Package ‘coarseDataTools’

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**Title** Analysis of Coarsely Observed Data

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**License** GPL (>= 2)

**URL** [https://cran.r-project.org/package=coarseDataTools](https://cran.r-project.org/package=coarseDataTools)

**Imports** MCMCpack, graphics, stats, methods

**Description** Functions to analyze coarse data. Specifically, it contains functions to (1) fit parametric accelerated failure time models to interval-censored survival time data, and (2) estimate the case-fatality ratio in scenarios with under-reporting. This package's development was motivated by applications to infectious disease: in particular, problems with estimating the incubation period and the case fatality ratio of a given disease. Sample data files are included in the package. See Reich et al. (2009) <doi:10.1002/sim.3659>, Reich et al. (2012) <doi:10.1111/j.1541-0420.2011.01709.x>, and Lessler et al. (2009) <doi:10.1016/S1473-3099(09)70069-6>.

**Collate** 'CFR_estimation.R' 'dic.fit.mcmc.R' 'dic.fit.R'
   'get.obs.type.R' 'S4stuff.R' 'sampleSizeSimulation.R'
   'coarseDataTools-package.R'

**RoxygenNote** 6.1.1

**NeedsCompilation** no

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R topics documented:

- cd.fit ........................................... 2
- cd.fit.mcmc ..................................... 3
- dgammaOff1 ..................................... 4
- dic.fit .......................................... 4
- dic.fit.mcmc ..................................... 6
- EMforCFR ........................................ 7
- exp.win.lengths ................................ 9
- fluA.inc.per ................................... 10
- get.obs.type .................................... 11
- logLik,cd.fit-method ........................... 11
- loglikhd ......................................... 12
- mcmc.erlang ..................................... 12
- mcmcpack.ll ..................................... 13
- nycH1N1 ......................................... 14
- pgammaOff1 ...................................... 15
- plot,cd.fit-method .............................. 15
- precision.simulation ............................ 16
- simulated.outbreak.deaths ..................... 17

Index 18

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cd.fit  An S4 Class that stores a fitted coarse data object

Description

This is the output from dic.fit(), which contains the important bits of information about the model fit and key options used.

Slots

- `ests`: Matrix of class "numeric". This matrix summarizes the results of fitting the model. Rows correspond to the first parameter, the second parameter and then percentiles specified by the `ptiles` argument. Columns correspond to the point estimate, the lower and upper bounds on the 95% confidence interval and the standard error of the point estimate. If the maximization does not converge, this matrix is filled with NAs.
- `conv`: Object of class "numeric". A value of 1 indicates successful convergence; 0 indicates unsuccessful convergence.
- `MSG`: Object of class "character". The error message returned from optim() if the routine fails to converge.
- `loglik`: Object of class "numeric". Value of the estimated maximum log-likelihood.
- `samples`: Object of class "data.frame". Data frame of bootstrap estimates of parameters (if bootstraps were performed).
- `data`: Object of class "data.frame". Original data used to fit model.
dist: Object of class "character". Failure time distribution fit to data. "L" for log-normal, "G" for gamma, "W" for Weibull, and "E" for Erlang.

inv.hessian: Object of class "matrix". The inverse of the hessian matrix for the likelihood surface at the MLE. Used to determine the standard errors for the percentiles. Note that optimization is done on a transformed scale with all parameters logged for all distributions except the first parameter of the log-normal distribution.

est.method: Object of class "character". Method used for estimation.

ci.method: Object of class "character". Method used for estimation of confidence/credible intervals.

---

An S4 Class that stores a MCMC fit coarse data object

**Description**

This is the output from `dic.fit.mcmc()`, which contains the important bits of information about the model fit and key options used.

**Slots**

ests: Matrix of class "numeric". This matrix summarizes the results of fitting the model. Rows correspond to the first parameter, the second parameter and then percentiles specified by the ptiles argument. Columns correspond to the point estimate, the lower and upper bounds on the 95% credible interval and the standard error of the point estimate.

conv: Object of class "numeric". Not used in with `dic.fit.mcmc`

MSG: Object of class "character". The error message returned from optim() if the routine fails to converge.

loglik: Object of class "numeric". Not used in with `dic.fit.mcmc`.

samples: Object of class "data.frame". Data frame of posterior draws of parameters.

data: Object of class "data.frame". Original data used to fit model.

dist: Object of class "character". Failure time distribution fit to data. "L" for log-normal, "G" for gamma, "W" for Weibull, and "E" for Erlang.

