Package 'degreenet'

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Title Models for Skewed Count Distributions Relevant to Networks

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Imports igraph, network

Description Likelihood-based inference for skewed count distributions, typically of degrees used in network modeling. ``degreenet'' is a part of the ``statnet'' suite of packages for network analysis. See Jones and Handcock <doi:10.1098/rspb.2003.2369>.

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URL https://statnet.org

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Contents

degreenet-package   *Models for Skewed Count Distributions Relevant to Networks*

Description

degreenet is a collection of functions to fit, diagnose, and simulate from distributions for skewed
count data. The coverage of distributions is very selective, focusing on those that have been pro-
posed to model the degree distribution on networks. For the rationale for this choice, see the papers
in the references section below. For a list of functions type: help(package='degreenet')

For a complete list of the functions, use library(help="degreenet") or read the rest of the man-
ual. For a simple demonstration, use demo(packages="degreenet").

The **degreenet** package is part of the **statnet** suite of packages. The suite was developed to facilitate
the statistical analysis of network data.

When publishing results obtained using this package alone see the citation in citation(package="degreenet").
The citation for the original paper to use this package is Handcock and Jones (2003) and it should
be cited for the theoretical development.

If you use other packages in the **statnet** suite, please cite it as:

Mark S. Handcock, David R. Hunter, Carter T. Butts, Steven M. Goodreau, and Martina Morris.
2003 *statnet: Software tools for the Statistical Modeling of Network Data*
https://statnet.org. For complete citation information, use
citation(package="statnet").

All programs derived from this or other **statnet** packages must cite them appropriately.

Details

See the Handcock and Jones (2003) reference (and the papers it cites and is cited by) for more information on the methodology.

Recent advances in the statistical modeling of random networks have had an impact on the empirical study of social networks. Statistical exponential family models (Strauss and Ikeda 1990) are a generalization of the Markov random network models introduced by Frank and Strauss (1986). These models recognize the complex dependencies within relational data structures. To date, the use of stochastic network models for networks has been limited by three interrelated factors: the complexity of realistic models, the lack of simulation tools for inference and validation, and a poor understanding of the inferential properties of nontrivial models.

This package relies on the network package which allows networks to be represented in R. The **statnet** suite of packages allows maximum likelihood estimates of exponential random network models to be calculated using Markov Chain Monte Carlo, as well as a broad range of statistical analysis of networks, such as tools for plotting networks, simulating networks and assessing model goodness-of-fit.

For detailed information on how to download and install the software, go to the **statnet** website: https://statnet.org. A tutorial, support newsgroup, references and links to further resources are provided there.

Author(s)

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References

Frank, O., and Strauss, D.(1986). *Markov graphs.* Journal of the American Statistical Association, 81, 832-842.

Jones, J. H. and Handcock, M. S. (2003). *An assessment of preferential attachment as a mechanism for human sexual network formation*, Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

Handcock, M. S., Hunter, D. R., Butts, C. T., Goodreau, S. M., and Morris, M. (2003), *statnet: Software tools for the Statistical Modeling of Network Data.*, URL https://statnet.org

Strauss, D., and Ikeda, M.(1990). Pseudolikelihood estimation for social networks. Journal of the American Statistical Association, 85, 204-212.

| acmpmle | *Conway Maxwell Poisson Modeling of Discrete Data* |

Description

Functions to Estimate the Conway Maxwell Poisson Discrete Probability Distribution via maximum likelihood.

Usage

```
acmpmle(x, cutoff = 1, cutabove = 1000, guess=c(7,3),
    method="BFGS", conc=FALSE, hellinger=FALSE, hessian=TRUE)
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
method	Method of optimization. See "optim" for details.
conc	Calculate the concentration index of the distribution?
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
hessian	Calculate the hessian of the information matrix (for use with calculating the standard errors.

Value

theta	vector of MLE of the parameters.
asycov	asymptotic covariance matrix.
asycor	asymptotic correlation matrix.
se	vector of standard errors for the MLE.
conc	The value of the concentration index (if calculated).

Note

See the papers on https://handcock.github.io/?q=Holland for details.

Based on the C code in the package **compoisson** written by Jeffrey Dunn (2008).

References

compoisson: Conway-Maxwell-Poisson Distribution, Jeffrey Dunn, 2008, R package version 0.3

See Also

ayulemle, awarmle, simcmp

Examples

```
# Simulate a Conway Maxwell Poisson distribution over 100
# observations with mean of 7 and variance of 3
# This leads to a mean of 1

set.seed(1)
s4 <- simcmp(n=100, v=c(7,3))
```

```
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameters
#

acmpmle(s4)
```

---

adqemle   *Discrete version of q-Exponential Modeling of Discrete Data*

Description

Functions to Estimate the Discrete version of q-Exponential Probability Distribution via maximum likelihood.

Usage

```
adqemle(x, cutoff = 1, cutabove = 1000, guess = c(3.5,1),
    method = "BFGS", conc = FALSE, hellinger = FALSE, hessian=TRUE)
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
conc	Calculate the concentration index of the distribution?
method	Method of optimization. See "optim" for details.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
hessian	Calculate the hessian of the information matrix (for use with calculating the standard errors.

