

Package: FBMS (via r-universe)

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 FBMS-package

Flexible Bayesian Model Selection and Model Averaging

Description

Implements MJMCMC (mode jumping MCMC) described in Hubin and Storvik (2018) <doi:10.1016/j.csda.2018.05.020> and GMJMCMC (genetically modified MJMCMC) described in Hubin et al. (2021) <doi:10.1613/jair.1.13047> algorithms as well as the subsampling counterpart described in Lachmann et al. (2022) <doi:10.1016/j.jjar.2022.08.018> for flexible Bayesian model selection and model averaging.

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References

- Lachmann, J., Storvik, G., Frommlet, F., & Hubin, A. (2022). A subsampling approach for Bayesian model selection. *International Journal of Approximate Reasoning*, 151, 33-63. Elsevier.
- Hubin, A., Storvik, G., & Frommlet, F. (2021). Flexible Bayesian Nonlinear Model Configuration. *Journal of Artificial Intelligence Research*, 72, 901-942.
- Hubin, A., Frommlet, F., & Storvik, G. (2021). Reversible Genetically Modified MJMCMC. Under review in EYSM 2021.
- Hubin, A., & Storvik, G. (2018). Mode jumping MCMC for Bayesian variable selection in GLMM. *Computational Statistics & Data Analysis*, 127, 281-297. Elsevier.

breastcancer

Breast Cancer Wisconsin (Diagnostic) Data Set

Description

Features are computed from a digitized image of a fine needle aspirate (FNA) of a breast mass. They describe characteristics of the cell nuclei present in the image.

Usage

```
data(breastcancer)
```

Format

A data frame with 569 rows and 32 variables

Details

Separating plane described above was obtained using Multisurface Method-Tree (MSM-T) (K. P. Bennett, "Decision Tree Construction Via Linear Programming." Proceedings of the 4th Midwest Artificial Intelligence and Cognitive Science Society, pp. 97-101, 1992), a classification method which uses linear programming to construct a decision tree. Relevant features were selected using an exhaustive search in the space of 1-4 features and 1-3 separating planes.

The actual linear program used to obtain the separating plane in the 3-dimensional space is that described in: (K. P. Bennett and O. L. Mangasarian: "Robust Linear Programming Discrimination of Two Linearly Inseparable Sets", *Optimization Methods and Software* 1, 1992, 23-34).

The variables are as follows:

- ID number
- Diagnosis (1 = malignant, 0 = benign)
- Ten real-valued features are computed for each cell nucleus

Source

Dataset downloaded from the UCI Machine Learning Repository. [http://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+\(Diagnostic\)](http://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+(Diagnostic))

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References

W.N. Street, W.H. Wolberg and O.L. Mangasarian. Nuclear feature extraction for breast tumor diagnosis. IS&T/SPIE 1993 International Symposium on Electronic Imaging: Science and Technology, volume 1905, pages 861-870, San Jose, CA, 1993.

Lichman, M. (2013). UCI Machine Learning Repository <http://archive.ics.uci.edu/ml>. Irvine, CA: University of California, School of Information and Computer Science.

compute_effects

Compute effects for specified in labels covariates using a fitted model.

Description

This function computes model averaged effects for specified covariates using a fitted model object. The effects are expected change in the BMA linear predictor having an increase of the corresponding covariate by one unit, while other covariates are fixed to 0. Users can provide custom labels and specify quantiles for the computation of effects.

Usage

```
compute_effects(object, labels, quantiles = c(0.025, 0.5, 0.975))
```

Arguments

object	A fitted model object, typically the result of a regression or predictive modeling.
labels	A vector of labels for which effects are to be computed.
quantiles	A numeric vector specifying the quantiles to be calculated. Default is c(0.025, 0.5, 0.975).

Value

A matrix of treatment effects for the specified labels, with rows corresponding to labels and columns to quantiles.