inv.hessian: Object of class "matrix". Not used in with `dic.fit.mcmc`.

est.method: Object of class "character". Method used for estimation.

ci.method: Object of class "character". Method used for estimation of confidence/credible intervals.
**Description**

Function that calculates \( d\gamma \) with a offset of 1 (i.e., 1 is equivalent to 0)

**Usage**

\[
dgammaOff1(x, \text{replace0} = \text{FALSE}, \ldots)
\]

**Arguments**

- \( x \) value to calculate \( d\gamma \) at
- \( \text{replace0} \) should we replace 0 with epsilon
- \( \ldots \) other parameters to \( d\gamma \)

**Value**

d\gamma offset

---

**Description**

\texttt{dic.fit} fits a parametric accelerated failure time model to survival data. It was developed with the application to estimating incubation periods of infectious diseases in mind but is applicable to many general problems. The data can be a mixture of doubly interval-censored, single interval-censored or exact observations from a single univariate distribution. Currently, three distributions are supported: log-normal, gamma, and Weibull. (The Erlang distribution is supported in the \texttt{dic.fit.mcmc} function, which implements an MCMC version of this code.) We use a consistent \( \text{par1}, \text{par2} \) notation for each distribution, they map in the following manner:

- \text{Log – normal}(\text{meanlog} = \text{par1}, \text{sdlog} = \text{par2})
- \text{Gamma}(\text{shape} = \text{par1}, \text{scale} = \text{par2})
- \text{Weibull}(\text{shape} = \text{par1}, \text{scale} = \text{par2})

Standard errors of parameters can be computed using closed-form asymptotic formulae or using a bootstrap routine for log-normal and gamma models. Currently, bootstrap SEs are the only option for the gamma models, which do not have a closed form for the percentiles. \texttt{dic.fit()} calculates asymptotic SEs by default, or whenever the \texttt{n.boots} option is set to 0. To compute bootstrap SEs, just set \texttt{n.boots} to be greater than zero. \texttt{dic.fit.mcmc} also allows for Markov Chain Monte Carlo fitting of these three parametric models and Erlang models as well.
dic.fit

Usage

dic.fit(dat, start.par2 = log(2), opt.method = "L-BFGS-B",
  par1.int = c(log(0.5), log(13)), par2.int = c(log(1.01),
  log(log(5))), ptiles = c(0.05, 0.95, 0.99), dist = "L",
  n.boots = 0, ...)

Arguments

dat a matrix with columns named "EL", "ER", "SL", "SR", corresponding to the left
  (L) and right (R) endpoints of the windows of possible exposure (E) and symp-
  tomat onset (S). Also, a "type" column must be specified and have entries with 0,
  1, or 2, corresponding to doubly interval-censored, single interval-censored or
  exact observations, respectively.

start.par2 starting value for 2nd parameter of desired distribution

opt.method method used by optim

par1.int the log-scale interval of possible median values (in the same units as the obser-
  vations in dat). Narrowing this interval can help speed up convergence of the
  algorithm, but care must be taken so that possible values are not excluded or
  that the maximization does not return a value at an endpoint of this interval.

par2.int the log-scale interval of possible dispersion values

ptiles percentiles of interest

dist what distribution to use to fit the data. Default "L" for log-normal. "G" for
  gamma, and "W" for Weibull.

n.boots number of bootstrap resamples (0 means that asymptotic results are desired)

... additional options passed to optim

Value

a cd.fit S4 object.

References


See Also

cd.fit, dic.fit.mcmc

Examples

data(fluA.inc.per)
dic.fit(fluA.inc.per, dist="L")
**dic.fit.mcmc**

Fits the distribution to the passed-in data using MCMC as implemented in MCMCpack.

**Description**

Similar to **dic.fit** but uses MCMC instead of a direct likelihood optimization routine to fit the model. Currently, four distributions are supported: log-normal, gamma, Weibull, and Erlang. See Details for prior specification.