Value

theta	vector of MLE of the parameters.
asycov	asymptotic covariance matrix.
asycor	asymptotic correlation matrix.
se	vector of standard errors for the MLE.
conc	The value of the concentration index (if calculated).

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, adqemle, simdqe

Examples

```
# Simulate a Discrete version of q-Exponential distribution over 100
# observations with a PDF exponent of 3.5 and a
# sigma scale of 1

set.seed(1)
s4 <- simdqe(n=100, v=c(3.5,1))
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameters
#

s4est <- adqemle(s4)
s4est

# Calculate the MLE and an asymptotic confidence
# interval for rho under the Yule model
#

s4yuleest <- ayulemle(s4)
s4yuleest

#
# Compare the AICC and BIC for the two models
#

lldqeall(v=s4est$theta,x=s4)
llyuleall(v=s4yuleest$theta,x=s4)
```

---

aplnmle   *Poisson Lognormal Modeling of Discrete Data*

Description

Functions to Estimate the Poisson Lognormal Discrete Probability Distribution via maximum likelihood.

Usage

```
aplnmle(x, cutoff = 1, cutabove = 1000, guess = c(0.6,1.2),
    method = "BFGS", conc = FALSE, hellinger = FALSE, hessian=TRUE,logn=TRUE)
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
method	Method of optimization. See "optim" for details.
conc	Calculate the concentration index of the distribution?
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
hessian	Calculate the hessian of the information matrix (for use with calculating the standard errors.
logn	Use logn parametrization, that is, mean and variance on the observation scale.

Value

theta	vector of MLE of the parameters.
asycov	asymptotic covariance matrix.
asycor	asymptotic correlation matrix.
se	vector of standard errors for the MLE.
conc	The value of the concentration index (if calculated).

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, awarmle, simpln

Examples

```
# Simulate a Poisson Lognormal distribution over 100
# observations with lognormal mean of -1 and lognormal variance of 1
# This leads to a mean of 1

set.seed(1)
s4 <- simpln(n=100, v=c(-1,1))
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameters
#

s4est <- aplnmle(s4)
s4est

# Calculate the MLE and an asymptotic confidence
# interval for rho under the Yule model
#

s4yuleest <- ayulemle(s4)
s4yuleest

# Calculate the MLE and an asymptotic confidence
# interval for rho under the Waring model
#

s4warest <- awarmle(s4)
s4warest

#
# Compare the AICC and BIC for the three models
#

llplnall(v=s4est$theta,x=s4)
llyuleall(v=s4yuleest$theta,x=s4)
llwarall(v=s4warest$theta,x=s4)
```

---

awarmle   *Waring Modeling of Discrete Data*

Description

Functions to Estimate the Waring Discrete Probability Distribution via maximum likelihood.

Usage

```
awarmle(x, cutoff = 1, cutabove = 1000, guess = c(3.5,0.1),
     method = "BFGS", conc = FALSE, hellinger = FALSE, hessian=TRUE)
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
conc	Calculate the concentration index of the distribution?
method	Method of optimization. See "optim" for details.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
hessian	Calculate the hessian of the information matrix (for use with calculating the standard errors.

Value

theta	vector of MLE of the parameters.
asycov	asymptotic covariance matrix.
asycor	asymptotic correlation matrix.
se	vector of standard errors for the MLE.
conc	The value of the concentration index (if calculated).

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, awarmle, simwar

Examples

```
# Simulate a Waring distribution over 100
# observations with a PDf exponent of 3.5 and a
# probability of including a new actor of 0.1

set.seed(1)
s4 <- simwar(n=100, v=c(3.5,0.1))
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameters
#
```

```
s4est <- awarmle(s4)
s4est

# Calculate the MLE and an asymptotic confidence
# interval for rho under the Yule model
#

s4yuleest <- ayulemle(s4)
s4yuleest

#
# Compare the AICC and BIC for the two models
#

llwarall(v=s4est$theta,x=s4)
llyuleall(v=s4yuleest$theta,x=s4)
```

---

ayulemle   *Yule Distribution Modeling of Discrete Data*

Description

Functions to Estimate the Yule Discrete Probability Distribution via maximum likelihood.

