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Description Dictionary-like reference for computing scoring rules in a wide range of situations. Covers both parametric forecast distributions (such as mixtures of Gaussians) and distributions generated via simulation. Further details can be found in the package vignettes <doi:10.18637/jss.v090.i12>, <doi:10.18637/jss.v110.i08>.

URL https://github.com/FK83/scoringRules

License GPL (>= 2)

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ar_ms *Bayesian analysis of a Markov Switching autoregressive model*

Description

Bayesian analysis of a Markov Switching autoregressive model

Usage

```
ar_ms(
  y,
  nlag = 1,
  beta_switch = FALSE,
  variance_switch = TRUE,
  identification_constraint = "variance",
  n_burn = 5000,
  n_rep = 20000,
  forecast_periods = 5,
  printout = FALSE,
  Hm1_delta = 25,
  mu_delta = 0,
  s_ = 0.3,
  nu_ = 3,
  R = matrix(c(8, 2, 2, 8), nrow = 2)
)
```

Arguments

y	numeric vector (time series to be analyzed).
nlag	integer, number of autoregressive lags (defaults to one).
beta_switch, variance_switch	logicals, indicating whether there should be Markovian state dependence in regression parameters and residual variance, respectively. Defaults to beta_switch = FALSE, variance_switch = TRUE.
identification_constraint	character, indicating how to identify latent states. Possible values: "variance", "mean" and "persistence". Defaults to "variance".
n_burn, n_rep	integers, number of MCMC iterations for burn-in and main analysis.
forecast_periods	number of future periods for which forecasts are computed.
printout	logical, whether to print progress report during MCMC (defaults to FALSE).
Hm1_delta, mu_delta, s_, nu_, R	prior parameters as described in KLTG (2021, Appendix E and Table 4).

Details

The default parameters are as set by KLTG (2021, Section 5). The output matrices `fcMeans` and `fcSds` can be used to construct the mixture-of-parameters estimator analyzed by KLTG. While many of the model features can be changed as described above, the number of Markov regimes is always fixed at two.

ar_ms is an R/C++ implementation of Matlab code kindly shared by Gianni Amisano via his website (https://sites.google.com/site/gianniamisanowebsite/). See Amisano and Giacomini (2007) who analyze a similar model.

Value

List containing parameter estimates and forecasts, with the following elements:

- `pars`, matrix of posterior draws for parameters (rows are MCMC iterations, columns are parameters)
- `fcMeans` and `fcSds`, matrices of forecast means and standard deviations (rows are MCMC iterations, columns are forecast horizons)
- `probs`, matrix of filtered probabilities for first latent state (rows are MCMC iterations, columns are time periods, excluding the first `nlag` values for initialization).
- `count`, integer, counter for the number of states that were relabeled based on `identification_constraint`.

Author(s)

Fabian Krueger, based on Matlab code by Gianni Amisano (see details section)

References

Amisano, G. and R. Giacomini (2007), 'Comparing density forecasts via weighted likelihood ratio tests', Journal of Business and Economic Statistics 25, 177-190. doi:10.1198/073500106000000332

Krueger, F., Lerch, S., Thorarinsdottir, T.L. and T. Gneiting (2021): 'Predictive inference based on Markov chain Monte Carlo output', *International Statistical Review* 89, 274-301. doi:10.1111/insr.12405

See Also

run_casestudy uses ar_ms to replicate the results of KLTG (2021, Section 5).

Examples

```
## Not run:
# Use GDP data from 2014Q4 edition
data(gdp)
dat <- subset(gdp, vint == "2014Q4")
y <- dat$val[order(dat$dt)]

# Fit model, using the default settings
set.seed(816)
fit <- ar_ms(y)
```

```
# Histograms of parameter draws
par(mfrow = c(2, 2))
hist(fit$pars[,1], main = "Intercept (state-invariant)", xlab = "")
hist(fit$pars[,2], main = "AR(1) term (state-invariant)", xlab = "")
hist(1/fit$pars[,3], main = "Residual variance in 1st state", xlab = "")
hist(1/fit$pars[,4], main = "Residual variance in 2nd state", xlab = "")

# By construction, the residual variance is smaller in the 1st than in the 2nd state:
print(mean(1/fit$pars[,3] < 1/fit$pars[,4]))

## End(Not run)
```

`crps.numeric` *Continuous Ranked Probability Score for Parametric Forecast Distributions*

Description

Calculate the Continuous Ranked Probability Score (CRPS) given observations and parameters of a family of distributions.

Usage

```
## S3 method for class 'numeric'
crps(y, family, ...)
```

Arguments

`y`	vector of realized values.
`family`	string which specifies the parametric family; current options: `"2pexp"`, `"2pnorm"`, `"beta"`, `"binom"`, `"clogis"`, `"cnorm"`, `"ct"`, `"exp"`, `"expM"`,`"exponential"`, `"gamma"`, `"gev"`, `"gpd"`, `"gtclogis"`, `"gtcnorm"`, `"gtct"`, `"hyper"`, `"lapl"`,`"laplace"`, `"llapl"`, `"llogis"`, `"lnorm"`, `"log-laplace"`, `"log-logistic"`,`"log-normal"`, `"logis"`, `"logistic"`, `"mixnorm"`, `"mixture-normal"`, `"nbinom"`,`"negative-binomial"`, `"norm"`, `"normal"`, `"pois"`, `"poisson"`, `"t"`, `"tlogis"`,`"tnorm"`, `"tt"`, `"two-piece-exponentia` `"two-piece-normal"`, `"unif"`, `"uniform"`.
`...`	vectors of parameter values; expected input depends on the chosen `family`. See details below.

Details

Mathematical details are available in Appendix A of the vignette *Evaluating probabilistic forecasts with scoringRules* that accompanies the package.

The parameters supplied to each of the functions are numeric vectors:

1. Distributions defined on the real line:
   - `"laplace"` or `"lapl"`: `location` (real-valued location parameter), `scale` (positive scale parameter); see `crps_lapl`

- "logistic" or "logis": location (real-valued location parameter), scale (positive scale parameter); see crps_logis
- "normal" or "norm": mean, sd (mean and standard deviation); see crps_norm
- "normal-mixture" or "mixture-normal" or "mixnorm": m (mean parameters), s (standard deviations), w (weights); see crps_mixnorm; note: matrix-input for parameters
- "t": df (degrees of freedom), location (real-valued location parameter), scale (positive scale parameter); see crps_t
- "two-piece-exponential" or "2pexp": location (real-valued location parameter), scale1, scale2 (positive scale parameters); see crps_2pexp
- "two-piece-normal" or "2pnorm": location (real-valued location parameter), scale1, scale2 (positive scale parameters); see crps_2pnorm

2. Distributions for non-negative random variables:
   - "exponential" or "exp": rate (positive rate parameter); see crps_exp
   - "gamma": shape (positive shape parameter), rate (positive rate parameter), scale (alternative to rate); see crps_gamma
   - "log-laplace" or "llapl": locationlog (real-valued location parameter), scalelog (positive scale parameter); see crps_llapl
   - "log-logistic" or "llogis": locationlog (real-valued location parameter), scalelog (positive scale parameter); see crps_llogis
   - "log-normal" or "lnorm": locationlog (real-valued location parameter), scalelog (positive scale parameter); see crps_lnorm
3. Distributions with flexible support and/or point masses:
   - "beta": shape1, shape2 (positive shape parameters), lower, upper (lower and upper limits); see crps_beta
   - "uniform" or "unif": min, max (lower and upper limits), lmass, umass (point mass in lower or upper limit); see crps_unif
   - "expM": location (real-valued location parameter), scale (positive scale parameter), mass (point mass in location); see crps_expM
   - "gev": location (real-valued location parameter), scale (positive scale parameter), shape (real-valued shape parameter); see crps_gev
   - "gpd": location (real-valued location parameter), scale (positive scale parameter), shape (real-valued shape parameter), mass (point mass in location); see crps_gpd
   - "tlogis": location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); see crps_tlogis
   - "clogis": location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); see crps_clogis
   - "gtclogis": location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); lmass, umass (point mass in lower or upper limit); see crps_gtclogis
   - "tnorm": location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); see crps_tnorm
   - "cnorm": location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); see crps_cnorm
   - "gtcnorm": location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); lmass, umass (point mass in lower or upper limit); see crps_gtcnorm

- "tt": df (degrees of freedom), location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); see crps_tt
- "ct": df (degrees of freedom), location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); see crps_ct
- "gtct": df (degrees of freedom), location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); lmass, umass (point mass in lower or upper limit); see crps_gtct

4. Distributions of discrete variables:
   - "binom": size (number of trials (zero or more)), prob (probability of success on each trial); see crps_binom
   - "hyper": m (the number of white balls in the urn), n (the number of black balls in the urn), k (the number of balls drawn from the urn); see crps_hyper
   - "negative-binomial" or "nbinom": size (positive dispersion parameter), prob (success probability), mu (mean, alternative to prob); see crps_nbinom
   - "poisson" or "pois": lambda (positive mean); see crps_pois

All numerical arguments should be of the same length. An exception are scalars of length 1, which will be recycled.

Value

Vector of score values. *A lower score indicates a better forecast.*

Author(s)

Alexander Jordan, Fabian Krueger, Sebastian Lerch

References

Closed form expressions of the CRPS for specific distributions:

Baran, S. and S. Lerch (2015): 'Log-normal distribution based Ensemble Model Output Statistics models for probabilistic wind-speed forecasting', Quarterly Journal of the Royal Meteorological Society 141, 2289-2299. doi:10.1002/qj.2521 *(Log-normal)*

Friederichs, P. and T.L. Thorarinsdottir (2012): 'Forecast verification for extreme value distributions with an application to probabilistic peak wind prediction', Environmetrics 23, 579-594. doi:10.1002/env.2176 *(Generalized Extreme Value, Generalized Pareto)*

Gneiting, T., Larson, K., Westvelt III, A.H. and T. Goldman (2005): 'Calibrated probabilistic forecasting using ensemble model output statistics and minimum CRPS estimation', Monthly Weather Review 133, 1098-1118. doi:10.1175/mwr2904.1 *(Normal)*

Gneiting, T., Larson, K., Westrick, K., Genton, M.G. and E. Aldrich (2006): 'Calibrated probabilistic forecasting at the stateline wind energy center: The regime-switching space-time method', Journal of the American Statistical Association 101, 968-979. doi:10.1198/016214506000000456 *(Censored normal)*

Gneiting, T. and T.L. Thorarinsdottir (2010): 'Predicting inflation: Professional experts versus no-change forecasts', arXiv preprint arXiv:1010.2318. *(Two-piece normal)*

Grimit, E.P., Gneiting, T., Berrocal, V.J. and N.A. Johnson (2006): 'The continuous ranked probability score for circular variables and its application to mesoscale forecast ensemble verification',

Quarterly Journal of the Royal Meteorological Society 132, 2925-2942. doi:10.1256/qj.05.235 *(Mixture of normals)*

Scheuerer, M. and D. Moeller (2015): 'Probabilistic wind speed forecasting on a grid based on ensemble model output statistics', Annals of Applied Statistics 9, 1328-1349. doi:10.1214/15-aoas843 *(Gamma)*

Thorarinsdottir, T.L. and T. Gneiting (2010): 'Probabilistic forecasts of wind speed: ensemble model output statistics by using heteroscedastic censored regression', Journal of the Royal Statistical Society (Series A) 173, 371-388. doi:10.1111/j.1467985x.2009.00616.x *(Truncated normal)*

Wei, W. and L. Held (2014): 'Calibration tests for count data', TEST 23, 787-205. doi:10.1007/s1174901403808 *(Poisson, Negative Binomial)*

Independent listing of closed-form solutions for the CRPS:

Taillardat, M., Mestre, O., Zamo, M. and P. Naveau (2016): 'Calibrated ensemble forecasts using quantile regression forests and ensemble model output statistics', Monthly Weather Review 144, 2375-2393. doi:10.1175/mwrd150260.1

See Also

logs.numeric

Examples

```
crps(y = 1, family = "normal", mean = 0, sd = 2)
crps(y = rnorm(20), family = "normal", mean = 1:20, sd = sqrt(1:20))

## Arguments can have different lengths:
crps(y = rnorm(20), family = "normal", mean = 0, sd = 2)
crps(y = 1, family = "normal", mean = 1:20, sd = sqrt(1:20))

## Mixture of normal distributions requires matrix input for parameters:
mval <- matrix(rnorm(20*50), nrow = 20)
sdval <- matrix(runif(20*50, min = 0, max = 2), nrow = 20)
weights <- matrix(rep(1/50, 20*50), nrow = 20)
crps(y = rnorm(20), family = "mixnorm", m = mval, s = sdval, w = weights)
```

GDP data *Data and forecasts for US GDP growth*

Description

Historical data and forecast distributions for the growth rate of US gross domestic product (GDP). The forecasts are generated from a Bayesian Markov Switching model as described in Section 5 of KLTG (2021).

