Package ‘eggCounts’

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Imports actuar, boot, coda
Suggests lattice
Title Hierarchical Modelling of Faecal Egg Counts
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Description An implementation of hierarchical models
for faecal egg count data to assess anthelmintic
efficacy. Bayesian inference is done via MCMC sampling.
License GPL (>= 2)
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Description

This package implements hierarchical models for faecal egg count data to assess anthelmintic efficacy. Bayesian inference is done via MCMC sampling.

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See demo("fecm", package="eggCounts") for an illustration.

Author(s)

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de(nococcus

Description

This is an example data set containing 24 eggs per gram (epg) values of Taenia parasites (Echinococcus) in dogs. The correction factor of the diagnostic technique was 50.

Usage

data(echinococcus)

Examples

data(echinococcus)
table(echinococcus)
epgs

Faecal egg count samples (before and after treatment)

Description
This is an example data set containing 24 eggs per gram (epg) values before and after anthelmintic treatment. The correction factor of the diagnostic technique was 10.

Usage
data(epgs)

fecrtCI

Compute standard FECRT according to WAAVP guidelines

Description
Computes the standard Faecal Egg Count Reduction test together with approximate confidence intervals according to the WAAVP guidelines (Coles et al., 1992, 2006). The function also returns bootstrap percentile confidence intervals.

Usage
fecrtCI(epg1, epg2, paired = FALSE, alpha = 0.05, R = 1999, ...)

Arguments
epg1 faecal egg counts in untreated animals
epg2 faecal egg counts in treated animals
paired logical indication whether or not the samples are paired
alpha confidence level of the intervals
R number of bootstrap replicates
... extra arguments (not used)

Value
A list with
estimate the estimated percentage reduction in mean epg rate
bootCI corresponding percentile bootstrap confidence interval
approxCI corresponding approximate confidence interval
References

Examples
```r
data(epgs)
fecrtCI(epgs$before, epgs$after, paired=TRUE)
```

**fecr_mcmc**

Modelling of Faecal Egg Count data (two-sample case)

**Description**
Modelling of Faecal Egg Count data in a two-sample case using a paired or unpaired (ZI) Poisson gamma model formulation

**Usage**
```r
fecr_mcmc(fec.pre, fec.post, rawCounts = FALSE, f.pre = 50,
          f.post = f.pre, model = "paired", priors.mu = list(hyperpars = c(1,
          0.001), proposalDist = "kl"), priors.phi = list(hyperpars = c(1, 0.1),
          proposalDist = "unif", v = 0.5), priors.delta = list(priorDist = c("gamma",
          "beta")[1], hyperpars = c(1, 1), proposalDist = NULL),
          priors.psiB = list(hyperpars = c(1, 1)), priors.psiA = list(hyperpars =
          c(1, 1)), priors.deltapsi = list(hyperpars = c(1, 1), proposalDist =
          "beta"), maxiter.pilot = 15, nburnin = 5000, nsamples = 10000,
          thin = 1, initials = NULL, verbose = TRUE, .verboselevel = 0, ...)
```

**Arguments**
- **fec.pre**: vector with faecal egg counts before treatment
- **fec.post**: vector with faecal egg counts after treatment
- **rawCounts**: logical indicating whether fec.pre and fec.post corresponds to raw counts (as counted on the McMaster slide), or to calculated EpGs (raw counts times correction factor). Defaults to FALSE.
- **f.pre**: correction factor(s) before treatment
- **f.post**: correction factor(s) after treatment
- **model**: string with model formulation ("paired" or "unpaired")
- **priors.mu**: list with hyper-prior/proposal information for \( \mu \)
priors.phi list with hyper-prior/proposal information for $\phi$
priors.delta list with hyper-prior/proposal information for $\delta$
priors.psiA list with hyper-prior/proposal information for $\psi_A$
priors.psiB list with hyper-prior/proposal information for $\psi_B$
priors.deltaPsi list with hyper-prior/proposal information for $\delta_{\psi}$
maxiter.pilot maximal number of tries to determine a good tuning value for the proposal distribution for $\phi$
nburnin number of burn-in iterations
nsamples number of desired samples
thin thinning parameter
initials named list with starting values for the parameters $\mu$, $\phi$, $\mu_{\text{pre}}$, $\mu_{\text{post}}$, $y_{\text{pre}}$, $y_{\text{post}}$, $\delta$, $\psi_B$ and $\psi_A$
verbose print progress information
verboselevel print additional information, mainly for debugging information, larger values print more details
... extra arguments (not used atm)

Details
With many zeros, the pilot chain has difficulties to converge. Setting a different starting value for v.phi is done by setting priors.phi=list(v=somevalue). There are many more undocumented features implemented, including additional models.

Value
a named list with
samples list with samples and acceptance rates
priors list with prior specifications
v.phi tuning parameter for $\phi$
initials list with initial values
model name of the specified model
nburnin number of burnin iterations
nsamples number of returned samples
thin used thinning factor

Author(s)
Michaela Paul, with contributions from Reinhard Furrer

See Also
demo("fecn", package = "eggCounts")
fec_mcmc  
Modelling of Faecal Egg Count data (one-sample case)

Description

Modelling of Faecal Egg Count data in a one-sample case using either a Poisson gamma or a zero-inflated Poisson gamma model formulation.