Usage

```
ayulemle(x, cutoff = 1, cutabove = 1000, guess = 3.5, conc = FALSE,
    method = "BFGS", hellinger = FALSE, hessian = TRUE, weights = rep(1, length(x)))
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
conc	Calculate the concentration index of the distribution?
method	Method of optimization. See "optim" for details.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
hessian	Calculate the hessian of the information matrix (for use with calculating the standard errors.
weights	sample weights on the observed counts.

Value

theta	vector of MLE of the parameters.
asycov	asymptotic covariance matrix.
asycor	asymptotic correlation matrix.
se	vector of standard errors for the MLE.
conc	The value of the concentration index (if calculated).

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, awarmle, simyule

Examples

```
# Simulate a Yule distribution over 100
# observations with PDf exponent of 3.5

set.seed(1)
s4 <- simyule(n=100, rho=3.5)
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameters
#

s4est <- ayulemle(s4)
s4est

#
# Compute the AICC and BIC for the model
#

llyuleall(v=s4est$theta,x=s4)
```

---

bsdp	*Calculate Bootstrap Estimates and Confidence Intervals for the Discrete Pareto Distribution*

Description

Uses the parametric bootstrap to estimate the bias and confidence interval of the MLE of the Discrete Pareto Distribution.

Usage

```
bsdp(x, cutoff=1, m=200, np=1, alpha=0.95)
bootstrapdp(x,cutoff=1,cutabove=1000,
                          m=200,alpha=0.95,guess=3.31,hellinger=FALSE,
                          mle.meth="adpmle")
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
m	Number of bootstrap samples to draw.
np	Number of parameters in the model (1 by default).
alpha	Type I error for the confidence interval.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
mle.meth	Method to use to compute the MLE.

Value

dist	matrix of sample CDFs, one per row.
obsmle	The Discrete Pareto MLE of the PDF exponent.
bsmles	Vector of bootstrap MLE.
quantiles	Quantiles of the bootstrap MLEs.
pvalue	p-value of the Anderson-Darling statistics relative to the bootstrap MLEs.
obsmands	Observed Anderson-Darling Statistic.
meanmles	Mean of the bootstrap MLEs.
guess	Initial estimate at the MLE.
mle.meth	Method to use to compute the MLE.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

anbmle, simdp, lldp

Examples

```
## Not run:
# Now, simulate a Discrete Pareto distribution over 100
# observations with expected count 1 and probability of another
# of 0.2

set.seed(1)
s4 <- simdp(n=100, v=3.31)
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameter.
#

s4est <- adpmle(s4)
s4est

#
# Use the bootstrap to compute a confidence interval rather than using the
# asymptotic confidence interval for the parameter.
#

bsdp(s4, m=20)

## End(Not run)
```

---

bsnb	*Calculate Bootstrap Estimates and Confidence Intervals for the Negative Binomial Distribution*

Description

Uses the parametric bootstrap to estimate the bias and confidence interval of the MLE of the Negative Binomial Distribution.

Usage

```
bsnb(x, cutoff=1, m=200, np=2, alpha=0.95, hellinger=FALSE)
bootstrapnb(x,cutoff=1,cutabove=1000,
                        m=200,alpha=0.95,guess=c(5, 0.2),
                        file="none")
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
m	Number of bootstrap samples to draw.
np	Number of parameters in the model (1 by default).
alpha	Type I error for the confidence interval.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Guess at the parameter value.
file	Name of the file to store the results. By default do not save the results.

Value

dist	matrix of sample CDFs, one per row.
obsmle	The Negative Binomial MLE of the PDF exponent.
bsmles	Vector of bootstrap MLE.
quantiles	Quantiles of the bootstrap MLEs.
pvalue	p-value of the Anderson-Darling statistics relative to the bootstrap MLEs.
obsmands	Observed Anderson-Darling Statistic.
meanmles	Mean of the bootstrap MLEs.
guess	Initial estimate at the MLE.
mle.meth	Method to use to compute the MLE.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

anbmle, simnb, llnb

Examples

```
# Now, simulate a Negative Binomial distribution over 100
# observations with expected count 1 and probability of another
# of 0.2

set.seed(1)
s4 <- simnb(n=100, v=c(5,0.2))
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameter.
#

s4est <- anbmle(s4)
s4est

#
# Use the bootstrap to compute a confidence interval rather than using the
# asymptotic confidence interval for the parameter.
#

bsnb(s4, m=20)
```

---

bspln	*Calculate Bootstrap Estimates and Confidence Intervals for the Poisson Lognormal Distribution*

Description

Uses the parametric bootstrap to estimate the bias and confidence interval of the MLE of the Poisson Lognormal Distribution.

Usage

```
bspln(x, cutoff=1, m=200, np=2, alpha=0.95, v=NULL,
                    hellinger=FALSE)
bootstrappln(x,cutoff=1,cutabove=1000,
                         m=200,alpha=0.95,guess=c(0.6,1.2), file = "none")
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
m	Number of bootstrap samples to draw.
np	Number of parameters in the model (1 by default).
alpha	Type I error for the confidence interval.

v	Parameter value to use for the bootstrap distribution. By default it is the MLE of the data.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
file	Name of the file to store the results. By default do not save the results.

