

# Package ‘poilog’

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**Type** Package

**Title** Poisson Lognormal and Bivariate Poisson Lognormal Distribution

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**Description** Functions for obtaining the density, random deviates and maximum likelihood estimates of the Poisson lognormal distribution and the bivariate Poisson lognormal distribution.

**License** GPL-3

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### Description

Functions for obtaining the density, random deviates and maximum likelihood estimates of the Poisson lognormal distribution and the bivariate Poisson lognormal distribution.

### Details

Package: `poilog`  
 Type: Package  
 Version: 0.4.2  
 Date: 2022-10-07  
 License: GPL-3

`dpoilog` returns the density, `rpoilog` returns random deviates and `poilogMLE` performs maximum likelihood estimation of parameters for the Poisson lognormal distribution.

`dbipoilog` returns the density, `rbipoilog` returns random deviates and `bipoilogMLE` performs maximum likelihood estimation of parameters for the bivariate Poisson lognormal distribution.

### Author(s)

Vidar Grotan and Steinar Engen

Maintainer: Vidar Grotan <vidar.grotan@ntnu.no>

### References

Bulmer, M. G. 1974. On fitting the Poisson lognormal distribution to species abundance data. *Biometrics* **30**, 651-660.

Engen, S., R. Lande, T. Walla and P. J. DeVries. 2002. Analyzing spatial structure of communities using the two-dimensional Poisson lognormal species abundance model. *American Naturalist* **160**, 60-73.

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Bivariate Poisson lognormal

*Bivariate Poisson Lognormal Distribution*

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### Description

Density and random generation for the for the bivariate Poisson lognormal distribution with parameters  $\mu_1$ ,  $\mu_2$ ,  $\sigma_1$ ,  $\sigma_2$  and  $\rho$ .

### Usage

```
dbipoilog(n1, n2, mu1, mu2, sig1, sig2, rho)
rbipoilog(S, mu1, mu2, sig1, sig2, rho, nu1=1, nu2=1,
          condS=FALSE, keep0=FALSE)
```

### Arguments

<code>n1</code>	vector of observed individuals for each species in sample 1
<code>n2</code>	vector of observed individuals for each species in sample 2 (in the same order as in sample 1)
<code>mu1</code>	mean of lognormal distribution in sample 1

mu2	mean of lognormal distribution in sample 1
sig1	standard deviation of lognormal distribution in sample 1
sig2	standard deviation of lognormal distribution in sample 2
rho	correlation among samples
S	Total number of species in both communities
nu1	sampling intensity sample 1
nu2	sampling intensity sample 2
condS	logical; if TRUE random deviates are conditional on S
keep0	logical; if TRUE species with count 0 in both communities are included in the random deviates

### Details

The following is written from the perspective of using the Poisson lognormal distribution to describe community structure (the distribution of species when sampling individuals from a community of several species).

The following assumes knowledge of the **Details** section of [dpoilog](#).

Consider two communities jointly and assume that the log abundances among species have the binormal distribution with parameters (mu1,sig1,mu2,sig2,rho). If sampling intensities are nu1 = nu2 = 1, samples from the communities will have the bivariate Poisson lognormal distribution

$$P(N_1 = n_1, N_2 = n_2; \mu_1, \text{sig}_1, \mu_2, \text{sig}_2, \rho) =$$

$$q(n_1, n_2; \mu_1, \text{sig}_1, \mu_2, \text{sig}_2, \rho) =$$

$$\int_{-\infty}^{\infty} \int_{-\infty}^{\infty} g_{n_1}(\mu_1, \text{sig}_1, u) g_{n_2}(\mu_2, \text{sig}_2, v) \phi(u, v; \rho) du dv,$$

where  $\phi(u, v; \rho)$  here denotes the binormal distribution with zero means, unit variances and correlation  $\rho$ . In the general case with sampling intensities nu1 and nu2, mu1 and mu2 should be replaced by mu1 + ln nu1 and mu2 + ln nu2 respectively. In this case, some species will be missing from both samples. The number of individuals for observed species will then have the truncated distribution

$$\frac{q(n_1, n_2; \mu_1, \text{sig}_1, \mu_2, \text{sig}_2, \rho)}{1 - q(0, 0; \mu_1, \text{sig}_1, \mu_2, \text{sig}_2, \rho)}$$

### Value

dbipoilog returns the density  
rbipoilog returns random deviates

### Author(s)

Vidar Grotan <vidar.grotan@ntnu.no> and Steinar Engen

**References**

Engen, S., R. Lande, T. Walla and P. J. DeVries. 2002. Analyzing spatial structure of communities using the two-dimensional Poisson lognormal species abundance model. *American Naturalist* **160**, 60-73.