Format

gdp is a data frame which contains the real-time data set used in Section 5 of KLTG (2021), with the following columns:

- dt - date in question (e.g., "2013Q2" for the second quarter of 2013)
- vint - data vintage (i.e., the date at which the realization was recorded); same format as dt
- val - value of the GDP growth rate

gdp_mcmc is a list, whereby each element is a data frame. gdp_mcmc$forecasts contains the simulated forecast distributions. There are 20 columns (corresponding to quarters 2008:Q1 to 2012:Q4) and 5.000 rows (corresponding to simulation draws). gdp_mcmc$actuals contains the actual observations. There are 20 columns (again corresponding to quarterly dates) and a single row.

Details

The realizations in gdp_mcmc$actuals are also contained in gdp, based on the second available vintage for each date. For example, gdp_mcmc$actuals$X2008Q1 is the entry in gdp for which dt == "2008Q1" and vint == "2008Q3".

Source

The GDP growth rate is computed from real-time data provided by the Federal Reserve Bank of Philadelphia, https://www.philadelphiafed.org/surveys-and-data/real-time-data-research/real-time-data-set-for-macroeconomists (series code "ROUTPUT", second-vintage data). The same data also enters the model which is used to generate the forecast distribution. *Disclaimer: The provider of the raw data takes no responsibility for the accuracy of the data posted here. Furthermore, the raw data may be revised over time, and the website linked above should be consulted for the official, most recent version.*

The model from which the forecast draws are generated is described in Section 5 of KLTG (2021). Forecasts are one quarter ahead (that is, they are based on data until the previous quarter).

References

Krueger, F., Lerch, S., Thorarinsdottir, T.L. and T. Gneiting (2021): 'Predictive inference based on Markov chain Monte Carlo output', *International Statistical Review* 89, 274-301. doi:10.1111/insr.12405

Examples

```
## Not run:

# Load data
data(gdp_mcmc)

# Histogram of forecast draws for 2012Q4
fc_draws <- gdp_mcmc$forecasts[, "X2012Q4"]
hist(fc_draws, main = "Forecast draws for 2012:Q4", xlab = "Value")

# Add vertical line at realizing value
rlz <- gdp_mcmc$actuals[, "X2012Q4"]
```

```
abline(v = rlz, lwd = 3)

# Compute CRPS for this forecast case
crps_sample(y = rlz, dat = fc_draws)


## End(Not run)
```

`get_weight_func` *Default Weight and Chaining Functions*

Description

Get commonly used weight or chaining functions to use within weighted scoring rules. The normal and logistic distribution, density, and survival functions are available. Multivariate normal distribution functions are also available for multivariate scoring rules.

Usage

```
get_weight_func(name = "norm_cdf", mu = 0, sigma = 1, weight = TRUE)
```

Arguments

`name`	name of the weight function to extract.
`mu`	location parameter(s) of the normal or logistic distribution.
`sigma`	scale parameter(s) of the normal or logistic distribution.
`weight`	logical specifying whether to return a weight function (`weight = TRUE`) or chaining function (`weight = FALSE`).

Details

The weighted scoring rules in scores_sample_univ_weighted and scores_sample_multiv_weighted require a weight or chaining function argument (`weight_func` or `chain_func`) to target particular outcomes. `get_weight_func()` can be used to obtain the relevant R function corresponding to commonly-used weight and chaining functions.

These commonly-used weight and chaining functions correspond to cumulative distribution functions (cdf's), probability density function (pdf's) and survival functions of the normal and logistic distributions. The `name` argument specifies the desired weight or chaining function. This must be one of `'norm_cdf'`, `'norm_pdf'`, `'norm_surv'`, `'logis_cdf'`, `'logis_pdf'` and `'logis_surv'`, corresponding to the cdf, pdf and survival functions of the normal and logistic distribution, respectively.

`mu` and `sigma` represent the location and scale parameters of the normal or logistic distribution.

`weight` is a logical that specifies whether a weight or chaining function should be returned: if `weight = TRUE` (the default) the weight function is returned, and if `weight = FALSE` the chaining function is returned.

The normal weight and chaining functions are applicable in both the univariate and multivariate setting. In the univariate case, `mu` and `sigma` should be single numeric values. In the multivariate case, `'norm_cdf'` and `'norm_pdf'` represent the cdf and pdf of the multivariate normal distribution, with mean vector `mu` and covariance matrix `diag(sigma)`. Here, `mu` and `sigma` are vectors with length equal to the dimension of the multivariate outcomes.

Note that `get_weight_func()` can currently only return multivariate weight and chaining functions corresponding to the multivariate normal distribution with a diagonal covariance matrix.

Value

A weight or chaining function.

Author(s)

Sam Allen

References

Gneiting, T. and R. Ranjan (2011): 'Comparing density forecasts using threshold-and quantile-weighted scoring rules', *Journal of Business & Economic Statistics* 29, 411-422. doi:10.1198/jbes.2010.08110

Allen, S., Ginsbourger, D. and J. Ziegel (2023): 'Evaluating forecasts for high-impact events using transformed kernel scores', *SIAM/ASA Journal on Uncertainty Quantification* 11, 906-940. doi:10.1137/22M1532184

See Also

scores_sample_univ_weighted and scores_sample_multiv_weighted for weighted scoring rules.

Examples

```
## Not run:

## univariate
# generate data
y <- rnorm(10)
sample_fc <- matrix(rnorm(100), nrow = 10)

# normal cdf
mu <- 1
sigma <- 1

weight_func <- get_weight_func("norm_cdf", mu = mu, sigma = sigma)
chain_func <- get_weight_func("norm_cdf", mu = mu, sigma = sigma, weight = FALSE)
owcrps_sample(y = y, dat = sample_fc, weight_func = weight_func)
twcrps_sample(y = y, dat = sample_fc, chain_func = chain_func)

# results are the same if the weight function is input manually
weight_func <- function(x) pnorm(x, mu, sigma)
chain_func <- function(x) (x - mu)*pnorm(x, mu, sigma) + (sigma^2)*dnorm(x, mu, sigma)
owcrps_sample(y = y, dat = sample_fc, weight_func = weight_func)
```

```
twcrps_sample(y = y, dat = sample_fc, chain_func = chain_func)


# logistic pdf
mu <- 0
sigma <- 1

weight_func <- get_weight_func("logis_pdf", mu = mu, sigma = sigma)
chain_func <- get_weight_func("logis_pdf", mu = mu, sigma = sigma, weight = FALSE)
owcrps_sample(y = y, dat = sample_fc, weight_func = weight_func)
twcrps_sample(y = y, dat = sample_fc, chain_func = chain_func)


# normal survival function
mu <- -1
sigma <- 1

weight_func <- get_weight_func("norm_surv", mu = mu, sigma = sigma)
chain_func <- get_weight_func("norm_surv", mu = mu, sigma = sigma, weight = FALSE)
owcrps_sample(y = y, dat = sample_fc, weight_func = weight_func)
twcrps_sample(y = y, dat = sample_fc, chain_func = chain_func)


## multivariate
d <- 3  # number of dimensions
m <- 10  # number of samples from multivariate forecast distribution

# generate samples from multivariate normal distributions
mu0 <- rep(0, d)
mu <- rep(1, d)
S0 <- S <- diag(d)
S0[S0==0] <- 0.2
S[S==0] <- 0.1

y <- drop(mu0 + rnorm(d) %*% chol(S0))
sample_fc <- replicate(m, drop(mu + rnorm(d) %*% chol(S)))

# component-wise normal cdf
mu <- rep(1, d)
sigma <- rep(1, d)

weight_func <- get_weight_func("norm_cdf", mu = mu, sigma = sigma)
chain_func <- get_weight_func("norm_cdf", mu = mu, sigma = sigma, weight = FALSE)
owes_sample(y = y, dat = sample_fc, weight_func = weight_func)
twes_sample(y = y, dat = sample_fc, chain_func = chain_func)


## End(Not run)
```

`logs.numeric` *Logarithmic Score for Parametric Forecast Distributions*

Description

Calculate the logarithmic score (LogS) given observations and parameters of a family of distributions.

Usage

```
## S3 method for class 'numeric'
logs(y, family, ...)
```

Arguments

y	Vector of realized values.
family	String which specifies the parametric family; current options: "2pexp", "2pnorm", "beta", "binom", "exp", "exp2","exponential", "gamma", "gev", "gpd", "hyper", "lapl","laplace", "llapl", "llogis", "lnorm", "log-laplace", "log-logistic","log-normal", "logis", "logistic", "mixnorm", "mixture-normal", "nbinom","negative-binomial", "norm", "normal", "pois", "poisson", "t", "tlogis","tnorm", "tt", "two-piece-exponential", "two-piece-normal", "unif", "uniform".
...	Vectors of parameter values; expected input depends on the chosen family. See details below.