Value

dist	matrix of sample CDFs, one per row.
obsmle	The Poisson Lognormal MLE of the PDF exponent.
bsmles	Vector of bootstrap MLE.
quantiles	Quantiles of the bootstrap MLEs.
pvalue	p-value of the Anderson-Darling statistics relative to the bootstrap MLEs.
obsmands	Observed Anderson-Darling Statistic.
meanmles	Mean of the bootstrap MLEs.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

anbmle, simpln, llpln

Examples

```
# Now, simulate a Poisson Lognormal distribution over 100
# observations with expected count 1 and probability of another
# of 0.2

set.seed(1)
s4 <- simpln(n=100, v=c(5,0.2))
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameter.
#

s4est <- aplnmle(s4)
s4est
```

```
#
# Use the bootstrap to compute a confidence interval rather than using the
# asymptotic confidence interval for the parameter.
#

bspln(s4, m=5)
```

---

bswar   *Calculate Bootstrap Estimates and Confidence Intervals for the War-*
                                ing Distribution

Description

Uses the parametric bootstrap to estimate the bias and confidence interval of the MLE of the Waring
Distribution.

Usage

```
bswar(x, cutoff=1, m=200, np=2, alpha=0.95, v=NULL,
                  hellinger=FALSE)
bootstrapwar(x,cutoff=1,cutabove=1000,
            m=200,alpha=0.95,guess=c(3.31, 0.1),file="none",
            conc = FALSE)
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
m	Number of bootstrap samples to draw.
np	Number of parameters in the model (1 by default).
alpha	Type I error for the confidence interval.
v	Parameter value to use for the bootstrap distribution. By default it is the MLE of the data.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Guess at the parameter value.
file	Name of the file to store the results. By default do not save the results.
conc	Calculate the concentration index of the distribution?

Value

`dist`	matrix of sample CDFs, one per row.
`obsmle`	The Waring MLE of the PDF exponent.
`bsmles`	Vector of bootstrap MLE.
`quantiles`	Quantiles of the bootstrap MLEs.
`pvalue`	p-value of the Anderson-Darling statistics relative to the bootstrap MLEs.
`obsmands`	Observed Anderson-Darling Statistic.
`meanmles`	Mean of the bootstrap MLEs.
`guess`	Initial estimate at the MLE.
`mle.meth`	Method to use to compute the MLE.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

anbmle, simwar, llwar

Examples

```
# Now, simulate a Waring distribution over 100
# observations with expected count 1 and probability of another
# of 0.2

set.seed(1)
s4 <- simwar(n=100, v=c(5,0.2))
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameter.
#

s4est <- awarmle(s4)
s4est

#
# Use the bootstrap to compute a confidence interval rather than using the
# asymptotic confidence interval for the parameter.
#

bswar(s4, m=20)
```

---

bsyule	*Calculate Bootstrap Estimates and Confidence Intervals for the Yule Distribution*

Description

Uses the parametric bootstrap to estimate the bias and confidence interval of the MLE of the Yule Distribution.

Usage

```
bsyule(x, cutoff=1, m=200, np=1, alpha=0.95, v=NULL,
                    hellinger=FALSE, cutabove=1000)
bootstrapyule(x,cutoff=1,cutabove=1000,
                        m=200,alpha=0.95,guess=3.31,hellinger=FALSE,
                        mle.meth="ayulemle")
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
m	Number of bootstrap samples to draw.
np	Number of parameters in the model (1 by default).
alpha	Type I error for the confidence interval.
v	Parameter value to use for the bootstrap distribution. By default it is the MLE of the data.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
mle.meth	Method to use to compute the MLE.

Value

dist	matrix of sample CDFs, one per row.
obsmle	The Yule MLE of the PDF exponent.
bsmles	Vector of bootstrap MLE.
quantiles	Quantiles of the bootstrap MLEs.
pvalue	p-value of the Anderson-Darling statistics relative to the bootstrap MLEs.
obsmands	Observed Anderson-Darling Statistic.
meanmles	Mean of the bootstrap MLEs.