See Also[predict](#)**Examples**

```
data <- data.frame(matrix(rnorm(600), 100))
result <- mjcmc.parallel(runs = 2, cores = 1, data, gaussian.loglik)
compute_effects(result, labels = names(data)[-1])
```

cos_deg	<i>Cosine function for degrees</i>
---------	------------------------------------

Description

Cosine function for degrees

Usage

```
cos_deg(x)
```

Arguments

x The vector of values in degrees

Value

The cosine of x

Examples

```
cos_deg(0)
```

diag_plot	<i>Plot convergence of best/median/mean/other summary log posteriors in time</i>
-----------	--

Description

Plot convergence of best/median/mean/other summary log posteriors in time

Usage

```
diag_plot(res, FUN = median, conf = 0.95, burnin = 0, window = 10000)
```

Arguments

res	Object corresponding gmjcmc output
FUN	The summary statistics to check convergence
conf	which confidence intervals to plot
burnin	how many first populations to skip
window	sliding window for computing the standard deviation

Value

A list of summary statistics for checking convergence with given confidence intervals

Examples

```
result <- gmjcmc(matrix(rnorm(600), 100), P = 2, gaussian.loglik, NULL, c("p0", "exp_dbl"))
diagnstats <- diagn_plot(result)
```

erf *erf function*

Description

erf function

Usage

```
erf(x)
```

Arguments

x	The vector of values
---	----------------------

Value

$2 * \text{pnorm}(x * \text{sqrt}(2)) - 1$

Examples

```
erf(2)
```

exoplanet

Excerpt from the Open Exoplanet Catalogue data set

Description

Data fields include planet and host star attributes.

Usage

```
data(exoplanet)
```

Format

A data frame with 223 rows and 11 variables

Details

The variables are as follows:

- TypeFlag: Flag indicating the type of data
- PlanetaryMassJpt: Mass of the planetary object in Jupiter masses
- RadiusJpt: Radius of the planetary object in Jupiter radii
- PeriodDays: Orbital period of the planetary object in days
- SemiMajorAxisAU: Semi-major axis of the planetary object's orbit in astronomical units
- Eccentricity: Eccentricity of the planetary object's orbit
- HostStarMassSlrMass: Mass of the host star in solar masses
- HostStarRadiusSlrRad: Radius of the host star in solar radii
- HostStarMetallicity: Metallicity of the host star
- HostStarTempK: Effective temperature of the host star in Kelvin
- PlanetaryDensJpt: Density of the planetary object up to a constant

Source

Dataset downloaded from the Open Exoplanet Catalogue Repository. https://github.com/OpenExoplanetCatalogue/oec_tables/

Creators:

1. Prof. Hanno Rein, Department for Physical and Environmental Sciences. University of Toronto at Scarborough Toronto, Ontario M1C 1A4 hanno.rein@utoronto.ca

exp_dbl	<i>Double exponential function</i>
---------	------------------------------------

Description

Double exponential function

Usage

```
exp_dbl(x)
```

Arguments

x	The vector of values
---	----------------------

Value

$e^{-\text{abs}(x)}$

Examples

```
exp_dbl(2)
```

fbms	<i>Fit a BGNLM model using Genetically Modified Mode Jumping Markov Chain Monte Carlo (MCMC) sampling. Or Fit a BGLM model using Modified Mode Jumping Markov Chain Monte Carlo (MCMC) sampling.</i>
------	--

Description

This function fits a model using the relevant MCMC sampling. The user can specify the formula, family, data, transforms, and other parameters to customize the model.

Usage

```
fbms(
  formula = NULL,
  family = "gaussian",
  data = NULL,
  transforms = NULL,
  loglik.pi = gaussian.loglik,
  loglik.alpha = gaussian.loglik.alpha,
  P = 10,
  runs = 10,
```

```

    cores = 1,
    verbose = FALSE,
    ...
)

```

Arguments

formula	A formula object specifying the model structure. Default is NULL.
family	The distribution family of the response variable. Currently supports "gaussian" and "binomial". Default is "gaussian".
data	A data frame containing the variables in the model. If NULL, the variables are taken from the environment of the formula. Default is NULL.
transforms	A list of transformations for BGNLM model. Default is NULL.
loglik.pi	The log-likelihood function for estimating the marginal likelihood and posterior modes (only used if family = "custom")
loglik.alpha	The log-likelihood function for the alpha parameter in the model. Default is gaussian.loglik.alpha.
P	The number of GMJMCMC generations. Default is 10.
runs	The number of parallel chains in case of parallel processing. Default is 2.
cores	The number of CPU cores to use for parallel processing. Default is 2.
verbose	If TRUE, print detailed progress information during the fitting process. Default is FALSE.
...	Additional parameters to be passed to the underlying MCMC fitting functions.