Details

The parameters supplied to each of the functions are numeric vectors:

1. Distributions defined on the real line:
   - "laplace" or "lapl": location (real-valued location parameter), scale (positive scale parameter); see logs_lapl
   - "logistic" or "logis": location (real-valued location parameter), scale (positive scale parameter); see logs_logis
   - "normal" or "norm": mean, sd (mean and standard deviation); see logs_norm
   - "normal-mixture" or "mixture-normal" or "mixnorm": m (mean parameters), s (standard deviations), w (weights); see logs_mixnorm; note: matrix-input for parameters
   - "t": df (degrees of freedom), location (real-valued location parameter), scale (positive scale parameter); see logs_t
   - "two-piece-exponential" or "2pexp": location (real-valued location parameter), scale1, scale2 (positive scale parameters); see logs_2pexp
   - "two-piece-normal" or "2pnorm": location (real-valued location parameter), scale1, scale2 (positive scale parameters); see logs_2pnorm
2. Distributions for non-negative random variables:
   - "exponential" or "exp": rate (positive rate parameter); see logs_exp
   - "gamma": shape (positive shape parameter), rate (positive rate parameter), scale (alternative to rate); see logs_gamma
   - "log-laplace" or "llapl": locationlog (real-valued location parameter), scalelog (positive scale parameter); see logs_llapl

- "log-logistic" or "llogis": locationlog (real-valued location parameter), scalelog (positive scale parameter); see logs_llogis
- "log-normal" or "lnorm": locationlog (real-valued location parameter), scalelog (positive scale parameter); see logs_lnorm

3. Distributions with flexible support and/or point masses:
   - "beta": shape1, shape2 (positive shape parameters), lower, upper (lower and upper limits); see logs_beta
   - "uniform" or "unif": min, max (lower and upper limits); see logs_unif
   - "exp2": location (real-valued location parameter), scale (positive scale parameter); see logs_exp2
   - "gev": location (real-valued location parameter), scale (positive scale parameter), shape (real-valued shape parameter); see logs_gev
   - "gpd": location (real-valued location parameter), scale (positive scale parameter), shape (real-valued shape parameter); see logs_gpd
   - "tlogis": location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); see logs_tlogis
   - "tnorm": location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); see logs_tnorm
   - "tt": df (degrees of freedom), location (location parameter), scale (scale parameter), lower, upper (lower and upper limits); see logs_tt
4. Distributions of discrete variables:
   - "binom": size (number of trials (zero or more)), prob (probability of success on each trial); see crps_binom
   - "hyper": m (the number of white balls in the urn), n (the number of black balls in the urn), k (the number of balls drawn from the urn); see crps_hyper
   - "negative-binomial" or "nbinom": size (positive dispersion parameter), prob (success probability), mu (mean, alternative to prob); see logs_nbinom
   - "poisson" or "pois": lambda (positive mean); see logs_pois

All numerical arguments should be of the same length. An exception are scalars of length 1, which will be recycled.

Value

Vector of score values. *A lower score indicates a better forecast.*

Author(s)

Alexander Jordan, Fabian Krueger, Sebastian Lerch

See Also

crps.numeric

Examples

```
logs(y = 1, family = "normal", mean = 0, sd = 2)
logs(y = rnorm(20), family = "normal", mean = 1:20, sd = sqrt(1:20))

## Arguments can have different lengths:
logs(y = rnorm(20), family = "normal", mean = 0, sd = 2)
logs(y = 1, family = "normal", mean = 1:20, sd = sqrt(1:20))

## Mixture of normal distributions requires matrix input for parameters:
mval <- matrix(rnorm(20*50), nrow = 20)
sdval <- matrix(runif(20*50, min = 0, max = 2), nrow = 20)
weights <- matrix(rep(1/50, 20*50), nrow = 20)
logs(y = rnorm(20), family = "mixnorm", m = mval, s = sdval, w = weights)
```

`plot.casestudy` *Plot the output of run_casestudy*

Description

Plot the output of run_casestudy

Usage

```
## S3 method for class 'casestudy'
plot(x, ...)
```

Arguments

`x`	object of class `casestudy`, generated by run_casestudy
`...`	additional parameters, see details below.

Details

The plot is in the same format as Figure 3 in KLTG (2021). Its content (nr of MCMC chains, maximal sample size, etc) depends on the parameters used to generate run_casestudy. In terms of additional inputs (`...`), the following are currently implemented:

- `scoring_rule`, the scoring rule for which results are to be plotted, either `"crps"` or `"logs"`. Defaults to `"crps"`.
- `add_main_title`, logical, whether to add main title to plot. Defaults to `TRUE`.

Value

none, used for the effect of drawing a plot.

Author(s)

Fabian Krueger

References

Krueger, F., Lerch, S., Thorarinsdottir, T.L. and T. Gneiting (2021): 'Predictive inference based on Markov chain Monte Carlo output', *International Statistical Review* 89, 274-301. doi:10.1111/insr.12405

See Also

run_casestudy produces the forecast results summarized by plot.casestudy

---

`plot.mcstudy` *Plot the output of run_mcstudy*

Description

Plot the output of run_mcstudy

Usage

```
## S3 method for class 'mcstudy'
plot(x, ...)
```

Arguments

`x`	object of class `mcstudy`, generated by run_mcstudy
`...`	additional parameters, see details below.

Details

The plot is in the same format as Figure 1 or 2 in KLTG (2021), depending on the parameters set when running run_mcstudy. These parameters also determine the plot content (nr of MCMC chains, maximal sample size, etc). In terms of additional inputs (`...`), the following are currently implemented:

- `scoring_rule`, the scoring rule for which results are to be plotted, either `"crps"` or `"logs"`. Defaults to `"crps"`.
- `add_main_title`, logical, whether to add main title to plot. Defaults to `TRUE`.

Value

none, used for the effect of drawing a plot.

Author(s)

Fabian Krueger

References

Krueger, F., Lerch, S., Thorarinsdottir, T.L. and T. Gneiting (2021): 'Predictive inference based on Markov chain Monte Carlo output', *International Statistical Review* 89, 274-301. doi:10.1111/insr.12405

See Also

run_mcstudy produces the simulation results summarized by plot.mcstudy

---

print.casestudy *Simple print method for object of class casestudy*

Description

Simple print method for object of class casestudy

Usage

```
## S3 method for class 'casestudy'
print(x, ...)
```

Arguments

x	Object of class casestudy, generated via run_casestudy
...	Additional specifications (presently not in use)

---

print.mcstudy *Simple print function for object of class mcstudy*

Description

Simple print function for object of class mcstudy

Usage

```
## S3 method for class 'mcstudy'
print(x, ...)
```

Arguments

x	Object of class mcstudy, generated via run_mcstudy
...	Additional specifications (presently not in use)

rps_probs *Ranked Probability Score*

Description

Computes the Ranked Probability Score (RPS) for a given vector or matrix of probabilities.

Usage

```
rps_probs(y, x, tol = .Machine$double.eps)
```

Arguments

y	vector of realizations, taking integer values between 1 and K. For the RPS, outcomes have an ordinal interpretation only (see details).
x	vector or matrix (depending on y; see details) of probabilities.
tol	non-negative numeric value specifying the allowed deviation from 1 of the total (row-wise) probability in x.

Details

The RPS interprets the outcome variable as ordinal. That is, different outcome values can be ranked (e.g., y=1 is smaller than y=2), but their numerical difference has no meaningful interpretation. For simplicity, the outcome y is coded as an integer here, with y = 1 indicating the smallest possible realization and y = K indicating the largest possible realization. If y is a vector of length n >= 2, x should be given as a matrix with n rows and K columns. If y has length 1, then x may be a vector of length K.

References

Original proposal of the RPS

Epstein, E.S. (1969): 'A Scoring System for Probability Forecasts of Ranked Categories', Journal of Applied Meteorology and Climatology 8, 985-987.

Application example (see esp. Section 4 for comments on the RPS' ordinal interpretation)

Krueger, F. and L. Pavlova (2024): 'Quantifying Subjective Uncertainty in Survey Expectations', International Journal of Forecasting 40, 796-810, doi:10.1016/j.ijforecast.2023.06.001.

Examples

```
# Example with three outcome categories (a single observation)
p <- c(.3, .2, .5)
y <- 2
rps_probs(y, p)

# Example with three outcome categories (n = 2 observations)
p <- matrix(c(.2, .4, .4, .3, .6, .1), nrow = 2, byrow = TRUE)
y <- c(2, 3)
rps_probs(y, p)
```

`run_casestudy` *Run the case study in KLTG (2021), or a smaller version thereof*

Description

Run the case study in KLTG (2021), or a smaller version thereof

Usage

```
run_casestudy(
  data_df,
  burnin_size = 5000,
  max_mcmc_sample_size = 5000,
  nr_of_chains = 3,
  first_vint = "1996Q2",
  last_vint = "2014Q3",
  forecast_horizon = 1,
  random_seed = 816
)
```

Arguments

`data_df`	data frame in the same format as the gdp data set in this package.
`burnin_size`	length of the burn-in period used for each forecast.
`max_mcmc_sample_size`	maximal number of MCMC draws to consider (integer, must equal either 1000, 5000, 10000, 20000 or 40000). Defaults to 5000.
`nr_of_chains`	number of parallel MCMC for each forecast date (integer, defaults to 3).
`first_vint, last_vint`	first and last data vintage (= time point at which forecasts are made). Default to "19962Q2" and "2014Q3", respectively.
`forecast_horizon`	forecast horizon to be analyzed (integer, defaults to 1).
`random_seed`	seed for random numbers used during the MCMC sampling process. Defaults to 816.

Details

The full results in Section 5 of KLTG (2021) are based on the following setup: `burnin_size` = `10000`, `max_mcmc_sample_size` = `50000`, `nr_of_chains` = `16`, `data_df` = `gdp`, `first_vint` = `"1996Q2"`, `last_vint` = `"2014Q3"`, and `forecast_horizon` = `1`. Since running this full configuration is very time consuming, the default setup offers the possibility to run a small-scale study which reproduces the qualitative outcomes of the analysis. Running the small-scale study implied by the defaults of `run_study` as well as the GDP data (`data_df` = `gdp`) takes about 40 minutes on an Intel i7 processor.

Value

Object of class "casestudy", containing the results of the analysis. This object can be passed to `plot` for plotting, see the documentation for plot.casestudy.

Author(s)

Fabian Krueger

References

Krueger, F., Lerch, S., Thorarinsdottir, T.L. and T. Gneiting (2021): 'Predictive inference based on Markov chain Monte Carlo output', *International Statistical Review* 89, 274-301. doi:10.1111/insr.12405

See Also

plot.casestudy produces a summary plot of the results generated by run_casestudy run_casestudy uses ar_ms to fit a Bayesian Markov Switching model, recursively for several time periods.

Examples

```
## Not run:
data(gdp)
cs <- run_casestudy(data_df = gdp, last_vint = "1999Q4")
plot(cs)

## End(Not run)
```

`run_mcstudy` *Run the Monte Carlo study by KLTG (2021), or a smaller version thereof*

Description

Run the Monte Carlo study by KLTG (2021), or a smaller version thereof

Usage

```
run_mcstudy(
  s = 2,
  a = 0.5,
  n = 12,
  nr_iterations = 50,
  zoom = FALSE,
  random_seed = 816
)
```

Arguments

s, a, n	parameters characterizing the process from which data are simulated (see Section 4 and Table 4 of KLTG, 2021). Defaults to the values reported in the main text of the paper.
nr_iterations	number of Monte Carlo iterations (defaults to 50).
zoom	set to TRUE to produce results for a fine grid of small (MCMC) sample sizes, as in Figure 2 of KLTG (2021).
random_seed	seed used for running the simulation experiment. Defaults to 816.

Details

The full results in Section 4 of KLTG (2021) are based on s = 2, a = 0.5, n = 12 and nr_iterations = 1000. Producing these results takes about 140 minutes on an Intel i7 processor.

Value

Object of class "mcstudy", containing the results of the analysis. This object can be passed to plot for plotting, see the documentation for plot.mcstudy.