Note

See the papers on <https://handcock.github.io/?q=Holland> for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, simyule, llyule

Examples

```
# Now, simulate a Yule distribution over 100
# observations with rho=4.0

set.seed(1)
s4 <- simyule(n=100, rho=4)
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for rho
#

s4est <- ayulemle(s4)
s4est

#
# Use the bootstrap to compute a confidence interval rather than using the
# asymptotic confidence interval for rho.
#

bsyule(s4, m=20)
```

---

gyulemle   *Models for Count Distributions*

Description

Functions to Estimate Parametric Discrete Probability Distributions via maximum likelihood Based on categorical response

Usage

```
gyulemle(x, cutoff = 1, cutabove = 1000, guess = 3.5, conc = FALSE,
    method = "BFGS", hellinger = FALSE, hessian=TRUE)
```

Arguments

x	A vector of categories for counts (one per observation). The values of x and the categories are: `0=0, 1=1, 2=2, 3=3, 4=4, 5=5-10, 6=11-20, 7=21-100, 8=>100`
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
conc	Calculate the concentration index of the distribution?
method	Method of optimization. See "optim" for details.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
hessian	Calculate the hessian of the information matrix (for use with calculating the standard errors.

Value

result	vector of parameter estimates - lower 95% confidence value, upper 95% confidence value, the PDF MLE, the asymptotic standard error, and the number of data values >=cutoff and <=cutabove.
theta	The Yule MLE of the PDF exponent.
value	The maximized value of the function.
conc	The value of the concentration index (if calculated).

Note

See the papers on <https://handcock.github.io/?q=Holland> for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

Examples

```
#
# Simulate a Yule distribution over 100
# observations with rho=4.0
#

set.seed(1)
s4 <- simyule(n=100, rho=4)
table(s4)

#
# Recode it as categorical
#
```

```
s4[s4 >  4 & s4 < 11] <- 5
s4[s4 > 100] <- 8
s4[s4 >  20] <- 7
s4[s4 >  10] <- 6

#
# Calculate the MLE and an asymptotic confidence
# interval for rho
#

s4est <- gyulemle(s4)
s4est

#
# Calculate the MLE and an asymptotic confidence
# interval for rho under the Waring model (i.e., rho=4, p=2/3)
#

s4warest <- gwarmle(s4)
s4warest

#
# Compare the AICC and BIC for the two models
#

llgyuleall(v=s4est$theta,x=s4)
llgwarall(v=s4warest$theta,x=s4)
```

---

llgyule   *Calculate the Conditional log-likelihood for Count Distributions*

Description

Functions to Estimate the Conditional Log-likelihood for Discrete Probability Distributions. The likelihood is calcualted condition on the count being at least the cutoff value and less than or equal to the cutabove value.

Usage

```
llgyule(v, x, cutoff=1,cutabove=1000,xr=1:10000,hellinger=FALSE)
```

Arguments

v	A vector of parameters for the Yule (a 1-vector - the scaling exponent).
x	A vector of categories for counts (one per observation). The values of x and the categories are: 0=0, 1=1, 2=2, 3=3, 4=4, 5=5-10, 6=11-20, 7=21-100, 8=>100
cutoff	Calculate estimates conditional on exceeding this value.

cutabove	Calculate estimates conditional on not exceeding this value.
xr	range of count values to use to approximate the set of all realistic counts.
hellinger	Calculate the Hellinger distance of the parametric model from the data instead of the log-likelihood?

Value

the log-likelihood for the data x at parameter value v (or the Hellinder distance if `hellinger=TRUE`).

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

gyulemle, llgyuleall, dyule

Examples

```
#
# Simulate a Yule distribution over 100
# observations with rho=4.0
#

set.seed(1)
s4 <- simyule(n=100, rho=4)
table(s4)

#
# Recode it as categorical
#

s4[s4 >  4 & s4 < 11] <- 5
s4[s4 > 100] <- 8
s4[s4 >  20] <- 7
s4[s4 >  10] <- 6

#
# Calculate the MLE and an asymptotic confidence
# interval for rho
#

s4est <- gyulemle(s4)
s4est

#
```

```
# Calculate the MLE and an asymptotic confidence
# interval for rho under the Waring model (i.e., rho=4, p=2/3)
#

s4warest <- gwarmle(s4)
s4warest

#
# Compare the log-likelihoods for the two models
#

llgyule(v=s4est$theta,x=s4)
llgwar(v=s4warest$theta,x=s4)
```

---

llgyuleall   *Calculate the log-likelihood for Count Distributions*

Description

Functions to Estimate the Log-likelihood for Discrete Probability Distributions Based on Categorical Response.

Usage

```
llgyuleall(v, x, cutoff = 2, cutabove = 1000,  np=1)
```

Arguments

v	A vector of parameters for the Yule (a 1-vector - the scaling exponent).
x	A vector of categories for counts (one per observation). The values of x and the categories are: 0=0, 1=1, 2=2, 3=3, 4=4, 5=5-10, 6=11-20, 7=21-100, 8=>100
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
np	wnumber of parameters in the model. For the Yule this is 1.