**Usage**

```r
dic.fit.mcmc(dat, prior.par1 = NULL, prior.par2 = NULL, 
init.pars = c(1, 1), ptiles = c(0.05, 0.95, 0.99), verbose = 1000, 
burnin = 3000, n.samples = 5000, dist = "L", seed = NULL, 
...)```

**Arguments**

- **dat** the data
- **prior.par1** vector of first prior parameters for each model parameter. If NULL then default parameters are used (as described in Details section).
- **prior.par2** vector of second prior parameters for each model parameter. If NULL then default parameters are used (as described in Details section).
- **init.pars** the initial parameter values (vector length = 2)
- **ptiles** returned percentiles of the survival survival distribution
- **verbose** how often do you want a print out from MCMCpack on iteration number and M-H acceptance rate
- **burnin** number of burnin samples
- **n.samples** number of samples to draw from the posterior (after the burnin)
- **dist** distribution to be used (L for log-normal, W for weibull, G for Gamma, and E for erlang, off1G for 1 day right shifted gamma)
- **seed** seed for the random number generator for MCMC
- **...** additional parameters to MCMCmetrop1R

**Details**

The following models are used:

\[
\text{Log-normal model: } f(x) = \frac{1}{x \sigma \sqrt{2 \pi}} \exp\left\{-\frac{(\log x - \mu)^2}{2 \sigma^2}\right\}
\]

\[
\text{Log-normal Default Prior: } \mu \sim N(0, 1000), \log(\sigma) \sim N(0, 1000)
\]

\[
\text{Weibull model: } f(x) = \frac{\alpha}{\beta} \left(\frac{x}{\beta}\right)^{\alpha-1} \exp\left\{-\left(\frac{x}{\beta}\right)^\alpha\right\}
\]
WeibullDefaultPriorSpecification: \( \log(\alpha) \sim N(0, 1000), \beta \sim \Gamma(0.001, 0.001) \)

\[ \text{Gammanemodel: } f(x) = \frac{1}{\theta^k \Gamma(k)} x^{k-1} \exp\left\{ -\frac{x}{\theta} \right\} \]

\[ \text{GammaDefaultPriorSpecification: } \rho(k, \theta) \propto \frac{1}{\theta^* \sqrt{k} \cdot \text{TriGamma}(k) - 1} \]

(Note: this is Jeffery’s Prior when both parameters are unknown), and

\[ \text{Trigamma}(x) = \frac{\partial}{\partial x^2} \ln(\Gamma(x)) \]

\[ \text{Erlangmodel: } f(x) = \frac{1}{\theta^k (k-1)!} x^{k-1} \exp\left\{ -\frac{x}{\theta} \right\} \]

\[ \text{ErlangDefaultPriorSpecification: } k \sim \text{NBinom}(100, 1), \log(\theta) \sim N(0, 1000) \]

(Note: parameters in the negative binomial distribution above represent mean and size, respectively)

Value

a cd.fit.mcmc S4 object

DEmforCFR

A function to estimate the relative case fatality ratio when reporting
rates are time-varying and deaths are lagged because of survival time.

Description

This function implements an EM algorithm to estimate the relative case fatality ratio between two
groups when reporting rates are time-varying and deaths are lagged because of survival time.

Usage

EMforCFR(assumed.nu, alpha.start.values, full.data, max.iter = 50,
verb = FALSE, tol = 1e-10, SEM.var = TRUE)

Arguments

assumed.nu a vector of probabilities corresponding to the survival distribution, i.e. \( \text{nu}[i] = \text{Pr}(\text{surviving } i \text{ days | fatal case}) \)

alpha.start.values a vector starting values for the reporting rate parameter of the GLM model. This must have length which corresponds to one less than the number of unique integer values of full.data["new.times"].

full.data A matrix of observed data. See description below.

max.iter The maximum number of iterations for the EM algorithm and the accompanying SEM algorithm (if used).
verb An indicator for whether the function should print results as it runs.

tol A tolerance to use to test for convergence of the EM algorithm.

SEM.var If TRUE, the SEM algorithm will be run in addition to the EM algorithm to calculate the variance of the parameter estimates.

Details
The data matrix full.data must have the following columns:

- **grp** a 1 or a 2 indicating which of the two groups, j, the observation is for.
- **new.times** an integer value representing the time, t, of observation.
- **R** the count of recovered cases with onset at time t in group j.
- **D** the count of deaths which occurred at time t in group j (note that these deaths did not have disease onset at time t but rather died at time t).
- **N** the total cases at t, j, or the sum of R and D columns.

Value
A list with the following elements

- **naive.rel.cfr** the naive estimate of the relative case fatality ratio
- **glm.rel.cfr** the reporting-rate-adjusted estimate of the relative case fatality ratio
- **EM.rel.cfr** the lag-adjusted estimate of the relative case fatality ratio
- **EM.re.cfr.var** the variance for the log-scale lag-adjusted estimator taken from the final M-step
- **EM.rel.cfr.var.SEM** the Supplemented EM algorithm variance for the log-scale lag-adjusted estimator
- **EM.rel.cfr.chain** a vector of the EM algorithm iterates of the lag-adjusted relative CFR estimates
- **EMiter** the number of iterations needed for the EM algorithm to converge
- **EMconv** indicator for convergence of the EM algorithm. 0 indicates all parameters converged within max.iter iterations. 1 indicates that the estimate of the relative case fatality ratio converged but other did not. 2 indicates that the relative case fatality ratio did not converge.
- **SEMconv** indicator for convergence of SEM algorithm. Same scheme as EMconv.
- **ests** the coefficient estimates for the model
- **ests.chain** a matrix with all of the coefficient estimates, at each EM iteration
- **DM** the DM matrix from the SEM algorithm
- **DMiter** a vector showing how many iterations it took for the variance component to converge in the SEM algorithm
```r
## This is code from the CFR vignette provided in the documentation.