Author(s)

Fabian Krueger

References

Krueger, F., Lerch, S., Thorarinsdottir, T.L. and T. Gneiting (2021): 'Predictive inference based on Markov chain Monte Carlo output', *International Statistical Review* 89, 274-301. doi:10.1111/insr.12405

See Also

plot.mcstudy produces a summary plot of the results generated by run_mcstudy

---

scores *Generic Scoring Rule Calculation*

Description

Generic functions for calculating the Continuous Ranked Probability Score and the Logarithmic Score of R objects.

scoringRules provides default methods (crps.numeric, logs.numeric) to calculate scores of forecasts that are members of families of parametric distributions.

Usage

```
crps(y, ...)

logs(y, ...)
```

Arguments

y	an object for which the score is to be calculated
...	further arguments passed to or from other methods

Details

The mean logarithmic score corresponds to the negative of the log-likelihood logLik.

Value

Returns a vector of scores. One for each forecast-observation pair.

References

General background and further references on scoring rules:

Gneiting, T. and A.E. Raftery (2007): 'Strictly proper scoring rules, prediction and estimation', Journal of the American Statistical Association 102, 359-378. doi:10.1198/016214506000001437

Gneiting, T. and M. Katzfuss (2014): 'Probabilistic forecasting', Annual Review of Statistics and Its Application 1, 125-151. doi:10.1146/annurevstatistics062713085831

See Also

crps.numeric, logs.numeric

---

scores_2pexp *Calculating scores for the two-piece-exponential distribution*

Description

Calculating scores for the two-piece-exponential distribution

Usage

```
crps_2pexp(y, scale1, scale2, location = 0)

logs_2pexp(y, scale1, scale2, location = 0)
```

Arguments

y	vector of observations.
scale1, scale2	vectors of positive scale parameters.
location	vector of location parameters.

Value

A vector of score values.

`scores_2pnorm` *Calculating scores for the two-piece-normal distribution*

Description

Calculating scores for the two-piece-normal distribution

Usage

```
crps_2pnorm(y, scale1, scale2, location = 0)

logs_2pnorm(y, scale1, scale2, location = 0)
```

Arguments

`y`	vector of observations.
`scale1`, `scale2`	vectors of positive scale parameters.
`location`	vector of location parameters.

Value

A vector of score values.

`scores_beta` *Calculating scores for the beta distribution*

Description

Calculating scores for the beta distribution

Usage

```
crps_beta(y, shape1, shape2, lower = 0, upper = 1)

logs_beta(y, shape1, shape2, lower = 0, upper = 1)

dss_beta(y, shape1, shape2, lower = 0, upper = 1)
```

Arguments

`y`	vector of observations.
`shape1`, `shape2`	vectors of positive shape parameters.
`lower`, `upper`	vectors of lower and upper limits of the distribution. Must be finite.

Value

A vector of score values.

`scores_binom` *Calculating scores for the binomial distribution*

Description

Calculating scores for the binomial distribution

Usage

```
crps_binom(y, size, prob)

logs_binom(y, size, prob)
```

Arguments

`y`	vector of observations.
`size`	number of trials (zero or more).
`prob`	probability of success on each trial.

Value

A vector of score values.

`scores_exp` *Calculating scores for the exponential distribution*

Description

Calculating scores (CRPS, LogS, DSS) for the exponential distribution, and the exponential distribution with location-scale transformation and point mass in `location`.

Usage

```
crps_exp(y, rate = 1)

crps_expM(y, location = 0, scale = 1, mass = 0)

logs_exp(y, rate = 1)

logs_exp2(y, location = 0, scale = 1)

dss_exp(y, rate = 1)
```

Arguments

y	vector of observations.
rate	vector of rates.
location	vector of location parameters.
scale	vector of positive scale parameters.
mass	vector of point masses in location.

Value

A vector of score values.

---

scores_gamma *Calculating scores for the gamma distribution*

Description

Calculating scores for the gamma distribution

Usage

```
crps_gamma(y, shape, rate = 1, scale = 1/rate)

logs_gamma(y, shape, rate = 1, scale = 1/rate)

dss_gamma(y, shape, rate = 1, scale = 1/rate)
```

Arguments

y	vector of observations.
shape	vector of positive shape parameters.
rate	an alternative way to specify the scale.
scale	vector of positive scale parameters.

Value

A vector of score values.

scores_gev *Calculating scores for the generalized extreme value distribution*

Description

Calculating scores for the generalized extreme value distribution

Usage

```
crps_gev(y, shape, location = 0, scale = 1)

logs_gev(y, shape, location = 0, scale = 1)

dss_gev(y, shape, location = 0, scale = 1)
```

Arguments

y	vector of observations.
shape	vector of positive shape parameters.
location	vector of location parameters.
scale	vector of positive scale parameters.

Value

A vector of score values.

scores_gpd *Calculating scores for the generalized Pareto distribution*

Description

Calculating scores for the generalized Pareto distribution

Usage

```
crps_gpd(y, shape, location = 0, scale = 1, mass = 0)

logs_gpd(y, shape, location = 0, scale = 1)

dss_gpd(y, shape, location = 0, scale = 1)
```

Arguments

y	vector of observations.
shape	vector of positive shape parameters.
location	vector of location parameters.
scale	vector of positive scale parameters.
mass	vector of point masses in location.

Value

A vector of score values.

---

scores_hyper *Calculating scores for the hypergeometric distribution*

Description

Calculating scores for the hypergeometric distribution

Usage

```
crps_hyper(y, m, n, k)

logs_hyper(y, m, n, k)
```

Arguments

y	vector of observations / numbers of white balls drawn without replacement from an urn which contains both black and white balls.
m	the number of white balls in the urn.
n	the number of black balls in the urn.
k	the number of balls drawn from the urn, hence must be in $0, 1, \ldots, m + n$.

Value

A vector of score values.

scores_lapl *Calculating scores for the Laplace distribution*

Description

Calculating scores for the Laplace distribution

Usage

```
crps_lapl(y, location = 0, scale = 1)

logs_lapl(y, location = 0, scale = 1)

dss_lapl(y, location = 0, scale = 1)
```

Arguments

y	vector of observations.
location	vector of location parameters.
scale	vector of positive scale parameters.

Value

A vector of score values.

scores_llapl *Calculating scores for the log-Laplace distribution*

Description

Calculating scores for the log-Laplace distribution

Usage

```
crps_llapl(y, locationlog, scalelog)

logs_llapl(y, locationlog, scalelog)

dss_llapl(y, locationlog, scalelog)
```

Arguments

y	vector of observations.
locationlog	vector of location parameters on the log scale.
scalelog	vector of positive scale parameters on the log scale.

Value

A vector of score values.

`scores_llogis` *Calculating scores for the log-logistic distribution*

Description

Calculating scores for the log-logistic distribution

Usage

```
crps_llogis(y, locationlog, scalelog)

logs_llogis(y, locationlog, scalelog)

dss_llogis(y, locationlog, scalelog)
```

Arguments

`y`	vector of observations.
`locationlog`	vector of location parameters on the log scale.
`scalelog`	vector of positive scale parameters on the log scale.

Value

A vector of score values.

`scores_lnorm` *Calculating scores for the log-normal distribution*

Description

Calculating scores for the log-normal distribution

Usage

```
crps_lnorm(y, meanlog = 0, sdlog = 1, locationlog = meanlog, scalelog = sdlog)

logs_lnorm(y, meanlog = 0, sdlog = 1, locationlog = meanlog, scalelog = sdlog)

dss_lnorm(y, meanlog = 0, sdlog = 1, locationlog = meanlog, scalelog = sdlog)
```

Arguments

y	vector of observations.
meanlog	an alternative way to specify locationlog.
sdlog	an alternative way to specify scalelog.
locationlog	vector of location parameters on the log scale.
scalelog	vector of positive scale parameters on the log scale.

Value

A vector of score values.

---

scores_logis *Calculating scores for the logistic distribution*

Description

These functions calculate scores (CRPS, logarithmic score) and its gradient and Hessian with respect to the parameters of a location-scale transformed logistic distribution. Furthermore, the censoring transformation and the truncation transformation may be introduced on top of the location-scale transformed logistic distribution.

Usage

```
## score functions
crps_logis(y, location = 0, scale = 1)
crps_clogis(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
crps_tlogis(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
crps_gtclogis(y, location = 0, scale = 1, lower = -Inf, upper = Inf, lmass = 0, umass = 0)
logs_logis(y, location = 0, scale = 1)
logs_tlogis(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
dss_logis(y, location = 0, scale = 1)

## gradient (location, scale) functions
gradcrps_logis(y, location = 0, scale = 1)
gradcrps_clogis(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
gradcrps_tlogis(y, location = 0, scale = 1, lower = -Inf, upper = Inf)

## Hessian (location, scale) functions
hesscrps_logis(y, location = 0, scale = 1)
hesscrps_clogis(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
hesscrps_tlogis(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
```

Arguments

y	vector of observations.
location	vector of location parameters.
scale	vector of scale paramters.
lower, upper	lower and upper truncation/censoring bounds.
lmass, umass	vectors of point masses in lower and upper respectively.

Value

For the score functions: a vector of score values.

For the gradient and Hessian functions: a matrix with column names corresponding to the respective partial derivatives.

---

scores_mixnorm *Calculating scores for a mixture of normal distributions.*

Description

Calculating scores for a mixture of normal distributions.

Usage

```
crps_mixnorm(y, m, s, w = NULL)

crps_mixnorm_int(y, m, s, w = NULL, rel_tol = 1e-06)

logs_mixnorm(y, m, s, w = NULL)

dss_mixnorm(y, m, s, w = NULL)
```

Arguments

y	vector of observations.
m	matrix of mean parameters; rows represent observations, columns represent mixture components.
s	matrix of scale parameters; same structure as m.
w	optional; matrix of non-negative weights; same structure as m.
rel_tol	relative accuracy for numerical integration.

Details

logs_mixnorm and crps_mixnorm calculate scores via analytical formulas. crps_mixnorm_int uses numerical integration for the CRPS; this can be faster if there are many mixture components (i.e., if m, s and w have many columns). See examples below.

Value

A vector of score values.

Examples

```
# Example 1: 100 observations, 15 mixture components
mval <- matrix(rnorm(100*15), nrow = 100)
sdval <- matrix(rgamma(100*15, shape = 2), nrow = 100)
weights <- matrix(rep(1/15, 100*15), nrow = 100)
y <- rnorm(100)
crps1 <- crps_mixnorm(y = y, m = mval, s = sdval, w = weights)
crps2 <- crps_mixnorm_int(y = y, m = mval, s = sdval, w = weights)

## Not run:
# Example 2: 2 observations, 10000 mixture components
mval <- matrix(rnorm(2*10000), nrow = 2)
sdval <- matrix(rgamma(2*10000, shape = 2), nrow = 2)
weights <- matrix(rep(1/10000, 2*10000), nrow = 2)
y <- rnorm(2)
# With many mixture components, numerical integration is much faster
system.time(crps1 <- crps_mixnorm(y = y, m = mval, s = sdval, w = weights))
system.time(crps2 <- crps_mixnorm_int(y = y, m = mval, s = sdval, w = weights))

## End(Not run)
```

---

scores_moments *Scoring Rules for a Vector of Moments*

Description

Calculate scores (DSS, ESS) given observations and moments of the predictive distributions.

Usage

```
dss_moments(y, mean = 0, var = 1)

ess_moments(y, mean = 0, var = 1, skew = 0)
```

Arguments

y	vector of realized values.
mean	vector of mean values.
var	vector of variance values.
skew	vector of skewness values.