Value

the log-likelihood for the data x at parameter value v.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

gyulemle, llgyule, dyule, llgwarall

Examples

```
#
# Simulate a Yule distribution over 100
# observations with rho=4.0
#

set.seed(1)
s4 <- simyule(n=100, rho=4)
table(s4)

#
# Recode it as categorical
#

s4[s4 >  4 & s4 < 11] <- 5
s4[s4 > 100] <- 8
s4[s4 >  20] <- 7
s4[s4 >  10] <- 6


#
# Calculate the MLE and an asymptotic confidence
# interval for rho
#

s4est <- gyulemle(s4)
s4est

# Calculate the MLE and an asymptotic confidence
# interval for rho under the Waring model (i.e., rho=4, p=2/3)
#

s4warest <- gwarmle(s4)
s4warest

#
# Compare the AICC and BIC for the two models
#

llgyuleall(v=s4est$theta,x=s4)
llgwarall(v=s4warest$theta,x=s4)
```

---

llpln *Calculate the Conditional log-likelihood for the Poisson Lognormal Distributions*

Description

Compute the Conditional Log-likelihood for the Poisson Lognormal Discrete Probability Distribution. The likelihood is calculated conditionl on the count being at least the cutoff value and less than or equal to the cutabove value.

Usage

```
llpln(v, x, cutoff=1,cutabove=1000,xr=1:10000,hellinger=FALSE,logn = TRUE)
```

Arguments

v	A vector of parameters for the Yule (a 1-vector - the scaling exponent).
x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
xr	range of count values to use to approximate the set of all realistic counts.
hellinger	Calculate the Hellinger distance of the parametric model from the data instead of the log-likelihood?
logn	Use logn parametrization, that is, mean and variance on the observation scale.

Value

the log-likelihood for the data x at parameter value v (or the Hellinder distance if `hellinger=TRUE`).

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

aplnmle, llplnall, dpln

Examples

```
# Simulate a Poisson Lognormal distribution over 100
# observations with lognormal mean -1 and logormal standard deviation 1.

set.seed(1)
s4 <- simpln(n=100, v=c(-1,1))
table(s4)

#
# Calculate the MLE and an asymptotic confidence
```

```
# interval for rho
#

s4est <- aplnmle(s4)
s4est

#
# Calculate the MLE and an asymptotic confidence
# interval for rho under the Waring model
#

s4warest <- awarmle(s4)
s4warest

#
# Compare the log-likelihoods for the two models
#

llpln(v=s4est$theta,x=s4)
llwar(v=s4warest$theta,x=s4)
```

---

llyule   *Calculate the Conditional log-likelihood for Count Distributions*

Description

Functions to Estimate the Conditional Log-likelihood for Discrete Probability Distributions. The likelihood is calcualted condition on the count being at least the cutoff value and less than or equal to the cutabove value.

Usage

```
llyule(v, x, cutoff=1,cutabove=1000, xr=1:10000 ,hellinger=FALSE,
       weights = rep(1, length(x)))
```

Arguments

v	A vector of parameters for the Yule (a 1-vector - the scaling exponent).
x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
xr	range of count values to use to approximate the set of all realistic counts.
hellinger	Calculate the Hellinger distance of the parametric model from the data instead of the log-likelihood?
weights	sample weights on the observed counts.

Value

the log-likelihood for the data x at parameter value v (or the Hellinder distance if `hellinger=TRUE`).

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, llyuleall, dyule

Examples

```
# Simulate a Yule distribution over 100
# observations with rho=4.0

set.seed(1)
s4 <- simyule(n=100, rho=4)
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for rho
#

s4est <- ayulemle(s4)
s4est

#
# Calculate the MLE and an asymptotic confidence
# interval for rho under the Waring model (i.e., rho=4, p=2/3)
#

s4warest <- awarmle(s4)
s4warest

#
# Compare the log-likelihoods for the two models
#

llyule(v=s4est$theta,x=s4)
llwar(v=s4warest$theta,x=s4)
```

---

llyuleall	*Calculate the log-likelihood for Count Distributions*

Description

Functions to Estimate the Log-likelihood for Discrete Probability Distributions.

Usage

```
llyuleall(v, x, cutoff = 2, cutabove = 1000,  np=1)
```

Arguments

v	A vector of parameters for the Yule (a 1-vector - the scaling exponent).
x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
np	wnumber of parameters in the model. For the Yule this is 1.