**See Also**

[bipoilogMLE](#) for maximum likelihood estimation

**Examples**

```
### change in density of n2 for two different values of rho (given n1=10)
barplot(rbind(dbipoilog(n1=rep(10,21),n2=0:20,mu1=0,mu2=0,sig=1,sig2=1,rho=0.0),
              dbipoilog(n1=rep(10,21),n2=0:20,mu1=0,mu2=0,sig=1,sig2=1,rho=0.8)),
        beside=TRUE,space=c(0,0.2),names.arg=0:20,xlab="n2",col=1:2)
legend(35,0.0012,c("rho=0","rho=0.8"),fill=1:2)

### draw random deviates from a community of 50 species
rbipoilog(S=50,mu1=0,mu2=0,sig1=1,sig2=2,rho=0.7)

### draw random deviates including zeros
rbipoilog(S=50,mu1=0,mu2=0,sig1=1,sig2=2,rho=0.7,keep0=TRUE)

### draw random deviates with sampling intensities nu1=0.5 and nu2=0.7
rbipoilog(S=50,mu1=0,mu2=0,sig1=1,sig2=2,rho=0.7,nu1=0.5,nu2=0.7)

### draw random deviates conditioned on a certain number of species
rbipoilog(S=50,mu1=0,mu2=0,sig1=1,sig2=2,rho=0.7,nu1=0.5,nu2=0.7,condS=TRUE)

### how many species are likely to be observed in at least one of the samples
### (given S,mu1,mu2,sig1,sig2,rho)?
hist(replicate(1000,nrow(rbipoilog(S=50,mu1=0,mu2=0,sig1=1,sig2=2,rho=0.7))),
     main="", xlab = "Number of species observed in at least one of the samples")

### how many individuals are likely to be observed
### (given S,mu1,mu2,sig1,sig2,rho)?
hist(replicate(1000,sum(rbipoilog(S=50,mu1=0,mu2=0,sig1=1,sig2=2,rho=0.7))),
     main="", xlab="sum nr of individuals in both samples")
```

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MLE for bivariate Poisson lognormal distribution

*Maximum Likelihood Estimation for Bivariate Poisson Lognormal  
Distribution*

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**Description**

bipoilogMLE fits the bivariate Poisson lognormal distribution to data

**Usage**

```
bipoilogMLE(n1, n2 = NULL,
            startVals = c(mu1=1, mu2=1, sig1=2, sig2=2, rho=0.5),
            nboot = 0, zTrunc = TRUE, file = NULL,
            method = "BFGS", control = list(maxit=1000))
```

**Arguments**

n1	a vector or a matrix with two columns of pairwise counts of observed individuals for each species
n2	if n1 is not given as a matrix, a vector of counts with same ordering of species as in argument n1
startVals	starting values of parameters
nboot	number of parametric bootstraps, defaults to zero
zTrunc	logical; if TRUE (default) the zero-truncated distribution is fitted
file	text file to hold copies of bootstrap estimates
method	method to use during optimization, see details
control	a list of control parameters for the optimization routine, see details

**Details**

The function estimates the parameters  $\mu_1$ ,  $\text{sig}_1$ ,  $\mu_2$ ,  $\text{sig}_2$  and  $\rho$ . In cases of incomplete sampling the estimates of  $\mu_1$  and  $\mu_2$  will be confounded with the sampling intensities (see [rbipoilog](#)). Assuming sampling intensities  $\nu_1$  and  $\nu_2$ , the estimates of the means are  $\mu_1 + \ln \nu_1$  and  $\mu_2 + \ln \nu_2$ . Parameters  $\text{sig}_1$ ,  $\text{sig}_2$  and  $\rho$  can be estimated without any knowledge of sampling intensities. The parameters must be given starting values for the optimization procedure (default starting values are used if starting values are not specified in the function call).

A zero-truncated distribution (see [dbipoilog](#)) is assumed by default ( $\text{zTrunc} = \text{TRUE}$ ). In cases where the number of zeros is known the  $\text{zTrunc}$  argument should be set to `FALSE`.

The function uses the optimization procedures in [optim](#) to obtain the maximum likelihood estimate. The `method` and `control` arguments are passed to [optim](#), see the help page for this function for additional methods and control parameters.