data(simulated.outbreak.deaths)
min.cases <- 10
N.1 <- simulated.outbreak.deaths[1:60, "N"]
N.2 <- simulated.outbreak.deaths[61:120, "N"]
first.t <- min(which(N.1 > min.cases & N.2 > min.cases))
last.t <- max(which(N.1 > min.cases & N.2 > min.cases))
idx.for.Estep <- first.t: last.t
new.times <- 1:length(idx.for.Estep)
simulated.outbreak.deaths <- cbind(simulated.outbreak.deaths, new.times = NA)
simulated.outbreak.deaths[ c(idx.for.Estep, idx.for.Estep + 60), "new.times"] <- rep(new.times, + 2)
assumed.nu = c(0, 0.3, 0.4, 0.3)
alpha.start <- rep(0, 22)

## caution! this next line may take several minutes (5-10, depending on
## the speed of your machine) to run.
## Not run: cfr.ests <- EMforCFR(assumed.nu = assumed.nu,
alpha.start.values = alpha.start,
full.data = simulated.outbreak.deaths,
verb = FALSE,
SEM.var = TRUE,
max.iter = 500,
tol = 1e-05)

## End(Not run)
```

### exp.win.lengths

Exposure window lengths from an influenza outbreak at a NYC school

**Description**

A numeric vector of exposure window lengths taken from a dataset of doubly interval-censored incubation period observations. All observations came from a NYC public school. The outbreak has been described in full in Lessler et al. (see citation below).

**Usage**

```r
data(exp.win.lengths)
```

**Format**

A numeric vector with 134 positive values. Each value represents an exposure window length from an observation of the incubation period for that individual. The exposure window length is the length of time during which exposure could have occurred. For example, if an individual could have been exposed anytime between 6am on Monday to 6am on Wednesday, her exposure window length would be 2 days.
Source


Examples

data(exp.win.lengths)
summary(exp.win.lengths)
hist(exp.win.lengths)

fluA.inc.per  Coarse incubation period data for influenza A

Description

These observations on the incubation period of influenza A come from a variety of sources, and were gathered for a literature review. They report doubly interval-censored, single interval-censored or exact observations for the incubation period.

Usage

data(fluA.inc.per)

Format

A data frame with 151 observations on the following 7 variables.

author  the name of the primary author for the source of the observation
year  the year of the study which is the source of the observation
EL  the earliest possible time of infection
ER  the latest possible time of infection
SL  the earliest possible time of symptom onset
SR  the latest possible time of symptom onset
type  an indicator of the type of observation: 0 for doubly interval-censored, 1 for single-interval censored, 2 for exact

Source


Examples

data(fluA.inc.per)
head(fluA.inc.per)
get.obs.type

get.obs.type  
*Tries to guess the observation types (SIC, DIC, or exact).*

**Description**

Tries to guess the observation types (SIC, DIC, or exact).

**Usage**

get.obs.type(dat)

**Arguments**

- **dat**
  
a matrix of data, similar to what needs to be passed to `dic.fit()`.

**Value**

vector of guessed types

---

logLik,cd.fit-method

Get the log-likelihood value of a `cd.fit` or `cd.fit.mcmc` object

**Description**

Get the log-likelihood value of a `cd.fit` or `cd.fit.mcmc` object.

**Usage**