Details

The skewness of a random variable X is the third standardized moment

$$E[(\frac{X - \text{mean}}{\sqrt{\text{var}}})^3].$$

Value

Value of the score. *A lower score indicates a better forecast.*

Author(s)

Alexander Jordan, Sebastian Lerch

References

Dawid-Sebastiani score:

Dawid, A.P. and P. Sebastiani (1999): 'Coherent dispersion criteria for optimal experimental design' The Annals of Statistics, 27, 65-81. doi:10.1214/aos/1018031101

Error-spread score:

Christensen, H.M., I.M. Moroz, and T.N. Palmer (2015): 'Evaluation of ensemble forecast uncertainty using a new proper score: Application to medium-range and seasonal forecasts', Quarterly Journal of the Royal Meteorological Society, 141, 538-549. doi:10.1002/qj.2375

`scores_nbinom` *Calculating scores for the negative binomial distribution*

Description

Calculating scores for the negative binomial distribution

Usage

```
crps_nbinom(y, size, prob, mu)

logs_nbinom(y, size, prob, mu)

dss_nbinom(y, size, prob, mu)
```

Arguments

`y`	vector of observations.
`size`	target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be integer.
`prob`	probability of success in each trial. `0 < prob <= 1`.
`mu`	alternative parametrization via mean: see 'Details'.

Details

The mean of the negative binomial distribution is given by `mu = size*(1-prob)/prob`.

Value

A vector of score values.

`scores_norm` *Calculating scores for the normal distribution*

Description

These functions calculate scores (CRPS, LogS, DSS) and their gradient and Hessian with respect to the parameters of a location-scale transformed normal distribution. Furthermore, the censoring transformation and the truncation transformation may be introduced on top of the location-scale transformed normal distribution.

Usage

```
## score functions
crps_norm(y, mean = 0, sd = 1, location = mean, scale = sd)
crps_cnorm(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
crps_tnorm(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
crps_gtcnorm(y, location = 0, scale = 1, lower = -Inf, upper = Inf, lmass = 0, umass = 0)
logs_norm(y, mean = 0, sd = 1, location = mean, scale = sd)
logs_tnorm(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
dss_norm(y, mean = 0, sd = 1, location = mean, scale = sd)

## gradient (location, scale) functions
gradcrps_norm(y, location = 0, scale = 1)
gradcrps_cnorm(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
gradcrps_tnorm(y, location = 0, scale = 1, lower = -Inf, upper = Inf)

## Hessian (location, scale) functions
hesscrps_norm(y, location = 0, scale = 1)
hesscrps_cnorm(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
hesscrps_tnorm(y, location = 0, scale = 1, lower = -Inf, upper = Inf)
```

Arguments

`y`	vector of observations.
`mean`	an alternative way to specify `location`.
`sd`	an alternative way to specify `scale`.
`location`	vector of location parameters.
`scale`	vector of scale parameters.
`lower, upper`	lower and upper truncation/censoring bounds.
`lmass, umass`	vectors of point masses in `lower` and `upper` respectively.

Value

For the score functions: a vector of score values.

For the gradient and Hessian functions: a matrix with column names corresponding to the respective partial derivatives.

Examples

```
## Not run:
# Illustrations: Compare CRPS of analytical distribution to
# CRPS of a large sample drawn from this distribution
# (expect scores to be similar)

# First illustration: Standard normal
# Consider CRPS at arbitrary evaluation point (value of outcome)
y <- 0.3
crps_norm(y = y) # score of analytical dist.
# draw standard normal sample of size 10000
dat <- rnorm(1e4)
crps_sample(y = y, dat = dat) # score of sample

# Second illustration: Truncated standard normal
# truncation point
upper <- 1
crps_tnorm(y = y, upper = upper) # score of analytical dist.
# sample from truncated normal
dat_trunc <- dat[dat <= upper]
crps_sample(y = y, dat = dat_trunc) # score of sample

# Third illustration: Censored standard normal (censoring at \code{upper})
crps_cnorm(y = y, upper = upper) # score of analytical dist.
# sample from censored normal
dat_cens <- ifelse(dat <= upper, dat, upper)
crps_sample(y = y, dat = dat_cens) # score of sample

## End(Not run)
```

`scores_pois` *Calculating scores for the Poisson distribution*

Description

Calculating scores for the Poisson distribution

Usage

```
crps_pois(y, lambda)

logs_pois(y, lambda)

dss_pois(y, lambda)
```

Arguments

y	vector of observations.
lambda	vector of (non-negative) means.

Value

A vector of score values.

---

scores_quantiles *Quantile and interval scores*

Description

Compute quantile and interval scores, for given quantile predictions

Usage

```
qs_quantiles(y, x, alpha)

ints_quantiles(y, x_lower, x_upper, target_coverage)

qs_sample(y, dat, alpha, w = NULL, type = 7, show_messages = TRUE)

ints_sample(y, dat, target_coverage, w = NULL, type = 7, show_messages = TRUE)
```

Arguments

y	vector of observations
x	vector of quantile predictions
alpha	quantile level of interest
x_lower, x_upper	vector of quantile predictions (lower and upper endpoints of prediction intervals)
target_coverage	target (i.e., nominal) coverage level of prediction interval
dat	vector or matrix (depending on y; see details) of simulation draws from forecast distribution.
w	vector of observation weights (currently ignored)
type	integer between 1 and 9 that is passed on to stats function quantile (specifies algorithm for empirical quantile estimation; defaults to 7)
show_messages	logical; display of messages (does not affect warnings and errors).

Details

For a vector y of length n, dat should be given as a matrix with n rows. If y has length 1, then dat may be a vector.

Value

A vector of score values. Smaller values indicate better forecasts. Note that the interval score refers to the central prediction interval at level `target_coverage`.

References

Quantile score

Koenker, R. and G. Bassett (1978): 'Regression quantiles', Econometrica 46, 33-50. doi:10.2307/1913643

Interval score

Gneiting, T. and A.E. Raftery (2007): 'Strictly proper scoring rules, prediction and estimation', Journal of the American Statistical Association 102, 359-378. doi:10.1198/016214506000001437

See Also

The syntax of `qs_sample` and `ints_sample` is analogous to the functions documented on `scores_sample_univ`.

Examples

```
# Example 1: Illustrate that interval score is proportional to sum of two quantile scores
target_coverage <- .8
# corresponding quantile levels
alpha_1 <- .5*(1-target_coverage)
alpha_2 <- 1-.5*(1-target_coverage)
# compute interval score
ints_quantiles(y = 1, x_lower = qnorm(alpha_1),
x_upper = qnorm(alpha_2), target_coverage = target_coverage)
# compute sum of quantile scores (scaled by 2/(1-target_coverage))
(2/(1-target_coverage))*(qs_quantiles(y = 1, x = qnorm(alpha_1), alpha = alpha_1) +
qs_quantiles(y = 1, x = qnorm(alpha_2), alpha = alpha_2))

# Example 2: Compare exact to simulated quantile forecast from standard normal distribution
qs_quantiles(y = 1, x = qnorm(.1), alpha = .1)
qs_sample(y = 1, dat = rnorm(500), alpha = .1)
```

---

scores_sample_multiv *Multivariate Scoring Rules for Simulated Forecast Distributions*

Description

Compute multivariate scores of the form $S(y, dat)$, where S is a proper scoring rule, y is a d-dimensional realization vector and dat is a simulated sample of multivariate forecasts. Three scores are available: The energy score, a score based on a Gaussian kernel (mmds_sample, see details below) and the variogram score of order p.

Usage

```
es_sample(y, dat, w = NULL)

mmds_sample(y, dat, w = NULL)

vs_sample(y, dat, w = NULL, w_vs = NULL, p = 0.5)
```

Arguments

y	realized values (numeric vector of length d).
dat	numeric matrix of data (columns are simulation draws from multivariate forecast distribution).
w	numeric vector of weights for forecast draws (length equal to number of columns of dat)
w_vs	numeric matrix of weights for dat used in the variogram score. This matrix must be square and symmetric, with all elements being non-negative. If no weights are specified, constant weights (with all elements of w_vs equal to one) are used.
p	order of variogram score. Standard choices include $p = 1$ and $p = 0.5$.

Details

In the input matrix dat each column is expected to represent a sample from the multivariate forecast distribution, the number of rows of dat thus has to match the length of the observation vector y, and the number of columns of dat is the number of simulated samples.

In es_sample and mmds_sample it is possible to specify a vector w of weights attached to each forecast draw (i.e. each column of matrix dat). These weights are analogous to the input w in crps_sample.

In vs_sample it is possible to specify a matrix w_vs of non-negative weights that allow to emphasize or downweight pairs of component combinations based on subjective expert decisions. w_vs is a square, symmetric matrix with dimensions equal to the length of the input vector y, and the entry in the i-th row and j-th column of w_vs corresponds to the weight assigned to the combination of the corresponding i-th and j-th component. A small example is provided below. For details and further examples, see Scheuerer and Hamill (2015).

The 'MMD score' in mmds_sample is a kernel scoring rule as described in Gneiting and Raftery (2007, Section 5). As for all other scores, we use a negative orientation, such that a smaller score corresponds to a better forecast. We use a Gaussian kernel with standard deviation 1. This kernel is the same as the one obtained by setting rbfdot(sigma = .5) in the R package kernlab (Karatzoglou et al., 2004). The naming prefix 'MMD' is motivated by the machine learning literature on two sample testing (e.g. Gretton et al., 2012), where this type of kernel function is popular.

Value

Value of the score. *A lower score indicates a better forecast.*

Author(s)

Maximiliane Graeter, Sebastian Lerch, Fabian Krueger

References

Energy score

Gneiting, T., Stanberry, L.I., Grimit, E.P., Held, L. and N.A. Johnson (2008): 'Assessing probabilistic forecasts of multivariate quantities, with an application to ensemble predictions of surface winds', TEST, 17, 211-235. doi:10.1007/s117490080114x

MMD score

Gneiting, T. and A.E. Raftery (2007): 'Strictly proper scoring rules, prediction and estimation', Journal of the American Statistical Association 102, 359-378. doi:10.1198/016214506000001437

Gretton, A., Borgwardt, K. M., Rasch, M. J., Schölkopf, B. and A. Smola (2012): 'A kernel two-sample test', Journal of' Machine Learning Research, 13, 723-773.

Karatzoglou, A., Smola, A., Hornik, K. and A. Zeileis (2004). kernlab - An S4 Package for Kernel Methods in R. Journal of Statistical Software 11, 1-20. doi:10.18637/jss.v011.i09

Variogram-based proper scoring rules

Scheuerer, M. and T.M. Hamill (2015): 'Variogram-based proper scoring rules for probabilistic forecasts of multivariate quantities', Monthly Weather Review, 143, 1321-1334. doi:10.1175/mwr-d1400269.1

See Also

`scores_sample_multiv_weighted` for weighted versions of the scoring rules documented here.