Value

the log-likelihood for the data x at parameter value v.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, llyule, dyule, llwarall

Examples

```
# Simulate a Yule distribution over 100
# observations with rho=4.0

set.seed(1)
s4 <- simyule(n=100, rho=4)
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for rho
```

```
#

s4est <- ayulemle(s4)
s4est

# Calculate the MLE and an asymptotic confidence
# interval for rho under the Waring model (i.e., rho=4, p=2/3)
#

s4warest <- awarmle(s4)
s4warest

#
# Compare the AICC and BIC for the two models
#

llyuleall(v=s4est$theta,x=s4)
llwarall(v=s4warest$theta,x=s4)
```

---

reedmolloy   *Generate a undirected network with a given sequence of degrees*

Description

Generate a undirected network where the degree of each actor is specified. The degree is the number of actors the actor is tied to. This returns a `network` object and requires the `igraph` package.

Usage

```
reedmolloy(deg, maxit=10, verbose=TRUE)
```

Arguments

deg	vector of counts where element i is the degree of actor i. Its sum should be even.
maxit	integer; maximum number of jitterings of the degree sequence to find a valid network.
verbose	Print out details of the progress of the algorithm.

Value

The network is returned as a `network` object.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, dyule

Examples

```
# Now, simulate a Poisson Lognormal distribution over 100
# observations with mean = -1 and s.d. = 1.

set.seed(2)
s4 <- simpln(n=100, v=c(-1,1))
table(s4)
#
simr <- reedmolloy(s4)
simr
```

---

rplnmle   *Rounded Poisson Lognormal Modeling of Discrete Data*

Description

Functions to Estimate the Rounded Poisson Lognormal Discrete Probability Distribution via maximum likelihood.

Usage

```
rplnmle(x, cutoff = 1, cutabove = 1000, guess = c(0.6,1.2),
    method = "BFGS", conc = FALSE, hellinger = FALSE, hessian=TRUE)
```

Arguments

x	A vector of counts (one per observation).
cutoff	Calculate estimates conditional on exceeding this value.
cutabove	Calculate estimates conditional on not exceeding this value.
guess	Initial estimate at the MLE.
conc	Calculate the concentration index of the distribution?
method	Method of optimization. See "optim" for details.
hellinger	Minimize Hellinger distance of the parametric model from the data instead of maximizing the likelihood.
hessian	Calculate the hessian of the information matrix (for use with calculating the standard errors.

Value

theta	vector of MLE of the parameters.
asycov	asymptotic covariance matrix.
asycor	asymptotic correlation matrix.
se	vector of standard errors for the MLE.
conc	The value of the concentration index (if calculated).

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

aplnmle

Examples

```
# Simulate a Poisson Lognormal distribution over 100
# observations with lognormal mean of -1 and lognormal variance of 1
# This leads to a mean of 1

set.seed(1)
s4 <- simpln(n=100, v=c(-1,1))
table(s4)

#
# Calculate the MLE and an asymptotic confidence
# interval for the parameters
#

s4est <- rplnmle(s4)
s4est
```

---

ryule	*Generate a (non-random) network from a Yule Distribution*

Description

Generate a network with a given number of actors having a degree distribution draw from a Yule distribution. The resultant network is not random - that is, is not a random draw from all such networks.

Usage

```
ryule(n=20,rho=2.5, maxdeg=n-1, maxit=10, verbose=FALSE)
```

Arguments

n	Number of actors in the network.
rho	PDF exponent of the Yule distribution.
maxdeg	Maximum degree to sample (using truncation of the distribution). If this is greater then n-1 then n-1 is used.
maxit	integer; maximum number of resamplings of the degree sequence to find a valid network.
verbose	Print out details of the progress of the algorithm.

Value

If the `network` package is available, the network is returned as a `network` object. If not a sociomatrix is returned.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, dyule, reedmolloy

Examples

```
# Now, simulate a Yule network of 30
# actors with rho=4.0
ryule(n=30, rho=4)
```

---

simcmp	*Simulate from a Conway Maxwell Poisson Distribution*

Description

Functions to generate random samples from a Conway Maxwell Poisson Probability Distribution

Usage

```
simcmp(n=100, v=c(7,2.6), maxdeg=10000)
```

Arguments

n	number of samples to draw.
v	Conway Maxwell Poisson parameters: lognormal mean and lognormal s.d.
maxdeg	Maximum degree to sample (using truncation of the distribution).

Value

vector of random draws or samples.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

acmpmle, dcmp

Examples

```
# Now, simulate a Conway Maxwell Poisson distribution over 100
# observations with lognormal mean -1 and lognormal standard deviation 1.

set.seed(1)
s4 <- simcmp(n=100, v=c(7,3))
table(s4)
```

---

simdp	*Simulate from a Discrete Pareto Distribution*

Description

Functions to generate random samples from a Discrete Pareto Probability Distribution

Usage

```
simdp(n=100, v=3.5, maxdeg=10000)
```

Arguments

n	number of samples to draw.
v	Discrete Pareto parameters: PDF exponent.
maxdeg	Maximum degree to sample (using truncation of the distribution).

Value

vector of random draws or samples.