Value

An object containing the results of the fitted model and MCMC sampling.

See Also

[mjmcmc](#), [gmjmcmc](#), [gmjmcmc.parallel](#)

Examples

```

# Fit a Gaussian multivariate time series model
fbms_result <- fbms(
  X1 ~ .,
  family = "gaussian",
  data = data.frame(matrix(rnorm(600), 100)),
  P = 10,
  runs = 1,
  cores = 1
)
summary(fbms_result)
plot(fbms_result)

```

gauss	<i>Gaussian function</i>
-------	--------------------------

Description

Gaussian function

Usage

gauss(x)

Arguments

x The vector of values

Value

e^{-x^2}

Examples

gauss(2)

gaussian.loglik	<i>Log likelihood function for gaussian regression with a prior $p(m)=r*\text{sum}(\text{total_width})$.</i>
-----------------	--

Description

Log likelihood function for gaussian regression with a prior $p(m)=r*\text{sum}(\text{total_width})$.

Usage

gaussian.loglik(y, x, model, complex, params)

Arguments

y A vector containing the dependent variable
x The matrix containing the precalculated features
model The model to estimate as a logical vector
complex A list of complexity measures for the features
params A list of parameters for the log likelihood, supplied by the user

Value

A list with the log marginal likelihood combined with the log prior (crit) and the posterior mode of the coefficients (coefs).

Examples

```
gaussian.loglik(rnorm(100), matrix(rnorm(100)), TRUE, list(oc = 1), NULL)
```

`gaussian.loglik.alpha` *Log likelihood function for gaussian regression for alpha calculation*
This function is just the bare likelihood function Note that it only gives a proportional value and is equivalent to least squares

Description

Log likelihood function for gaussian regression for alpha calculation This function is just the bare likelihood function Note that it only gives a proportional value and is equivalent to least squares

Usage

```
gaussian.loglik.alpha(a, data, mu_func)
```

Arguments

<code>a</code>	A vector of the alphas to be used
<code>data</code>	The data to be used for calculation
<code>mu_func</code>	The function linking the mean to the covariates, as a string with the alphas as <code>a[i]</code> .

Value

A numeric with the log likelihood.

Examples

```
gaussian.loglik.alpha(1, matrix(rnorm(100), 50), "a * data[, 2]")
```

gelu	<i>GELU function</i>
------	----------------------

Description

GELU function

Usage

```
gelu(x)
```

Arguments

x The vector of values

Value

$x * \text{pnorm}(x)$

Examples

```
gelu(2)
```

gen.params.gmjcmc	<i>Generate a parameter list for GMJMCMC (Genetically Modified MJMCMC)</i>
-------------------	--

Description

Generate a parameter list for GMJMCMC (Genetically Modified MJMCMC)

Usage

```
gen.params.gmjcmc(data)
```

Arguments

data The dataset that will be used in the algorithm

Value

A list of parameters to use when running the mjcmc function.

Examples

```
gen.params.gmjcmc(matrix(rnorm(600), 100))
```

gen.params.mjcmc	<i>Generate a parameter list for MJMCMC (Mode Jumping MCMC)</i>
------------------	---

Description

Generate a parameter list for MJMCMC (Mode Jumping MCMC)

Usage

```
gen.params.mjcmc(data)
```

Arguments

data	The dataset that will be used in the algorithm
------	--

Value

A list of parameters to use when running the mjcmc function.

Note that the \$loglik item is an empty list, which is passed to the log likelihood function of the model, intended to store parameters that the estimator function should use.

Examples

```
gen.params.mjcmc(matrix(rnorm(600), 100))
```

gen.probs.gmjcmc	<i>Generate a probability list for GMJMCMC (Genetically Modified MJMCMC)</i>
------------------	--

Description

Generate a probability list for GMJMCMC (Genetically Modified MJMCMC)

Usage

```
gen.probs.gmjcmc(transforms)
```

Arguments

transforms	A list of the transformations used (to get the count).
------------	--

Value

A list of probabilities to be used as input for the gmjcmc function.