Examples

```
d <- 10  # number of dimensions
m <- 50  # number of samples from multivariate forecast distribution

# parameters for multivariate normal example
mu0 <- rep(0, d)
mu <- rep(1, d)
S0 <- S <- diag(d)
S0[S0==0] <- 0.2
S[S==0] <- 0.1

# generate samples from multivariate normal distributions
obs <- drop(mu0 + rnorm(d) %*% chol(S0))
fc_sample <- replicate(m, drop(mu + rnorm(d) %*% chol(S)))

# compute Energy Score
es_sample(y = obs, dat = fc_sample)

# in the univariate case, Energy Score and CRPS are the same
# illustration: Evaluate forecast sample for the first variable
es_sample(y = obs[1], dat = fc_sample[1, , drop = FALSE])
crps_sample(y = obs[1], dat = fc_sample[1, ])

# illustration of observation weights for Energy Score
# example: equal weights for first half of draws; zero weights for other draws
w <- rep(c(1, 0), each = .5*m)/(.5*m)
```

```
es_sample(y = obs, dat = fc_sample, w = w)

# weighting matrix for variogram score
# note that, unlike for w, weights in w_vs refer to dimensions
# (rows of dat) rather than draws (cols of dat)
w_vs <- outer(1:d, 1:d, function(x, y) .5^abs(x-y))

vs_sample(y = obs, dat = fc_sample)
vs_sample(y = obs, dat = fc_sample, w_vs = w_vs)
vs_sample(y = obs, dat = fc_sample, w_vs = w_vs, p = 1)
```

`scores_sample_multiv_weighted`

Weighted Multivariate Scoring Rules for Simulated Forecast Distributions

---

Description

Compute weighted versions of multivariate scores $S(y, dat)$, where S is a proper scoring rule, y is a d-dimensional realization vector and dat is a simulated sample of multivariate forecasts. The weighted scores allow particular outcomes of interest to be emphasised during forecast evaluation. Threshold-weighted and outcome-weighted versions of three multivariate scores are available: the energy score, a score based on a Gaussian kernel (mmds_sample, see details below) and the variogram score of order p.

Usage

```
twes_sample(y, dat, a = -Inf, b = Inf, chain_func = NULL, w = NULL)

owes_sample(y, dat, a = -Inf, b = Inf, weight_func = NULL, w = NULL)

twmmds_sample(y, dat, a = -Inf, b = Inf, chain_func = NULL, w = NULL)

owmmds_sample(y, dat, a = -Inf, b = Inf, weight_func = NULL, w = NULL)

twvs_sample(
  y,
  dat,
  a = -Inf,
  b = Inf,
  chain_func = NULL,
  w = NULL,
  w_vs = NULL,
  p = 0.5
)
```

```
owvs_sample(
  y,
  dat,
  a = -Inf,
  b = Inf,
  weight_func = NULL,
  w = NULL,
  w_vs = NULL,
  p = 0.5
)
```

Arguments

y	realized values (numeric vector of length d).
dat	numeric matrix of data (columns are simulation draws from multivariate forecast distribution).
a	numeric vector of of length d containing lower bounds for the indicator weight function w(z) = 1{a[1] < z[1] < b[1], ..., a[d] < z[d] < b[d]}.
b	numeric vector of of length d containing upper bounds for the indicator weight function w(z) = 1{a[1] < z[1] < b[1], ..., a[d] < z[d] < b[d]}.
chain_func	function used to target particular outcomes in the threshold-weighted scores; the default corresponds to the weight function above.
w	numeric vector of weights for forecast draws (length equal to number of columns of dat)
weight_func	function used to target particular outcomes in the outcome-weighted scores; the default corresponds to the weight function above.
w_vs	numeric matrix of weights for dat used in the variogram score. This matrix must be square and symmetric, with all elements being non-negative. If no weights are specified, constant weights (with all elements of w_vs equal to one) are used.
p	order of variogram score. Standard choices include $p = 1$ and $p = 0.5$.

Details

In the input matrix dat each column is expected to represent a sample from the multivariate forecast distribution, the number of rows of dat thus has to match the length of the observation vector y, and the number of columns of dat is the number of simulated samples.

The threshold-weighted scores (twes_sample, twmmds_sample, twvs_sample) transform y and dat using the chaining function chain_func and then call the relevant unweighted score function (es_sample, mmds_sample, vs_sample). The outcome-weighted scores (owes_sample, owmmds_sample, owvs_sample) weight y and dat using the weight function weight_func and then call the relevant unweighted score function (es_sample, mmds_sample, vs_sample). See the documentation for e.g. es_sample for further details.

The default weight function used in the weighted scores is w(z) = 1{a[1] < z[1] < b[1], ..., a[d] < z[d] < b[d]}, which is equal to one if z is in the 'box' defined by the vectors a and b, and is equal to zero otherwise. This weight function emphasises outcomes between the vectors a and b,

and is commonly used in practical applications when interest is on values above a threshold along multiple dimensions.

Alternative weight functions can also be employed using the `chain_func` and `weight_func` arguments. Computation of the threshold-weighted scores for samples from a predictive distribution requires a chaining function rather than a weight function. This is why a chaining function is an input for `twes_sample`, `twmmds_sample`, and `twvs_sample`, whereas a weight function is an input for `owes_sample`, `owmmds_sample`, and `owvs_sample`.

The `chain_func` and `weight_func` arguments are functions that will be applied to the elements in `y` and `dat`. `weight_func` must input a numeric vector of length `d`, and output a single numeric value. An error will be returned if `weight_func` returns negative values. `chain_func` must input a numeric vector of length `d`, and return a numeric vector of length `d`.

If no custom argument is given for `a`, `b`, `chain_func` or `weight_func`, then all weighted scores are equivalent to the standard unweighted scores `es_sample`, `mmds_sample`, and `vs_sample`.

The `w` argument is also present in the unweighted scores. `w` is used to weight the draws from the predictive distribution, and does not weight particular outcomes within the weighted scoring rules. This should not be confused with the `weight_func` argument.

Value

Value of the score. *A lower score indicates a better forecast.*

Author(s)

Sam Allen

References

Allen, S. (2024): 'Weighted scoringRules: Emphasising Particular Outcomes when Evaluating Probabilistic Forecasts', *Journal of Statistical Software*. doi:10.18637/jss.v110.i08

Threshold-weighted scores

Allen, S., Ginsbourger, D. and J. Ziegel (2023): 'Evaluating forecasts for high-impact events using transformed kernel scores', *SIAM/ASA Journal on Uncertainty Quantification* 11, 906-940. doi:10.1137/22M1532184

Outcome-weighted scores:

Holzmann, H. and B. Klar (2017): 'Focusing on regions of interest in forecast evaluation', *Annals of Applied Statistics* 11, 2404-2431. doi:10.1214/17AOAS1088

See Also

scores_sample_multiv for standard (unweighted) scores based on simulated multivariate forecast distributions. scores_sample_univ_weighted for weighted scores based on simulated univariate forecast distributions

Examples

```
## Not run:
d <- 3  # number of dimensions
m <- 10  # number of samples from multivariate forecast distribution

# parameters for multivariate normal example
mu0 <- rep(0, d)
mu <- rep(1, d)
S0 <- S <- diag(d)
S0[S0==0] <- 0.2
S[S==0] <- 0.1

# generate samples from multivariate normal distributions
obs <- drop(mu0 + rnorm(d) %*% chol(S0))
sample_fc <- replicate(m, drop(mu + rnorm(d) %*% chol(S)))

# if no additional parameters are provided, the weighted scores are the same as
# the unweighted scores:
es_sample(y = obs, dat = sample_fc) # energy score
twes_sample(y = obs, dat = sample_fc) # threshold-weighted energy score
owes_sample(y = obs, dat = sample_fc) # outcome-weighted energy score

mmds_sample(y = obs, dat = sample_fc) # Gaussian kernel score
twmmds_sample(y = obs, dat = sample_fc) # threshold-weighted Gaussian kernel score
owmmds_sample(y = obs, dat = sample_fc) # outcome-weighted Gaussian kernel score

vs_sample(y = obs, dat = sample_fc) # variogram score
twvs_sample(y = obs, dat = sample_fc) # threshold-weighted variogram score
owvs_sample(y = obs, dat = sample_fc) # outcome-weighted variogram score


# the outcome-weighted scores are undefined if none of dat are between a and b
# this can lead to NaNs in some of the scores calculated below, particularly
# if the thresholds are extreme, or if the dimension is large


# emphasise outcomes greater than 0 in all dimensions
twes_sample(y = obs, dat = sample_fc, a = 0)
owes_sample(y = obs, dat = sample_fc, a = 0)
twmmds_sample(y = obs, dat = sample_fc, a = 0)
owmmds_sample(y = obs, dat = sample_fc, a = 0)
twvs_sample(y = obs, dat = sample_fc, a = 0)
owvs_sample(y = obs, dat = sample_fc, a = 0)

# this can also be done more explicitly by setting a = rep(0, d)
twes_sample(y = obs, dat = sample_fc, a = rep(0, d))
owes_sample(y = obs, dat = sample_fc, a = rep(0, d))

# a should also be specified fully if the threshold changes in each dimension
a <- rnorm(d)
twes_sample(y = obs, dat = sample_fc, a = a)
owes_sample(y = obs, dat = sample_fc, a = a)
```

```
twmmds_sample(y = obs, dat = sample_fc, a = a)
owmmds_sample(y = obs, dat = sample_fc, a = a)
twvs_sample(y = obs, dat = sample_fc, a = a)
owvs_sample(y = obs, dat = sample_fc, a = a)

# emphasise outcomes smaller than 0 in all dimensions
twes_sample(y = obs, dat = sample_fc, b = 0)
owes_sample(y = obs, dat = sample_fc, b = 0)
twmmds_sample(y = obs, dat = sample_fc, b = 0)
owmmds_sample(y = obs, dat = sample_fc, b = 0)
twvs_sample(y = obs, dat = sample_fc, b = 0)
owvs_sample(y = obs, dat = sample_fc, b = 0)

# emphasise outcomes between (-1, -1, -1) and (1, 1, 1)
twes_sample(y = obs, dat = sample_fc, a = -1, b = 1)
owes_sample(y = obs, dat = sample_fc, a = -1, b = 1)
twmmds_sample(y = obs, dat = sample_fc, a = -1, b = 1)
owmmds_sample(y = obs, dat = sample_fc, a = -1, b = 1)
twvs_sample(y = obs, dat = sample_fc, a = -1, b = 1)
owvs_sample(y = obs, dat = sample_fc, a = -1, b = 1)

# emphasise outcomes between (-2, 0, -1) and (0, 2, 1)
a <- c(-2, 0, -1)
b <- c(0, 2, 1)
twes_sample(y = obs, dat = sample_fc, a = a, b = b)
owes_sample(y = obs, dat = sample_fc, a = a, b = b)
twmmds_sample(y = obs, dat = sample_fc, a = a, b = b)
owmmds_sample(y = obs, dat = sample_fc, a = a, b = b)
twvs_sample(y = obs, dat = sample_fc, a = a, b = b)
owvs_sample(y = obs, dat = sample_fc, a = a, b = b)


# values of a cannot be larger than the corresponding values of b
twes_sample(y = obs, dat = sample_fc, a = c(0, 0, 0), b = c(0, 0, 1))
twes_sample(y = obs, dat = sample_fc, a = c(0, 0, 0), b = c(0, 0, 0)) # error
twes_sample(y = obs, dat = sample_fc, a = c(0, 0, 0), b = c(1, 1, -1)) # error

# a and b must be of the same length (and of the same length as y)
owmmds_sample(y = obs, dat = sample_fc, a = c(0, 0), b = 1) # error
owmmds_sample(y = obs, dat = sample_fc, a = c(0, 0), b = c(1, 1)) # error


# alternative custom weight and chaining functions can also be used

# Example 1: the default weight function with an alternative chaining function
# the default weight function is
# w(z) = 1{a[1] < z[1] < b[1], ..., a[d] < z[d] < b[d]}
# the default chaining function is
# v(z) = (min(max(z[1], a[1]), b[1]), ..., min(max(z[d], a[d]), b[d]))
a <- -2
b <- 2
weight_func <- function(x) as.numeric(all(x > a & x < b))
chain_func <- function(x) pmin(pmax(x, a), b)
```

```
owes_sample(y = obs, dat = sample_fc, a = a, b = b)
owes_sample(y = obs, dat = sample_fc, weight_func = weight_func)
twes_sample(y = obs, dat = sample_fc, a = a, b = b)
twes_sample(y = obs, dat = sample_fc, chain_func = chain_func)

# consider an alternative chaining function: v(z) = z if w(z) = 1, else v(z) = 0
chain_func <- function(x) x*weight_func(x)
twes_sample(y = obs, dat = sample_fc, chain_func = chain_func)


# Example 2: a mulivariate Gaussian weight function with mean vector mu and
# diagonal covariance matrix sigma
mu <- rep(0, d)
sigma <- diag(d)
weight_func <- function(x) prod(pnorm(x, mu, diag(sigma)))
# the corresponding chaining function is
chain_func <- function(x){
 (x - mu)*pnorm(x, mu, diag(sigma)) + (diag(sigma)^2)*dnorm(x, mu, diag(sigma))
}

owvs_sample(y = obs, dat = sample_fc, a = mu)
owvs_sample(y = obs, dat = sample_fc, weight_func = weight_func)
twvs_sample(y = obs, dat = sample_fc, a = mu)
twvs_sample(y = obs, dat = sample_fc, chain_func = chain_func)

## End(Not run)
```