Usage

fec_mcmc(fec, rawCounts = FALSE, f = 50, model = c("PoGa", "ZIPoGa")[1],
priors.mu = list(hyperpars = c(1, 0.001), proposalDist = "kl"),
priors.phi = list(hyperpars = c(1, 0.1), proposalDist = "unif", v = 0.5),
priors.psi = list(hyperpars = c(1, 1)), maxiter.pilot = 10,
 nburnin = 1000, nsamples = 10000, thin = 1, initials = NULL,
 verbose = TRUE, .verboselevel = 0, ...)

Arguments

fec vector with faecal egg counts
rawCounts logical indicating whether fec corresponds to raw counts (as counted on the McMaster slide), or to calculated EpGs (raw counts times correction factor). Defaults to FALSE.
f correction factor for the McMaster technique (e.g. 50). Either a number or a vector with different correction factors for each FEC
model either "PoGa" or "ZIPoGa"
priors.mu list with hyper-prior/proposal information for \( \mu \)
priors.phi list with hyper-prior/proposal information for \( \phi \)
priors.psi list with hyper-prior information for \( \psi \)
maxiter.pilot maximal number of tries to determine a good tuning value for the proposal distribution for \( \phi \)
nburnin number of burn-in iterations
nsamples number of desired samples
thin thinning parameter
initials named list with starting values for the parameters \( \mu, \phi, \mu_i, \psi \)
verbose print progress information
.verboselevel print additional information, mainly for debugging information, larger values print more details
... extra arguments (not used)
**Value**

a named list with

- **samples** list with samples and acceptance rates
- **priors** list with prior specifications
- **v.phi** tuning parameter for \( \phi \)
- **initials** list with initial values
- **model** name of the specified model
- **nburnin** number of burnin iterations
- **nsamples** number of returned samples
- **thin** used thinning factor

**Author(s)**

Michaela Paul, with contributions from Reinhard Furrer

**See Also**

demo("fecm", package = "eggCounts")

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**simData1s**

Simulate faecal egg count data (1-sample situation)

**Description**

Simulates (zero-inflated) egg count data

**Usage**

```r
simData1s(n = 10, m = 500, k = 0.5, psi = 1, f = 50)
```

**Arguments**

- **n** sample size (number of faeces collected)
- **m** true number of eggs per gram (EPG) (i.e. worm burden)
- **k** overdispersion factor, \( k \to \infty \) corresponds to Poisson
- **psi** prevalence (i.e. proportion of infected animals)
- **f** correction factor of the egg counting technique

**Value**

a data-frame with the observed EPG (obs), number of eggs counted on microscope slide (master) and true egg counts (true).

**Examples**

```r
fec <- simData1s(n=10, m=500, k=0.5, psi=0.7)
```
### simData2s

**Simulate faecal egg count data (2-sample situation)**

**Description**

Generates two samples of (zero-inflated) egg count data

**Usage**

```r
simData2s(n = 10, m.pre = 500, delta = 0.1, k = 0.5, psi = 1,
          psiA = psi, f = 50, paired = TRUE)
```

**Arguments**

- `n`: sample size (number of faeces collected pre and post treatment)
- `m.pre`: true number of eggs per gram (EPG) (i.e. worm burden) before treatment
- `delta`: reduction in mean after treatment
- `k`: overdispersion factor, $k \to \infty$ corresponds to Poisson
- `psi`: prevalence (i.e. proportion of infected animals)
- `psiA`: prevalence after treatment
- `f`: correction factor of the egg counting technique
- `paired`: logical indicating a paired or unpaired situation

**Value**

a data-frame with the observed EPGs (obs.prePost), number of eggs counted on microscope slide (master) and true egg counts (true).

**Examples**

```r
fec <- simData2s(n=10, m.pre=500, delta=0.8, k=0.5, psi=0.7)
```

### tab1morgan

**Abundance of trichostrongylid eggs in sheep faeces**

**Description**

This data set contains information about the abundance and distribution of trichostrongylid eggs in the faeces of 14 groups of commercially farmed sheep given in Table 1 in Morgan et al. (2005). The faecal egg counts were assumed to follow a negative binomial distribution with mean $m$ and overdispersion parameter $k$. 

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Usage

data(tab1morgan)

Format

A data frame with 14 rows and 13 variables

Details

The data set has columns:

- **group**: ID number for the groups
- **ageclass**: age class of sheep: "Lambs" or "Ewes"
- **month**: month when samples were taken
- **n**: number of sheep in group
- **meanFEC**: mean number of eggs per gram (epg) of faeces
- **k**: estimated overdispersion parameter $k$
- **k.low**: lower limit of a 95% confidence interval for $k$
- **k.up**: lower limit of a 95% confidence interval for $k$
- **maxFEC**: maximal number of eggs per gram of faeces per group
- **percentageLarger1000**: percentage of samples with more than 1000 epg
- **Chi2**: goodness-of-fit statistic for the negative binomial distribution
- **df**: corresponding degrees of freedom
- **p**: corresponding p-value

Source


Examples

data(tab1morgan)
if (require("lattice"))
  xyplot(k.low+k.up+k ~meanFEC, type="p", pch=19, col=c(8,8,1), data=tab1morgan)
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