Examples

```
gen.probs.gmjcmc(c("p0", "exp_dbl"))
```

gen.probs.mjmcmc	<i>Generate a probability list for MJMCMC (Mode Jumping MCMC)</i>
------------------	---

Description

Generate a probability list for MJMCMC (Mode Jumping MCMC)

Usage

```
gen.probs.mjmcmc()
```

Value

A list of probabilities to be used as input for the mjmcmc function.

Examples

```
gen.probs.mjmcmc()
```

gmjcmc	<i>Main algorithm for GMJMCMC (Genetically Modified MJMCMC)</i>
--------	---

Description

Main algorithm for GMJMCMC (Genetically Modified MJMCMC)

Usage

```
gmjcmc(  
  data,  
  loglik.pi = gaussian.loglik,  
  loglik.alpha = gaussian.loglik.alpha,  
  transforms,  
  P = 10,  
  N.init = 100,  
  N.final = 100,  
  probs = NULL,  
  params = NULL,  
  sub = FALSE,  
  verbose = TRUE  
)
```

Arguments

data	A matrix containing the data to use in the algorithm, first column should be the dependent variable, second should be the intercept and the rest of the columns should be the independent variables.
loglik.pi	The (log) density to explore
loglik.alpha	The likelihood function to use for alpha calculation
transforms	A Character vector including the names of the non-linear functions to be used by the modification and the projection operator.
P	The number of generations for GMJMCMC (Genetically Modified MJMCMC). The default value is $P = 10$. A larger value like $P = 50$ might be more realistic for more complicated examples where one expects a lot of non-linear structures.
N.init	The number of iterations per population (total iterations = $(T-1)*N.init+N.final$)
N.final	The number of iterations for the final population (total iterations = $(T-1)*N.init+N.final$)
probs	A list of the various probability vectors to use
params	A list of the various parameters for all the parts of the algorithm
sub	An indicator that if the likelihood is inexact and should be improved each model visit (EXPERIMENTAL!)
verbose	A logical denoting if messages should be printed

Value

A list containing the following elements:

models	All models per population.
lo.models	All local optimization models per population.
populations	All features per population.
marg.probs	Marginal feature probabilities per population.
model.probs	Marginal feature probabilities per population.
model.probs.idx	Marginal feature probabilities per population.
best.margs	Best marginal model probability per population.
accept	Acceptance rate per population.
accept.tot	Overall acceptance rate.
best	Best marginal model probability throughout the run, represented as the maximum value in <code>unlist(best.margs)</code> .

Examples

```
result <- gmjcmc(matrix(rnorm(600), 100), P = 2, gaussian.loglik, NULL, c("p0", "exp_dbl"))
summary(result)
plot(result)
```

gmjcmc.parallel	<i>Run multiple gmjcmc (Genetically Modified MJMCMC) runs in parallel returning a list of all results.</i>
-----------------	--

Description

Run multiple gmjcmc (Genetically Modified MJMCMC) runs in parallel returning a list of all results.

Usage

```
gmjcmc.parallel(
  runs,
  cores = getOption("mc.cores", 2L),
  merge.options = list(populations = "best", complex.measure = 2, tol = 1e-07),
  data,
  loglik.pi = gaussian.loglik,
  loglik.alpha = gaussian.loglik.alpha(),
  transforms,
  ...
)
```

Arguments

runs	The number of runs to run
cores	The number of cores to run on
merge.options	A list of options to pass to the merge_results() function run after the
data	A matrix containing the data to use in the algorithm, first column should be the dependent variable, second should be the intercept and the rest of the columns should be the independent variables.
loglik.pi	The (log) density to explore
loglik.alpha	The likelihood function to use for alpha calculation
transforms	A Character vector including the names of the non-linear functions to be used by the modification and the projection operator.
...	Further params passed to mjcmc.