The approximate fraction of species revealed by each sample is estimated as 1 minus the zero term of the univariate Poisson lognormal distribution:  $1 - q(0; \mu_1, \text{sig}_1)$  and  $1 - q(0; \mu_2, \text{sig}_2)$ .

Parametric bootstrapping could be time consuming for large data sets. If argument `file` is specified, e.g. `file = 'C:\myboots.txt'`, the matrix with bootstrap estimates are copied into a tab-separated text-file providing extra backup. Bootstrapping is done by simulating new sets of observations conditioned on the observed number of species (see [rbipoilog](#)).

**Value**

par	Maximum likelihood estimates of the parameters
p	Approximate fraction of species revealed by the samples for sample 1 and 2 respectively
logLval	Log likelihood of the data given the estimated parameters

gof	Goodness of fit measure obtained by checking the rank of logLval against logLval's obtained during the bootstrap procedure, (gof < 0.05) or (gof > 0.95) indicates lack of fit
boot	A data frame containing the bootstrap replicates of parameters and logLval

**Author(s)**

Vidar Grotan <vidar.grotan@ntnu.no>, Steinar Engen

**References**

Engen, S., R. Lande, T. Walla and P. J. DeVries. 2002. Analyzing spatial structure of communities using the two-dimensional Poisson lognormal species abundance model. *American Naturalist* **160**, 60-73.

**See Also**

[optim](#), [dbipoilog](#), [rbipoilog](#)

**Examples**

```
## simulate observations
xy <- rbipoilog(S=30,mu1=1,mu2=1,sig1=2,sig2=2,rho=0.5)

## obtain estimates of parameters
est <- bipoilogMLE(xy)

## change start values and request tracing information
## from optimization procedure
## Not run: est <- bipoilogMLE(xy,startVals=c(2,2,4,4,0.3),
##       control=list(maxit=1000,trace=1, REPORT=1))
## End(Not run)

## effect of sampling intensity
xy <- rbipoilog(S=100,mu1=1,mu2=1,sig1=2,sig2=2,rho=0.5,nu1=0.5,nu2=0.5)
## Not run: est <- bipoilogMLE(xy)
## the expected estimates of mu1 and mu2 are now 1-log(0.5) = 0.3 (approximately)
```

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MLE for Poisson lognormal distribution

*Maximum Likelihood Estimation for Poisson Lognormal Distribution*

---

**Description**

pologMLE fits the Poisson lognormal distribution to data and estimates parameters mean mu and standard deviation sig in the lognormal distribution

**Usage**

```
poilogMLE(n, startVals = c(mu=1, sig=2),
          nboot = 0, zTrunc = TRUE,
          method = "BFGS", control = list(maxit=1000))
```

**Arguments**

n	A vector of counts
startVals	Starting values of parameters, see details
nboot	Number of parametric bootstraps, defaults to zero
zTrunc	Zero-truncated distribution, defaults to TRUE
method	Method to use during optimization, see details
control	A list of control parameters for the optimization routine, see details

**Details**

The function estimates parameters mean  $\mu$  and standard deviation  $\sigma$ . In cases of incomplete sampling the estimate of  $\mu$  will be confounded with the sampling intensity (see [rpoilog](#)). Assuming sampling intensity  $\nu$ , the estimates of the mean is  $\mu + \ln(\nu)$ . Parameter  $\sigma$  can be estimated without any knowledge of sampling intensity.

The parameters must be given starting values for the optimization procedure (default starting values are used if starting values are not specified in the function call).

The function uses the optimization procedures in [optim](#) to obtain the maximum likelihood estimate. The method and control arguments are passed to [optim](#), see the help page for this function for additional methods and control parameters.

A zero-truncated distribution (see [dpoilog](#)) is assumed by default (`zTrunc = TRUE`). In cases where the number of zeros is known the `zTrunc` argument should be set to `FALSE`.

The approximate fraction of species revealed by the sample is  $1 - q(0; \mu, \sigma)$ .

Parametric bootstrapping is done by simulating new sets of observations using the estimated parameters (see [rbipoilog](#)).

**Value**

par	Maximum likelihood estimates of the parameters
p	Approximate fraction of species revealed by the sample
logLval	Log likelihood of the data given the estimated parameters
gof	Goodness of fit measure obtained by checking the rank of logLval against logLval's obtained during the bootstrap procedure, ( <code>gof &lt; 0.05</code> ) or ( <code>gof &gt; 0.95</code> ) indicates lack of fit
boot	A data frame containing the bootstrap replicates of parameters and logLval

**Author(s)**

Vidar Grotan <vidar.grotan@ntnu.no>, Steinar Engen

**References**

- Bulmer, M. G. 1974. On fitting the Poisson lognormal distribution to species abundance data. *Biometrics* **30**, 651-660.
- Engen, S., R. Lande, T. Walla and P. J. DeVries. 2002. Analyzing spatial structure of communities using the two-dimensional Poisson lognormal species abundance model. *American Naturalist* **160**, 60-73.