`scores_sample_univ` *Scoring Rules for Simulated Forecast Distributions*

Description

Calculate scores (CRPS, LogS, DSS) given observations and draws from the predictive distributions.

Usage

```
crps_sample(
  y,
  dat,
  method = "edf",
  w = NULL,
  bw = NULL,
  num_int = FALSE,
  show_messages = TRUE
)

logs_sample(y, dat, bw = NULL, show_messages = FALSE)
```

```
dss_sample(y, dat, w = NULL)
```

Arguments

y	vector of realized values.
dat	vector or matrix (depending on y; see details) of simulation draws from forecast distribution.
method	string; approximation method. Options: "edf" (empirical distribution function) and "kde" (kernel density estimation).
w	optional; vector or matrix (matching dat) of weights for method "edf".
bw	optional; vector (matching y) of bandwidths for kernel density estimation; see details.
num_int	logical; if TRUE numerical integration is used for method "kde".
show_messages	logical; display of messages (does not affect warnings and errors).

Details

For a vector y of length n >= 2, dat should be given as a matrix with n rows. If y has length 1, then dat may be a vector.

crps_sample employs an empirical version of the quantile decomposition of the CRPS (Laio and Tamea, 2007) when using method = "edf". For method = "kde", it uses kernel density estimation using a Gaussian kernel. The logarithmic score always uses kernel density estimation.

The bandwidth (bw) for kernel density estimation can be specified manually, in which case it must be a vector (matching y) of positive numbers. If bw == NULL, the bandwidth is selected using the core function bw.nrd. Numerical integration may speed up computation for crps_sample in case of large samples dat.

Value

Value of the score. *A lower score indicates a better forecast.*

Author(s)

Alexander Jordan, Fabian Krueger, Sebastian Lerch

References

Evaluating simulation based forecast distributions:

Krueger, F., Lerch, S., Thorarinsdottir, T.L. and T. Gneiting (2021): 'Predictive inference based on Markov chain Monte Carlo output', *International Statistical Review* 89, 274-301. doi:10.1111/insr.12405

Empirical quantile decomposition of the CRPS:

Laio, F. and S. Tamea (2007): 'Verification tools for probabilistic forecasts of continuous hydrological variables', Hydrology and Earth System Sciences, 11, 1267-1277. doi:10.5194/hess1112672007

See Also

scores_sample_univ_weighted for weighted versions of the scoring rules documented here.

Examples

```
## Not run:

# y has length greater than 1
y <- 1:2
sample <- matrix(rnorm(20), nrow = 2)
crps_sample(y = y, dat = sample)
logs_sample(y = y, dat = sample)

y <- 1:2
sample <- rnorm(10)
crps_sample(y = y, dat = sample) # error

# y has length 1
y <- 1
sample <- rnorm(10)
crps_sample(y = y, dat = sample)

sample <- matrix(rnorm(10), nrow = 1)
crps_sample(y = y, dat = sample)

sample <- matrix(rnorm(20), nrow = 2)
crps_sample(y = y, dat = sample) # error

## End(Not run)
```

---

scores_sample_univ_weighted

Weighted Scoring Rules for Simulated Forecast Distributions

Description

Calculate weighted scores given observations and draws from univariate predictive distributions. The weighted scoring rules that are available are the threshold-weighted CRPS, outcome-weighted CRPS, and conditional and censored likelihood scores.

Usage

```
twcrps_sample(
  y,
  dat,
  a = -Inf,
  b = Inf,
  chain_func = NULL,
```

```
  w = NULL,
  show_messages = TRUE
)

owcrps_sample(
  y,
  dat,
  a = -Inf,
  b = Inf,
  weight_func = NULL,
  w = NULL,
  show_messages = TRUE
)

clogs_sample(
  y,
  dat,
  a = -Inf,
  b = Inf,
  bw = NULL,
  show_messages = FALSE,
  cens = TRUE
)
```

Arguments

y	vector of realized values.
dat	vector or matrix (depending on y; see details) of simulation draws from forecast distribution.
a	numeric lower bound for the indicator weight function w(z) = 1{a < z < b}.
b	numeric upper bound for the indicator weight function w(z) = 1{a < z < b}.
chain_func	function used to target particular outcomes in the threshold-weighted CRPS; the default corresponds to the weight function w(z) = 1{a < z < b}.
w	optional; vector or matrix (matching dat) of ensemble weights. Note that these weights are not used in the weighted scoring rules; see details.
show_messages	logical; display of messages (does not affect warnings and errors).
weight_func	function used to target particular outcomes in the outcome-weighted CRPS; the default corresponds to the weight function w(z) = 1{a < z < b}.
bw	optional; vector (matching y) of bandwidths for kernel density estimation for clogs_sample; see details.
cens	logical; if TRUE, clogs_sample returns the censored likelihood score; if FALSE, clogs_sample returns the conditional likelihood score.

Details

For a vector y of length n, dat should be given as a matrix with n rows. If y has length 1, then dat may be a vector.

twcrps_sample transforms y and dat using the chaining function chain_func and then calls crps_sample. owcrps_sample weights y and dat using the weight function weight_func and then calls crps_sample. See the documentation for crps_sample for further details.

The default weight function used in the weighted scores is w(z) = 1{a < z < b}, which is equal to one if z is between a and b, and zero otherwise. This weight function emphasises outcomes between a and b, and is commonly used in practical applications when interest is on values above a threshold (set b = Inf and a equal to the threshold) or below a threshold (set a = -Inf and b equal to the threshold).

Alternative weight functions can also be employed using the chain_func and weight_func arguments to twcrps_sample and owcrps_sample, respectively. Computation of the threshold-weighted CRPS for samples from a predictive distribution requires a chaining function rather than a weight function. This is why a chaining function is an input for twcrps_sample whereas a weight function is an input for owcrps_sample. Since clogs_sample requires kernel density estimation to approximate the forecast density, it cannot readily be calculated for arbitrary weight functions, and is thus only available for the canonical weight function w(z) = 1{a < z < b}.

The chain_func and weight_func arguments are functions that will be applied to the vector y and the columns of dat. It is assumed that these functions are vectorised. Both functions must take a vector as an input and output a vector of the same length, containing the weight (for weight_func) or transformed value (for chain_func) corresponding to each element in the input vector. An error will be returned if weight_func returns negative values, and a warning message will appear if chain_func is not increasing.

If no custom argument is given for a, b, chain_func or weight_func, then both twcrps_sample and owcrps_sample are equivalent to the standard unweighted crps_sample, and clogs_sample is equivalent to logs_sample.

The w argument is also present in the unweighted scores (e.g. crps_sample). w is used to weight the draws from the predictive distribution, and does not weight particular outcomes within the weighted scoring rules. This should not be confused with the weight_func argument, which is used within the weighted scores.

Value

Value of the score. *A lower score indicates a better forecast.*

Author(s)

Sam Allen

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Conditional and censored likelihood scores:

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See Also

scores_sample_univ for standard (unweighted) scores based on simulated forecast distributions. scores_sample_multiv_weighted for weighted scores based on simulated multivariate forecast distributions.

Examples

```
## Not run:

y <- rnorm(10)
sample_fc <- matrix(rnorm(100), nrow = 10)

crps_sample(y = y, dat = sample_fc)
twcrps_sample(y = y, dat = sample_fc)
owcrps_sample(y = y, dat = sample_fc)

logs_sample(y = y, dat = sample_fc)
clogs_sample(y = y, dat = sample_fc)
clogs_sample(y = y, dat = sample_fc, cens = FALSE)

# emphasise outcomes above 0
twcrps_sample(y = y, dat = sample_fc, a = 0)
owcrps_sample(y = y, dat = sample_fc, a = 0)
clogs_sample(y = y, dat = sample_fc, a = 0)
clogs_sample(y = y, dat = sample_fc, a = 0, cens = FALSE)

# emphasise outcomes below 0
twcrps_sample(y = y, dat = sample_fc, b = 0)
owcrps_sample(y = y, dat = sample_fc, b = 0)
clogs_sample(y = y, dat = sample_fc, b = 0)

# emphasise outcomes between -1 and 1
twcrps_sample(y = y, dat = sample_fc, a = -1, b = 1)
owcrps_sample(y = y, dat = sample_fc, a = -1, b = 1)
clogs_sample(y = y, dat = sample_fc, a = -1, b = 1)


# a must be smaller than b
twcrps_sample(y = y, dat = sample_fc, a = 1, b = -1) # error
```

```
owcrps_sample(y = y, dat = sample_fc, a = 0, b = 0) # error
clogs_sample(y = y, dat = sample_fc, a = 10, b = 9) # error

# a and b must be single numeric values (not vectors)
twcrps_sample(y = y, dat = sample_fc, a = rnorm(10)) # error


# the owCRPS is not well-defined if none of dat are between a and b
y <- rnorm(10)
sample_fc <- matrix(runif(100, -5, 1), nrow = 10)
owcrps_sample(y = y, dat = sample_fc, a = 1)
# the twCRPS is zero if none of y and dat are between a and b
twcrps_sample(y = y, dat = sample_fc, a = 1)


# alternative custom weight and chaining functions can also be used

# Example 1: a Gaussian weight function with location mu and scale sigma
mu <- 0
sigma <- 0.5
weight_func <- function(x) pnorm(x, mu, sigma)
# or weight_func <- get_weight_func("norm_cdf", mu, sigma)
# a corresponding chaining function is
chain_func <- function(x) (x - mu)*pnorm(x, mu, sigma) + (sigma^2)*dnorm(x, mu, sigma)
# or chain_func <- get_weight_func("norm_cdf", mu, sigma, weight = FALSE)

x <- seq(-2, 2, 0.01)
plot(x, weight_func(x), type = "l") # positive outcomes are given higher weight
plot(x, chain_func(x), type = "l")

owcrps_sample(y = y, dat = sample_fc, a = mu)
owcrps_sample(y = y, dat = sample_fc, weight_func = weight_func)
twcrps_sample(y = y, dat = sample_fc, a = mu)
twcrps_sample(y = y, dat = sample_fc, chain_func = chain_func)


# Example 2: a sigmoid (or logistic) weight function with location mu and scale sigma
weight_func <- function(x) plogis(x, mu, sigma)
# or weight_func <- get_weight_func("logis_cdf", mu, sigma)
chain_func <- function(x) sigma*log(exp((x - mu)/sigma) + 1)
# or chain_func <- get_weight_func("logis_cdf", mu, sigma, weight = FALSE)

x <- seq(-2, 2, 0.01)
plot(x, weight_func(x), type = "l") # positive outcomes are given higher weight
plot(x, chain_func(x), type = "l")

owcrps_sample(y = y, dat = sample_fc, a = mu)
owcrps_sample(y = y, dat = sample_fc, weight_func = weight_func)
twcrps_sample(y = y, dat = sample_fc, a = mu)
twcrps_sample(y = y, dat = sample_fc, chain_func = chain_func)


# Example 3: the weight function w(z) = 1{z < a or z > b}
```

```
a <- -1
b <- 1
weight_func <- function(x) as.numeric(x < a | x > b)
chain_func <- function(x) (x < a)*(x - a) + (x > b)*(x - b) + a

x <- seq(-2, 2, 0.01)
plot(x, weight_func(x), type = "l")
plot(x, chain_func(x), type = "l")

owcrps_sample(y = y, dat = sample_fc, weight_func = weight_func)
twcrps_sample(y = y, dat = sample_fc, chain_func = chain_func)
twcrps_sample(y = y, dat = sample_fc, b = -1) + twcrps_sample(y = y, dat = sample_fc, a = 1)
crps_sample(y = y, dat = sample_fc) - twcrps_sample(y = y, dat = sample_fc, a = -1, b = 1)

## End(Not run)
```

