

Program "SCATMAN" : User Instructions

by

James E. Hines and William A. Link

USGS, Biological Resources Division
Patuxent Wildlife Research Center
11510 American Holly Drive
Laurel, Maryland 20708

Introduction

This program is used to test the hypothesis of prey-selectivity based on random samples of predator scats. Suppose that prey species i has population density d_i , and that a single kill of species i typically results in λ_i scats. Under the null hypothesis of no prey specificity (i.e., that the frequencies of prey species in a predators' diet is proportional to availability), the proportion of scats identified to species i is expected to be

$$\pi_i = \frac{d_i \lambda_i}{\sum_i d_i \lambda_i}$$

If the quantities d_i and λ_i are known, a chi-squared goodness of fit test can be used to test the hypothesis of no prey specificity (Manly et al. 1972, Chesson 1978). Typically, however, d_i and λ_i are estimated rather than precisely known; furthermore, the number of scats produced by a single kill is variable. These sources of variation cause an inflation of the Type 1 error rate of the hypothesis test (Link and Karanth 1994). This program implements a parametric bootstrap designed to handle these problems; for details, see Link and Karanth (1994).

Data input:

The input file for program **SCATMAN** consists of a list of prey species, a list of estimated densities, standard errors of estimated densities, scat production rates, and scat production variability. The user also specifies the number of bootstrap replications.

Example (Tiger scat data from Link and Karanth, 1994):

Sample data

Prey:	SBR	PIG	CHT	GAR	MJK	LGR
Scat Freq:	118.5	35	143	82.5	24	16
Scat Production:	22.55	11.48	14.09	23.87	7.46	3.54
SD(Scat Production):	9.02	4.59	5.64	9.55	2.98	1.42
Density:	1.80	1.28	5.94	0.84	3.80	4.77
SE(Density):	0.62	0.23	0.81	0.34	1.55	0.63

Explanation:

In this example, the predator species is the tiger (*Panthera tigris*); prey species are

- SBR: Sambar (*Cervus unicolor*)
- PIG: Wild pig (*Sus scrofa*)
- CHT: Chital (*Axis axis*)
- GAR: Gaur (*Bos gaurus*)
- MJK: Muntjac (*Muntiacus muntjak*)
- LGR: Hanuman Langur (*Presbytis entellus*)

Input file: (scatman2.inp):

```
200,54321
SBR
118.5,1.8,0.62,22.553
PIG
35,1.28,.23,11.48
CHT
143,5.94,.81,14.085
GAR
82.5,.84,.34,23.867
MJK
24,3.8,1.55,7.463
LGR
16,4.77,.63,3.54
```

The line containing 200,54321 tells the program how many bootstrap replications (200) to perform, and a seed number (54321) for the random number generator. You probably don't need to change these.

The next line is the first prey species name (SBR). The following line contains the scat frequency for SBR (118.5), the density for SBR (1.8), the standard error of the density (0.62), and the scat production (22.55).

The other pairs of lines contain the data for the other 5 prey species.

Program Operation:

The first step is to create an input file. The easiest way to do this is to look at the sample input file provided, scatman.inp. Use any editor and create an input file similar to the sample input file. Just make sure to save the file as ASCII text. Next, run the program as described below, then view the output using your editor. If you are running Windows, open a MSDOS window and type the following:

```
cd \scatman
scatman <scatman.inp >scatman.out
```

Variability in scat production rates was set at 40% of the mean level.

Program Output

```
bootreps=      200 ix=      54321
SBR      118.5000  1.8000  0.6200 22.5530
PIG      35.0000  1.2800  0.2300 11.4800
CHT     143.0000  5.9400  0.8100 14.0850
GAR      82.5000  0.8400  0.3400 23.8670
MJK      24.0000  3.8000  1.5500  7.4630
LGR      16.0000  4.7700  0.6300  3.5400
```

species	observed	estimated	expected
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SBR	118.5000	83.2785
PIG	35.0000	30.1445
CHT	143.0000	171.6323
GAR	82.5000	41.1276
MJK	24.0000	58.1772
LGR	16.0000	34.6400

CV(SCATRATE)= 10%

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species	Chi squared	Unadjusted p-value	Adjusted p-value	standard error
~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
SBR	18.5917	0.0000	0.0010	0.0003
PIG	0.8427	0.3586	0.3887	0.0024
CHT	8.0907	0.0044	0.0539	0.0046
GAR	46.1486	0.0000	0.0000	0.0000
MJK	23.3153	0.0000	0.0003	0.0001
LGR	10.9342	0.0009	0.0027	0.0002
Composite	92.1822	0.0000	0.0000	0.0000

CV(SCATRATE)= 20%

species	Chi squared	Unadjusted p-value	Adjusted p-value	standard error
~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
SBR	18.5917	0.0000	0.0026	0.0006
PIG	0.8427	0.3586	0.4043	0.0035
CHT	8.0907	0.0044	0.0536	0.0054
GAR	46.1486	0.0000	0.0000	0.0000
MJK	23.3153	0.0000	0.0009	0.0003
LGR	10.9342	0.0009	0.0030	0.0002
Composite	92.1822	0.0000	0.0000	0.0000

CV(SCATRATE)= 30%

*****

species	Chi squared	Unadjusted p-value	Adjusted p-value	standard error
~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
SBR	18.5917	0.0000	0.0042	0.0010
PIG	0.8427	0.3586	0.4227	0.0052
CHT	8.0907	0.0044	0.0812	0.0094
GAR	46.1486	0.0000	0.0000	0.0000
MJK	23.3153	0.0000	0.0011	0.0003
LGR	10.9342	0.0009	0.0044	0.0004
Composite	92.1822	0.0000	0.0000	0.0000

CV(SCATRATE)= 40%

species	Chi squared	Unadjusted p-value	Adjusted p-value	standard error
~~~~~	~~~~~	~~~~~	~~~~~	~~~~~
SBR	18.5917	0.0000	0.0062	0.0018
PIG	0.8427	0.3586	0.4402	0.0064
CHT	8.0907	0.0044	0.1268	0.0128
GAR	46.1486	0.0000	0.0000	0.0000
MJK	23.3153	0.0000	0.0025	0.0007
LGR	10.9342	0.0009	0.0056	0.0006
Composite	92.1822	0.0000	0.0000	0.0000

## REFERENCES

Chesson, J. (1989). The effect of alternative prey on the functional response of *Notonecta hoffmani*. *Ecology* 70: 1227-1235.

Link, W.A. and Karanth, K.U. (1994). Correcting for overdispersion in tests of prey selectivity. *Ecology* 75: 2456-2459.

Manly, B.F.J., Miller, P., and Cook, L.M. (1972). Analysis of a selective predation experiment. *American Naturalist* 106: 719-736.

If you have questions, problems or comments with this program please contact:

Jim Hines, USGS-PWRC  
11510 American Holly Dr. #201  
Laurel, Md. 20708-4017

Phone:(301)497-5661  
email:[Jim_Hines%40usgs.gov](mailto:Jim_Hines%40usgs.gov)  
web :<http://www.mbr-pwrc.usgs.gov/software>