```r
## S4 method for signature 'cd.fit'
logLik(object)
```

**Arguments**

- **object**
  
A `cd.fit` or `cd.fit.mcmc` object.

**Value**

log-likelihood value
Description

Negative log likelihood for a dataset of interval-censored data, given a distribution and its parameters.

Usage

loglikhd(pars, dat, dist)

Arguments

pars vector of the transformed (estimation scale) parameters
dat a dataset, as in dic.fit
dist a distribution, as in dic.fit

Details

This package uses two versions of each parameter, the estimation scale, or the scale that is used for numerical optimization, and the reporting scale, or the natural scale of the parameters. For all likelihood calculations, this loglikhd function expects parameters that are on the estimation scale, i.e. have range \((-\infty, \infty)\). Specifically, this translates into all parameters for all distributions being log-transformed except for the meanlog (i.e. "par1") for the log-normal distribution.

Value

negative log-likelihood for a given dataset, parameters, and distribution.

mcmc.erlang

**Does a metropolis hastings for the Erlang distribution**

Description

Does a metropolis hastings for the Erlang distribution

Usage

mcmc.erlang(dat, prior.par1, prior.par2, init.pars, verbose, burnin, n.samples, sds = c(1, 1))
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dat</td>
<td>the data to fit</td>
</tr>
<tr>
<td>prior.par1</td>
<td>mean of priors. A negative binomial (for shape) and a normal for log(scale)</td>
</tr>
<tr>
<td>prior.par2</td>
<td>dispersion parameters for priors, dispersion for negative binomial, log scale sd for normal</td>
</tr>
<tr>
<td>init.pars</td>
<td>the starting parameters on the reporting scale</td>
</tr>
<tr>
<td>verbose</td>
<td>how often to print an update</td>
</tr>
<tr>
<td>burnin</td>
<td>how many burnin iterations to do</td>
</tr>
<tr>
<td>n.samples</td>
<td>the number of samples to keep and report back</td>
</tr>
<tr>
<td>sds</td>
<td>the standard deviations for the proposal distribution</td>
</tr>
</tbody>
</table>

Value

a matrix of n.samples X 2 parameters, on the estimation scale

---

mcmcpack.ll

*posterior log likelihood function to pass to MCMCpack sampler*

Description

posterior log likelihood function to pass to MCMCpack sampler

Usage

mcmcpack.ll(pars, dat, prior.par1, prior.par2, dist)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pars</td>
<td>the parameters to calculate the ll at</td>
</tr>
<tr>
<td>dat</td>
<td>the date to base it on</td>
</tr>
<tr>
<td>prior.par1</td>
<td>first parameter of each prior</td>
</tr>
<tr>
<td>prior.par2</td>
<td>second parameter of each prior</td>
</tr>
<tr>
<td>dist</td>
<td>the distribution the likelihood is being calculated for</td>
</tr>
</tbody>
</table>

Value

the posterior log likelihood
nycH1N1

*Incubation period data from New York City Public Schools, 2009 H1N1 influenza outbreak*

**Description**

These observations on the incubation period of influenza A come from the investigation of the H1N1 outbreak in NYC schools in the spring of 2009. They report doubly interval-censored observations for the incubation period.

**Usage**

```R
data(nycH1N1)
```

**Format**

A data frame with 134 observations on the following 5 variables.

- **EL** the earliest possible time of infection
- **ER** the latest possible time of infection
- **SL** the earliest possible time of symptom onset
- **SR** the latest possible time of symptom onset
- **type** an indicator of the type of observation: 0 for doubly interval-censored, 1 for single-interval censored, 2 for exact. All of these observations are doubly interval-censored.

**Source**


**Examples**

```R
data(nycH1N1)
head(nycH1N1)
## Not run: dic.fit(nycH1N1)
```
pgammaOff1

Function that calculates pgamma with a offset of 1 (i.e., 1 is equivalent to 0)

Description
Function that calculates pgamma with a offset of 1 (i.e., 1 is equivalent to 0)

Usage
pgammaOff1(x, replace0 = FALSE, ...)  

Arguments
  x  
  replace0  
  ...  

Value
pgamma offset

plot,cd.fit-method
Plots the estimated survival function with an option to plot the posterior draws or bootstraps behind the fit

Description
Plots the estimated survival function with an option to plot the posterior draws or bootstraps behind the fit

Usage
## S4 method for signature 'cd.fit'
plot(x, y, col.main = rgb(230, 85, 13, maxColorValue = 255), col.samps = rgb(99, 99, 99, 10, maxColorValue = 255), plot.n.samps = 200, add = F, xlim = range(x@data), ...)
precision.simulation

Simulate incubation period analyses with coarse data

Description

These functions simulate coarse incubation period data sets and analyze them. The goal is for these simulations to provide evidence for how much information a given dataset contains about a characteristic of the incubation period distribution.

Usage