---

scores_t *Calculating scores for Student's t-distribution*

Description

These functions calculate scores (CRPS, logarithmic score) and their gradient and Hessian with respect to the parameters of a location-scale transformed Student's t-distribution. Furthermore, the censoring transformation and the truncation transformation may be introduced on top of the location-scale transformed t-distribution.

Usage

```
## score functions
crps_t(y, df, location = 0, scale = 1)
crps_ct(y, df, location = 0, scale = 1, lower = -Inf, upper = Inf)
crps_tt(y, df, location = 0, scale = 1, lower = -Inf, upper = Inf)
crps_gtct(y, df, location = 0, scale = 1, lower = -Inf, upper = Inf, lmass = 0, umass = 0)
logs_t(y, df, location = 0, scale = 1)
logs_tt(y, df, location = 0, scale = 1, lower = -Inf, upper = Inf)
dss_t(y, df, location = 0, scale = 1)

## gradient (location, scale) functions
gradcrps_t(y, df, location = 0, scale = 1)
gradcrps_ct(y, df, location = 0, scale = 1, lower = -Inf, upper = Inf)
gradcrps_tt(y, df, location = 0, scale = 1, lower = -Inf, upper = Inf)

## Hessian (location, scale) functions
hesscrps_t(y, df, location = 0, scale = 1)
hesscrps_ct(y, df, location = 0, scale = 1, lower = -Inf, upper = Inf)
hesscrps_tt(y, df, location = 0, scale = 1, lower = -Inf, upper = Inf)
```

Arguments

y	vector of observations.
df	vector of degrees of freedom.
location	vector of location parameters.
scale	vector of scale paramters.
lower, upper	lower and upper truncation/censoring bounds.
lmass, umass	vectors of point masses in lower and upper respectively.

Value

For the CRPS functions: a vector of score values.

For the gradient and Hessian functions: a matrix with column names corresponding to the respective partial derivatives.

---

scores_unif *Calculating scores for the uniform distribution*

Description

Calculating scores for the uniform distribution

Usage

```
crps_unif(y, min = 0, max = 1, lmass = 0, umass = 0)

logs_unif(y, min = 0, max = 1)

dss_unif(y, min = 0, max = 1)
```

Arguments

y	vector of observations.
min, max	lower and upper limits of the distribution. Must be finite.
lmass, umass	vectors of point masses in min and max respectively.

Value

A vector of score values.

summary.casestudy *Summary method for class casestudy*

Description

Summary method for class casestudy

Usage

```
## S3 method for class 'casestudy'
summary(object, ...)
```

Arguments

object	Object of class casestudy, generated via run_casestudy
...	Additional specifications (presently not in use)

summary.mcstudy *Simple summary method for class mcstudy*

Description

Simple summary method for class mcstudy

Usage

```
## S3 method for class 'mcstudy'
summary(object, ...)
```

Arguments

object	Object of class mcstudy, generated via run_mcstudy
...	Additional specifications (presently not in use)

`Supplementary distributions: Positive real line`
Supplementary distributions (not in base R) supported on the positive real line.

Description

We include the probability density functions of some distributions which are part of scoringRules, but are not part of base R. The parametrizations used here are identical to the ones used when calling `crps` and `logs`.

Here we document distributions on the positive real line: `fllapl` - log-Laplace distribution; `fllogis` - log-logistic distribution.

Usage

```
fllapl(x, locationlog, scalelog)
fllogis(x, locationlog, scalelog)
```

Arguments

`x`	vector of quantiles
`locationlog`	vector of location parameters on the log scale
`scalelog`	vector of scale parameters on the log scale

Details

To be added.

Value

Probability density function of the relevant distribution, evaluated at `x`.

Author(s)

Alexander Jordan

See Also

The documentation for crps.numeric contains the full list of distributions supported by scoringRules (includes the ones documented here, as well as many others).

`Supplementary distributions: Real line`

Supplementary distributions (not in base R) supported on the real line.

Description

We include the probability density functions of some distributions which are part of scoringRules, but are not part of base R. The parametrizations used here are identical to the ones used when calling `crps` and `logs`.

Here we document distributions with support on the real line: `flapl` - Laplace distribution; `f2pexp` - two-piece exponential distribution; `fmixnorm` - mixture of normal distributions; `f2pnorm` - two-piece normal distribution.

Usage

```
flapl(x, location, scale)

f2pexp(x, location, scale1, scale2)
f2pnorm(x, location, scale1, scale2)

fmixnorm(x, m, s, w)
```

Arguments

`x`	vector of quantiles
`location`	vector of location parameters
`scale`, `scale1`, `scale2`	vector of scale parameters
`m`	matrix of means (rows correspond to observations, columns correspond to mixture components)
`s`	matrix of standard deviations (same structure as `m`)
`w`	matrix of weights (same structure as `m`)

Details

The Laplace distribution (`flapl`) is described on https://en.wikipedia.org/wiki/Laplace_distribution. It is a special case of the two-piece exponential distribution (`f2pexp`), which allows for different scale parameters to the left and right of `location`.

The density function of a mixture of normal distributions (`fmixnorm`) is given by the weighted sum over the mixture components,

$$f(x) = \sum w_i / s_i \phi((x - m_i)/s_i),$$

where ϕ is the pdf of the standard normal distribution.

For details on the two-piece normal distribution (`f2pnorm`), see Box A of Wallis (2004, "An Assessment of Bank of England and National Institute Inflation Forecast Uncertainties", National Institute Economic Review).

Value

Probability density function of the relevant distribution, evaluated at `x`.

Author(s)

Alexander Jordan

See Also

The documentation for crps.numeric contains the full list of distributions supported by scoringRules (includes the ones documented here, as well as many others).

fnorm, flogis, ft

Examples

```
# Plot PDF of Laplace distribution
ff <- function(x) flapl(x, location = 0, scale = 2)
curve(ff, from = -8, to = 8, bty = "n", xlab = "Value",
      ylab = "PDF",
      main = "Laplace distribution with location 0 and scale 2")
```

`Supplementary distributions: Variable support`

Supplementary distributions (not in base R) with variable support.

Description

We include the probability density functions of some distributions which are part of scoringRules, but are not part of base R. The parametrizations used here are identical to the ones used when calling `crps` and `logs`.

Here we document distributions with variable support: `fexp` - location-scale exponential distribution with a point mass on the lower boundary; `fgdp` - generalized Pareto distribution with a point mass on the lower boundary; `fgev` - generalized extreme value distribution; `fnorm`, `flogis`, `ft` - (normal/logistic/Student's t)-distribution with flexible domain and point masses on the boundaries.

Usage

```
fexp(x, location, scale, mass = 0, log = FALSE)
fgpd(x, location, scale, shape, mass = 0, log = FALSE)

fgev(x, location, scale, shape)

fnorm(x, location, scale, lower = -Inf, upper = Inf, lmass = 0, umass = 0, log = FALSE)
ft(x, df, location, scale, lower = -Inf, upper = Inf, lmass = 0, umass = 0, log = FALSE)
flogis(x, location, scale, lower = -Inf, upper = Inf, lmass = 0, umass = 0, log = FALSE)
```

Arguments

x	vector of quantiles
df	vector of degrees of freedom parameters
location	vector of location parameters
scale	vector of scale parameters (positive)
shape	vector of shape parameters
mass	vector of point masses in location
lower	vector of lower bounds
upper	vector of upper bounds
lmass	vector of point masses in lower, or strings "trunc" / "cens"
umass	vector of point masses in upper, or strings "trunc" / "cens"
log	logical; if TRUE, the log of the density is returned

Details

For details on generalized extreme value and generalized Pareto distributions, see Friederichs, F. and T.L. Thorarinsdottir (2012, "Forecast verification for extreme value distributions with an application to probabilistic peak wind prediction", Environmetrics 23, 579-594). Note that the support of both distributions depends on the input parameters; see https://en.wikipedia.org/wiki/Generalized_extreme_value_distribution and https://en.wikipedia.org/wiki/Generalized_Pareto_distribution.

Sometimes truncated or censored versions of the normal distribution are used to model variables with a restricted domain (e.g. precipitation). We allow the flexible specification of lower and upper boundaries and point masses in those boundaries. The truncated normal distribution assumes no point masses (i.e. redistributes the cut-off) and can be specified using the string "trunc" instead of a numerical probability. In contrast, the censored distribution introduces a point mass at the bound in the amount of the cut-off. Here, the string "cens" may be used for lmass or umass. The most common use in practice lies in the context of non-negative quantities. For example, a truncated standard normal distribution (left truncation at zero) has pdf $f(x) = \phi(x)/(1 - \Phi(0))$, for $x \geq 0$ and 0 otherwise. A censored standard normal distribution (left censoring at zero) has point mass $\Phi(0)$ at zero, and density $\phi(x)$ for $x > 0$.

The location-scale family based on Student's t-distribution (ft) has mean $location$ for $df > 1$ and variance $df/(df - 2) * scale^2$ for $df > 2$. Note that the crps exists only for $df > 1$. For details, see https://en.wikipedia.org/wiki/Student's_t-distribution#Non-standardized_Student.27s_t-distribution.

Value

Density function of the relevant distribution, evaluated at x. NOTE: For distributions involving a point mass (e.g., when lmass = "cens" in fnorm), the density functions do not integrate to one.

Author(s)

Alexander Jordan

See Also

The documentation for crps.numeric contains the full list of distributions supported by scoringRules (includes the ones documented here, as well as many others).

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