**See Also**

[optim](#), [dpoilog](#), [rpoilog](#)

**Examples**

```
### simulate observations

n <- rpoilog(S=80,mu=1,sig=2)

### obtain estimates of parameters
est <- poilogMLE(n)

### similar, but now with bootstrapping ###
## Not run: est <- poilogMLE(n,nboot=10)

### change start values and request tracing information
### from optimization procedure
est <- poilogMLE(n,startVals=c(2,3),
                 control=list(maxit=1000,trace=1, REPORT=1))
```

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Poisson lognormal      *Poisson lognormal distribution*

---

**Description**

Density and random generation for the Poisson lognormal distribution with parameters `mu` and `sig`.

**Usage**

```
dpoilog(n, mu, sig)
rpoilog(S, mu, sig, nu=1, condS=FALSE, keep0=FALSE)
```

**Arguments**

<code>n</code>	vector of observed individuals for each species
<code>S</code>	number of species in the community
<code>mu</code>	mean of lognormal distribution
<code>sig</code>	standard deviation of lognormal distribution
<code>nu</code>	sampling intensity, defaults to 1
<code>condS</code>	logical; if TRUE random deviates are conditional on S
<code>keep0</code>	logical; if TRUE species with count 0 are included in the random deviates



## Details

The following is written from the perspective of using the Poisson lognormal distribution to describe community structure (the distribution of species when sampling individuals from a community of several species).

Under the assumption of random sampling, the number of individuals sampled from a given species with abundance  $y$ , say  $N$ , is Poisson distributed with mean  $\nu y$  where the parameter  $\nu$  expresses the sampling intensity. If  $\ln y$  is normally distributed with mean  $\mu$  and standard deviation  $\sigma$  among species, then the vector of individuals sampled from all  $S$  species then constitutes a sample from the Poisson lognormal distribution with parameters  $(\mu + \ln \nu, \sigma)$ , where  $\mu$  and  $\sigma$  are the mean and standard deviation of the log abundances. For  $\nu = 1$ , this is the Poisson lognormal distribution with parameters  $(\mu, \sigma)$  which may be written in the form

$$P(N = n; \mu, \sigma) = q(n; \mu, \sigma) = \int_{-\infty}^{\infty} g_n(\mu, \sigma, u) \phi(u) du,$$

where  $\phi(u)$  is the standard normal distribution and

$$g_n(\mu, \sigma, u) = \frac{\exp(u \sigma n + \mu n - \exp(u \sigma + \mu))}{n!}$$

Since  $S$  is usually unknown, we only consider the observed number of individuals for the observed species. With a general sampling intensity  $\nu$ , the distribution of the number of individuals then follows the zero-truncated Poisson lognormal distribution

$$\frac{q(n; \mu, \sigma)}{1 - q(0; \mu, \sigma)}$$

## Value

`dpoilog` returns the density  
`rpoilog` returns random deviates

## Author(s)

Vidar Grotan <vidar.grotan@ntnu.no> and Steinar Engen

## References

Engen, S., R. Lande, T. Walla & P. J. DeVries. 2002. Analyzing spatial structure of communities using the two-dimensional Poisson lognormal species abundance model. *American Naturalist* 160: 60-73.

## See Also

[poilogMLE](#) for ML estimation

**Examples**

```
### plot density for given parameters
barplot(dpoilog(n=0:20,mu=2,sig=1),names.arg=0:20)

### draw random deviates from a community of 50 species
rpoilog(S=50,mu=2,sig=1)

### draw random deviates including zeros
rpoilog(S=50,mu=2,sig=1,keep0=TRUE)

### draw random deviates with sampling intensity = 0.5
rpoilog(S=50,mu=2,sig=1,nu=0.5)

### how many species are likely to be observed
### (given S,mu,sig2 and nu)?
hist(replicate(1000,length(rpoilog(S=30,mu=0,sig=3,nu=0.7))))

### how many individuals are likely to be observed
### (given S,mu,sig2 and nu)?
hist(replicate(1000,sum(rpoilog(S=30,mu=0,sig=3,nu=0.7))))
```

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