1573 -5.451 5.00e-08 ***  
factor(class)2:factor(surv)0  0.1604    0.1738  0.923   0.356    
factor(class)3:factor(surv)0  0.9201    0.1486  6.192 5.93e-10 ***  
factor(class)1:factor(surv)1    NA        NA       NA       NA      
factor(class)2:factor(surv)1    NA        NA       NA       NA      
factor(class)3:factor(surv)1    NA        NA       NA       NA      
factor(age)1:factor(surv)0   1.0615    0.2440  4.350 1.36e-05 ***  
factor(age)1:factor(surv)1    NA        NA       NA       NA      
factor(sex)1:factor(surv)0   2.4201    0.1404  17.236 < 2e-16 ***  
factor(sex)1:factor(surv)1    NA        NA       NA       NA      
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 4953.14  on 31  degrees of freedom
Residual deviance: 112.57  on 10  degrees of freedom
AIC: 283.97

```

Number of Fisher Scoring iterations: 15

The variable `alpha` is added to correspond to the  $\alpha_i$  terms from (2). Consider the gender effect in specific. Here, 2.42 suggests the odds of surviving for a male were roughly 9% that of a female. Furthermore, the estimate is highly significant. To calculate an exact P-value for this problem we use `simulateConditional` to simulate tables conditioning on all of the parameters except the one corresponding to the factor(`surv`) : factor(`sex`) interaction.

```
> chain <- simulateConditional(y ~ factor(surv) +
+                               (factor(class) + factor(age)) : factor(surv) +
+                               factor(alpha),
+                               dat = titanic.dat,
+                               nosim = 10 ^ 3,
+                               method = "cab",
+                               p = .1)
```

A P-value for a score test of  $H_0 : \gamma = 0$  versus  $H_a : \gamma < 0$  simply counts the proportion of tables with sufficient statistic for  $\gamma$  is smaller than the observed value. Using the notation from (2) the sufficient statistic for  $\gamma$  is  $s_\gamma = \sum_i z_i y_i \equiv z'y$ . We calculate the chain of sufficient statistics and the observed sufficient statistic below.

```
> z <- titanic.dat$sex * titanic.dat$surv
> sgamma <- chain %*% z
> sgamma.obs <- titanic.dat$y %*% z
> mean(sgamma <= sgamma.obs[1])
[1] 0.032
```

Apparently, none of the simulated tables have sufficient statistics for  $\gamma$  below that of the observed, which agrees closely with large sample results above.

## 5 Discussion and To Do

In this manual we investigated three straightforward examples of `exactLoglinTest` and considered two useful extensions of the program. The program was initially constructed calculate P-values for goodness of fit tests for contingency tables. However, the latter examples suggest a more user friendly interface for those problems would be useful.

Finally, it should be noted that only the inner-most calculations have been migrated to C. Possibly great gains in the speed of the algorithm could be attained by migrating more of the code (or more efficient R coding).

## References

- [1] Alan Agresti. *Categorical Data Analysis*. Wiley, New York, 1990.
- [2] J.G. Booth and R.W. Butler. An importance sampling algorithm for exact conditional test in log-linear models. *Biometrika*, 86:321–332, 1999.
- [3] Brian S. Caffo and James G. Booth. A markov chain monte carlo algorithm for approximating exact conditional probabilities. *the Journal of Computational and Graphical Statistics*, 10:730–745, 2001.
- [4] Adrian Dobra, Claudia Tebaldi, and Mike West. Reconstruction of contingency tables with missing data. Technical report, Duke University, 2002.
- [5] D. E. Edwards and T. Havranek. A fast procedure for model search in multidimesional contingency tables. *Biometrika*, 72:339–351, 1985.
- [6] Friedrich Leisch. *Sweave User Manual*.
- [7] W. N. Venables and B. D. Ripley. *Modern Applied Statistics with S*. Springer, New York, fourth edition, 2002.

## A Tables

Residence in 1980	Residence in 1985			
	Northeast	Midwest	South	West
Northeast	11,607	100	366	124
Midwest	87	13,677	515	302
South	172	225	17,819	270
West	63	176	286	10,192

Source [1]

Table 1: Residency Data

Pathologist A	Pathologist B				
	1	2	3	4	5
1	22	2	2	0	0
2	5	7	14	0	0
3	0	2	36	0	0
4	0	1	14	7	0
5	0	0	3	0	3

Source [1]

Table 2: Pathologist Agreement Data

Lake	Gender	Size	Primary Food Choice				
			Fish	Invert	Reptile	Bird	Other
1	Male	Small	7	1	0	0	5
	Male	Large	4	0	0	1	2
	Female	Small	16	3	2	2	3
	Female	Large	3	0	1	2	3
2	Male	Small	2	2	0	0	1
	Male	Large	13	7	6	0	0
	Female	Small	3	9	1	0	2
	Female	Large	0	1	0	1	0
3	Male	Small	3	7	1	0	1
	Male	Large	8	6	6	3	5
	Female	Small	2	4	1	1	4
	Female	Large	0	1	0	0	0
4	Male	Small	13	10	0	2	2
	Male	Large	9	0	0	1	2
	Female	Small	3	9	1	0	1
	Female	Large	8	1	0	0	1

Source [1]

Model (FG, FL, FS, LGS) where F=food choice, L=lake, S=size, G=gender.

Table 3: Alligator Data

				B		no		yes	
				A	no	yes	no	yes	
neg	small	small	no		44	40	112	67	
			yes		129	145	12	23	
			large	no	35	12	80	33	
	large	small	yes		109	67	7	9	
			no		23	32	70	66	
			yes		50	80	7	13	
	large	large	no		24	25	73	57	Source [4] originally appeared in [5].
			yes		51	63	7	16	
pos	small	small	no		5	7	21	9	
			yes		9	17	1	4	
			large	no	4	3	11	8	
	large	small	yes		14	17	5	2	
			no		7	3	14	14	
			yes		9	16	2	3	
	large	large	no		4	0	13	11	
			yes		5	14	4	4	

Table 4: Czech Auto Workers Data

Surv	Sex	Age	Class			
			Crew	First	Second	Third
yes	F	Child	0	0	0	17
		Adult	3	4	13	89
		M	0	0	0	35
		Child	670	118	154	387
	M	Adult	0	1	13	14
		Child	20	140	80	76
		Adult	0	5	11	13
		Child	192	57	14	75