Value

Results from multiple gmjcmc runs

Examples

```
result <- gmjcmc.parallel(
  runs = 1,
  cores = 1,
```

```
list(populations = "best", complex.measure = 2, tol = 0.0000001),
matrix(rnorm(600), 100),
P = 2,
gaussian.loglik,
loglik.alpha = gaussian.loglik.alpha,
c("p0", "exp_dbl")
)

summary(result)

plot(result)
```

hs	<i>heavy side function</i>
----	----------------------------

Description

heavy side function

Usage

hs(x)

Arguments

x The vector of values

Value

as.integer(x>0)

Examples

hs(2)

linear.g.prior.loglik *Log likelihood function for linear regression using Zellners g-prior*

Description

Log likelihood function for linear regression using Zellners g-prior

Usage

```
linear.g.prior.loglik(y, x, model, complex, params = list(g = 4))
```

Arguments

y	A vector containing the dependent variable
x	The matrix containing the precalculated features
model	The model to estimate as a logical vector
complex	A list of complexity measures for the features
params	A list of parameters for the log likelihood, supplied by the user

Value

A list with the log marginal likelihood combined with the log prior (crit) and the posterior mode of the coefficients (coefs).

Examples

```
linear.g.prior.loglik(rnorm(100), matrix(rnorm(100)), TRUE, list(oc=1))
```

logistic.loglik	<i>Log likelihood function for logistic regression with a prior $p(m)=\text{sum}(\text{total_width})$ This function is created as an example of how to create an estimator that is used to calculate the marginal likelihood of a model.</i>
-----------------	--

Description

Log likelihood function for logistic regression with a prior $p(m)=\text{sum}(\text{total_width})$ This function is created as an example of how to create an estimator that is used to calculate the marginal likelihood of a model.

Usage

```
logistic.loglik(y, x, model, complex, params = list(r = 1))
```

Arguments

y	A vector containing the dependent variable
x	The matrix containing the precalculated features
model	The model to estimate as a logical vector
complex	A list of complexity measures for the features
params	A list of parameters for the log likelihood, supplied by the user

Value

A list with the log marginal likelihood combined with the log prior (crit) and the posterior mode of the coefficients (coefs).

Examples

```
logistic.loglik(as.integer(rnorm(100) > 0), matrix(rnorm(100)), TRUE, list(oc = 1))
```

logistic.loglik.alpha *Log likelihood function for logistic regression for alpha calculation*
This function is just the bare likelihood function

Description

Log likelihood function for logistic regression for alpha calculation This function is just the bare likelihood function

Usage

```
logistic.loglik.alpha(a, data, mu_func)
```

Arguments

a	A vector of the alphas to be used
data	The data to be used for calculation
mu_func	The function linking the mean to the covariates, as a string with the alphas as a[i].

Value

A numeric with the log likelihood.

marginal.probs	<i>Function for calculating marginal inclusion probabilities of features given a list of models</i>
----------------	---

Description

Function for calculating marginal inclusion probabilities of features given a list of models

Usage

```
marginal.probs(models)
```

Arguments

models The list of models to use.

Value

A numeric vector of marginal model probabilities based on relative frequencies of model visits in MCMC.

Examples

```
result <- gmjcmc(matrix(rnorm(600), 100), P = 2, gaussian.loglik, NULL, c("p0", "exp_db1"))
marginal.probs(result$models[[1]])
```

merge_results	<i>Merge a list of multiple results from many runs This function will weight the features based on the best mlk in that population and merge the results together, simplifying by merging equivalent features (having high correlation).</i>
---------------	--

Description

Merge a list of multiple results from many runs This function will weight the features based on the best mlk in that population and merge the results together, simplifying by merging equivalent features (having high correlation).

Usage

```
merge_results(
  results,
  populations = NULL,
  complex.measure = NULL,
  tol = NULL,
  data = NULL
)
```

Arguments

results	A list containing multiple results from GMJMCMC (Genetically Modified MJMCMC).
populations	Which populations should be merged from the results, can be "all", "last" (default) or "best".
complex.measure	The complex measure to use when finding the simplest equivalent feature, 1=total width, 2=operation count and 3=depth.
tol	The tolerance to use for the correlation when finding equivalent features, default is 0.
data	Data to use when comparing features, default is NULL meaning that mock data will be generated, if data is supplied it should be of the same form as is required by gmjcmc, i.e. with both x, y and an intercept.