Note

See the papers on <https://handcock.github.io/?q=Holland> for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

adpmle, ddp

Examples

```
## Not run:
# Now, simulate a Discrete Pareto distribution over 100
# observations with lognormal mean -1 and lognormal standard deviation 1.

set.seed(1)
s4 <- simdp(n=100, v=3.5)
table(s4)

## End(Not run)
```

---

simnb   *Simulate from a Negative Binomial Distribution*

Description

Functions to generate random samples from a Negative Binomial Probability Distribution

Usage

```
simnb(n=100, v=c(5,0.2), maxdeg=10000)
```

Arguments

n	number of samples to draw.
v	Negative Binomial parameters: expected count and probability of another.
maxdeg	Maximum degree to sample (using truncation of the distribution).

Value

vector of random draws or samples.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

anbmle, dnb

Examples

```
# Now, simulate a Negative Binomial distribution over 100
# observations with lognormal mean -1 and lognormal standard deviation 1.

set.seed(1)
s4 <- simnb(n=100, v=c(5,0.2))
table(s4)
```

---

simpln	*Simulate from a Poisson Lognormal Distribution*

Description

Functions to generate random samples from a Poisson Lognormal Probability Distribution

Usage

```
simpln(n=100, v=c(0.6,1.2), maxdeg=10000, cutoff=1)
```

Arguments

n	number of samples to draw.
v	Poisson Lognormal parameters: lognormal mean and lognormal s.d.
maxdeg	Maximum degree to sample (using truncation of the distribution).
cutoff	Calculate estimates conditional on exceeding this value.

Value

vector of random draws or samples.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

aplnmle, dpln

Examples

```
# Now, simulate a Poisson Lognormal distribution over 100
# observations with lognormal mean -1 and lognormal standard deviation 1.

set.seed(1)
s4 <- simpln(n=100, v=c(-1,1))
table(s4)
```

---

simwar   *Simulate from a Waring Distribution*

Description

Functions to generate random samples from a Waring Probability Distribution

Usage

```
simwar(n=100, v=c(3.5, 0.1), maxdeg=10000)
```

Arguments

n	number of samples to draw.
v	Waring parameters: scaling exponent and probability of a new actor.
maxdeg	Maximum degree to sample (using truncation of the distribution).

Value

vector of random draws or samples.

Note

See the papers on https://handcock.github.io/?q=Holland for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

awarmle, dwar

Examples

```
# Now, simulate a Waring distribution over 100
# observations with Waring with exponent 3.5 and probability of a new
# actor 0.1.

set.seed(1)
s4 <- simwar(n=100, v=c(3.5, 0.1))
table(s4)
```

---

simyule   *Simulate from a Yule Distribution*

Description

Functions to generate random samples from a Yule Probability Distribution

Usage

```
simyule(n=100, rho=4, maxdeg=10000)
```

Arguments

n	number of samples to draw.
rho	Yule PDF exponent.
maxdeg	Maximum degree to sample (using truncation of the distribution).

Value

vector of random draws or samples.

Note

See the papers on <https://handcock.github.io/?q=Holland> for details

References

Jones, J. H. and Handcock, M. S. "An assessment of preferential attachment as a mechanism for human sexual network formation," Proceedings of the Royal Society, B, 2003, 270, 1123-1128.

See Also

ayulemle, dyule

Examples

```
# Now, simulate a Yule distribution over 100
# observations with rho=4.0

set.seed(1)
s4 <- simyule(n=100, rho=4)
table(s4)
```

---

sweden	*Number of sex partners in the last 12 months for men and women in Sweden*

Description

This is a data set used in Jones and Handcock (2002) and

The data are counts of the numbers of sex partners for men and women in the last twelve months. The data from the 1996 "Sex in Sweden" survey based on a nationwide probability sample and financed by the Swedish National Board of Health.

Usage

```
 data(sweden)
```

Source

We thanks Dr. Bo Lewin, Professor of Sociology, Uppsala University and head of the research team responsible for the "Sex in Sweden" study for providing the Swedish data used in this study. This research supported by Grant 7R01DA012831-02 from NIDA and Grant 1R01HD041877 from NICHD.

References

Lewin, B. (1996). *Sex in Sweden,* Stockholm: National Institute of Public Health.

Handcock, Mark S. and Jones, James Holland (2004), "Likelihood-Based Inference for Stochastic Models of Sexual Network Formation" *Theoretical Population Biology*, doi:10.1016/j.tpb.2003.09.006.

Jones, James Holland and Handcock, Mark S. (2003), *Nature*, 423, 6940, 605-606.

Handcock, Mark S. and Jones, James Holland (2003), "An assessment of preferential attachment as a mechanism for human sexual network formation" *Proceedings of the Royal Society*, B., 270, 1123-1128.

See Also

ayulemle

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