```r
precision.simulation(N, med = 2, disp = 1.3, percentile = 0.5, 
nsim = 100, exact.data = FALSE, pct.type.A = 0.5, 
exp.win.dat = NULL, verb = FALSE)
```

```r
precision.simulation.exact(N, med, disp, percentile, nsim, verb)
```

```r
precision.simulation.coarse(N, med, disp, percentile, nsim, pct.type.A, 
exp.win.dat, verb)
```

```r
generate.coarse.data(N, med, disp, pct.type.A, exp.win.dat)
```

Arguments

- **N**  
  Overall sample size for the datasets to be simulated.

- **med**  
  Median for the assumed log normal distribution of the incubation periods.

- **disp**  
  Dispersion for the assumed log normal distribution of the incubation periods.

- **percentile**  
  Percentile of the incubation period distribution which we want to estimate.

- **nsim**  
  Number of datasets to analyze in the simulation.

- **exact.data**  
  Either TRUE/FALSE. Incidates whether the data generated should be coarsened at all. If TRUE, pct.type.A and exp.win.dat are ignored.

- **pct.type.A**  
  Percent of the N observations that are assumed to be type A data. If N*pct.type.A is not an integer, it will be rounded to the nearest integer.
exp.win.dat  A vector of exposure window lengths. Defaults to the observed window lengths from Lessler et al. (see below).
verb  If TRUE, a message with the system time and iteration number will be printed ten times during the simulation run.

Value

The precision.simulation functions return a matrix with four columns and nsim rows. The "est" column gives the estimated percentiles for the incubation period distribution. The "SE" column gives the standard error for the estimate. The "conv" column is 1 if the doubly interval-censored likelihood maximization converged. Otherwise, it is 0. The "bias" column gives the estimated percentile - true percentile. The generate.coarse.data function returns a matrix with data suitable for analysis by the dic.fit function.

simulated.outbreak.deaths

Simulated case and death reports from a fictional outbreak

Description

This dataset provides reported counts of cases and deaths occurring at different time points across a simulated outbreak. Details of the data simulation algorithm are provided in the manuscript "Estimating case fatality ratios from infectious disease surveillance data" (Reich et al., under review, available upon request).

Usage

data(simulated.outbreak.deaths)

Format

time  time, t, after start of outbreak
grp  an categorical variable indicating membership in one of two groups of a covariate, j
R  number of recovered cases reported at the given t and j
D  number of deaths reported at the given t and j
N  total number of cases and deaths reported at t and j, or D+R

Source


Examples

data(simulated.outbreak.deaths)
head(simulated.outbreak.deaths)
plot(simulated.outbreak.deaths[,"grp"==1,"D"], type="l")
Index

*Topic case
   EMforCFR, 7
*Topic coarse
   EMforCFR, 7
*Topic datasets
   exp.win.lengths, 9
   fluA.inc.per, 10
   nycH1N1, 14
*Topic data
   EMforCFR, 7
*Topic disease
   EMforCFR, 7
*Topic fatality
   EMforCFR, 7
*Topic incomplete
   EMforCFR, 7
*Topic infectious
   EMforCFR, 7
*Topic ratio
   EMforCFR, 7

   cd.fit, 2, 5
   cd.fit-class (cd.fit), 2
   cd.fit.mcmc, 3
   cd.fit.mcmc-class (cd.fit.mcmc), 3

dgammaOff1, 4
 dic.fit, 4, 6
dic.fit.mcmc, 4, 5, 6

EMforCFR, 7
exp.win.lengths, 9
fluA.inc.per, 10

generate.coarse.data
   (precision.simulation), 16
get.obs.type, 11

logLik (logLik, cd.fit-method), 11
logLik, cd.fit-method, 11

loglikhd, 12
mcmc.erlang, 12
MCMCmetrop1R, 6
mcmcpack, 11, 13
nycH1N1, 14
pgammaOff1, 15
plot (plot, cd.fit-method), 15
plot, cd.fit-method, 15
precision.simulation, 16
simulated.outbreak.deaths, 17

18