Package 'gfiExtremes'

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Type Package

Title Generalized Fiducial Inference for Extremes

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License GPL (>= 2)

Depends coda

Imports Rcpp (>= 1.0.5), parallel, doParallel, foreach, stats

LinkingTo Rcpp, BH, RcppArmadillo

Encoding UTF-8

RoxygenNote 7.1.1

URL https://github.com/stla/gfiExtremes

BugReports https://github.com/stla/gfiExtremes/issues

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation yes

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R topics documented:

gfigpd1 ................................................................. 2
gfigpd2 ................................................................. 3
gfigpd1

Description

Runs the MCMC sampler of the fiducial distribution for the generalized Pareto model with known threshold.

Usage

```r
gfigpd1(
  X,
  beta,
  threshold,
  gamma.init = NA,
  sigma.init = NA,
  sd.gamma = NA,
  sd.sigma = NA,
  Jnumb = 50L,
  iter = 10000L,
  burnin = 2000L,
  thin = 6L,
  nchains = 4L,
  nthreads = parallel::detectCores(),
  seeds = NULL
)
```

Arguments

- `X`: numeric vector of data
- `beta`: vector of probabilities corresponding to the quantiles to be estimated
- `threshold`: value of the known threshold, must be smaller than the maximum of `X`
- `gamma.init`: starting value for gamma in the MCMC
- `sigma.init`: starting value for sigma in the MCMC
- `sd.gamma`: standard deviation for the proposed gamma in the MCMC
- `sd.sigma`: standard deviation for the proposed sigma in the MCMC
- `Jnumb`: number of subsamples that are taken from the Jacobian
- `iter`: number of iterations per chain (burnin excluded)
burnin number of the first MCMC iterations discarded
thin thinning number for the MCMC chain. (e.g. if it is 1 no iteration is skipped)
nchains number of MCMC chains to run
nthreads number of threads to run the chains in parallel
seeds the seeds used for the MCMC sampler; one seed per chain, or NULL to use random seeds

Value

An object of class `mcmc` if `nchains=1`, otherwise an object of class `mcmc.list`.

References


Examples

```r
set.seed(666L)
X <- rgpareto(200L, mu = 10, gamma = 0.5, sigma = 1)
gf <- gfigpd1(
  X, beta = c(0.98, 0.99), threshold = 10,
  iter = 2000L, nchains = 2L, nthreads = 2L
)
# note: 2*2000 iterations is not enough, I'm using these settings because
# of CRAN constraints (elapsed time must be < 5s)
summary(gf)
qgpareto(c(0.98, 0.99), mu = 10, gamma = 0.5, sigma = 1)
rejectionRate(gf)
HPDinterval(gf)
HPDinterval(joinMCMCchains(gf))
```

Fiducial inference for the generalized Pareto model with unknown threshold

Description

Runs the MCMC sampler of the fiducial distribution for the generalized Pareto model with unknown threshold.

Usage

```r
gfigpd2( 
  x, 
  beta, 
  threshold.init = NA, 
  gamma.init = NA, 
)```
sigma.init = NA,
sd.gamma = NA,
sd.sigma = NA,
p1 = 0.9,
p2 = 0.5,
lambda1 = 2,
lambda2 = 10,
Jnumb = 50L,
iter = 10000L,
burnin = 2000L,
thin = 6L,
nchains = 4L,
nthreads = parallel::detectCores(),
seeds = NULL,
allParameters = FALSE
)

Arguments

X numeric vector of data
beta vector of probabilities corresponding to the quantiles to be estimated
threshold.init a guess of the unknown threshold, must be in the range of X
gamma.init starting value for gamma in the MCMC
sigma.init starting value for sigma in the MCMC
sd.gamma standard deviation for the proposed gamma in the MCMC
sd.sigma standard deviation for the proposed sigma in the MCMC
p1 probability that the MCMC will propose a new \((gamma, sigma)\); \((1-p1)\) would be the probability that the MCMC chain will propose a new index for a new threshold
p2 probability that the new index proposed will be larger than the current index
lambda1 the small jump the index variable will make
lambda2 the large jump the index variable will make; happens 1 of every 10 iterations
Jnumb number of subsamples that are taken from the Jacobian
iter number of iterations per chain (burnin excluded)
burnin number of the first MCMC iterations discarded
thin thinning number for the MCMC chain. (e.g. if it is 1 no iteration is skipped)
nchains number of MCMC chains to run
nthreads number of threads to run the chains in parallel
seeds the seeds used for the MCMC sampler; one seed per chain, or NULL to use random seeds
allParameters logical, whether to return the MCMC chains of all parameters (pretty useless) or only the ones of the quantiles
**Value**

An object of class `mcmc` if `nchains=1`, otherwise an object of class `mcmc.list`.

**References**


**Examples**

```r
set.seed(31415L)
X <- rgamma(350L, shape = 10, rate = 1)
gf <- gfigpd2(X, beta = c(0.98, 0.99), iter = 3000L, nthreads = 2L)
summary(gf)
qgamma(c(0.98, 0.99), shape = 10, rate = 1)
traceplot(gf[, "beta1"])
traceplot(gf[, "beta2"])
thresholdEstimate(gf)
rejectionRate(gf)
HPDinterval(gf)
HPDinterval(joinMCMCchains(gf))
```

---

**GPareto**

**Generalized Pareto distribution**

**Description**

Density, distribution function, quantile function, and random generation for the generalized Pareto distribution.

**Usage**

```r
dgpareto(x, mu, gamma, sigma, log = FALSE)
pgpareto(q, mu, gamma, sigma)
rgpareto(n, mu, gamma, sigma)
qgpareto(p, mu, gamma, sigma)
```

**Arguments**

- `x`: numeric vector
- `mu`: location parameter
- `gamma`: shape parameter
- `sigma`: scale parameter, strictly positive
- `log`: logical, whether to return the log-density
**joinMCMCchains**

*Join MCMC chains*

**Description**

Joins multiple MCMC chains into a single chain.

**Usage**

`joinMCMCchains(gfi)`

**Arguments**

- `gfi`:
  
  An output of `gfigpd1` or `gfigpd2` containing more than one chain.

**Value**

A mcmc object.

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**thresholdEstimate**

*Threshold estimate*

**Description**

Returns the estimate of the threshold.

**Usage**

`thresholdEstimate(gfi)`

**Arguments**

- `gfi`:
  
  An output of `gfigpd2`.

**Value**

The estimated threshold.
Index

dgpareto (GPareto), 5

gfigpd1, 2, 6
  gfigpd2, 3, 6
  GPareto, 5

  joinMCMCchains, 6

  mcmc, 3, 5
  mcmc.list, 3, 5

  pgpareto (GPareto), 5

  qgpareto (GPareto), 5

  rgpareto (GPareto), 5

  thresholdEstimate, 6