Value

An object of class "gmjcmc_merged" containing the following elements:

features	The features where equivalent features are represented in their simplest form.
marg.probs	Importance of features.
counts	Counts of how many versions that were present of each feature.
results	Results as they were passed to the function.
pop.best	The population in the results which contained the model with the highest log marginal posterior.
thread.best	The thread in the results which contained the model with the highest log marginal posterior.
crit.best	The highest log marginal posterior for any model in the results.
reported	The highest log marginal likelihood for the reported populations as defined in the populations argument.
rep.pop	The index of the population which contains reported.
best.log.posterior	A matrix where the first column contains the population indices and the second column contains the model with the highest log marginal posterior within that population.
rep.thread	The index of the thread which contains reported.

```
result <- gmjcmc.parallel( runs = 1, cores = 1, list(populations = "best", complex.measure = 2, tol = 0.0000001), matrix(rnorm(600), 100), P = 2, gaussian.loglik, loglik.alpha = gaussian.loglik.alpha, c("p0", "exp_dbl") )
```

```
summary(result)
```

```
plot(result)
```

```
merge_results(result$results)
```

mjcmc

*Main algorithm for MJMCMC (Genetically Modified MJMCMC)***Description**

Main algorithm for MJMCMC (Genetically Modified MJMCMC)

Usage

```

mjcmc(
  data,
  loglik.pi,
  N = 100,
  probs = NULL,
  params = NULL,
  sub = FALSE,
  verbose = TRUE
)

```

Arguments

data	A matrix containing the data to use in the algorithm, first column should be the dependent variable, second should be the intercept and the rest of the columns should be the independent variables.
loglik.pi	The (log) density to explore
N	The number of iterations to run for
probs	A list of the various probability vectors to use
params	A list of the various parameters for all the parts of the algorithm
sub	An indicator that if the likelihood is inexact and should be improved each model visit (EXPERIMENTAL!)
verbose	A logical denoting if messages should be printed

Value

A list containing the following elements:

models	All visited models.
accept	Average acceptance rate of the chain.
lo.models	All models visited during local optimization.
best.crit	The highest log marginal probability of the visited models.
marg.probs	Marginal probabilities of the features.
model.probs	Marginal probabilities of all of the visited models.
model.probs.idx	Indices of unique visited models.
populations	The covariates represented as a list of features.

Examples

```
result <- mjmcmc(matrix(rnorm(600), 100), gaussian.loglik)
summary(result)
plot(result)
```

mjmcmc.parallel	<i>Run multiple mjmcmc runs in parallel, merging the results before returning.</i>
-----------------	--

Description

Run multiple mjmcmc runs in parallel, merging the results before returning.

Usage

```
mjmcmc.parallel(runs, cores = getOption("mc.cores", 2L), ...)
```

Arguments

runs	The number of runs to run
cores	The number of cores to run on
...	Further params passed to mjmcmc.

Value

Merged results from multiple mjmcmc runs

Examples

```
result <- mjmcmc.parallel(runs = 1, cores = 1, matrix(rnorm(600), 100), gaussian.loglik)
summary(result)
plot(result)
```

model.string	<i>Function to generate a function string for a model consisting of features</i>
--------------	--

Description

Function to generate a function string for a model consisting of features

Usage

```
model.string(model, features, link = "I", round = 2)
```

Arguments

model	A logical vector indicating which features to include
features	The population of features
link	The link function to use, as a string
round	Rounding error for the features in the printed format

Value

A character representation of a model

Examples

```
result <- gmjcmc(matrix(rnorm(600), 100), P = 2, gaussian.loglik, NULL, c("p0", "exp_dbl"))
summary(result)
plot(result)
model.string(c(TRUE, FALSE, TRUE, FALSE, TRUE), result$populations[[1]])
model.string(result$models[[1]][1][1][1]$model, result$populations[[1]])
```

ngelu	<i>Negative GELU function</i>
-------	-------------------------------

Description

Negative GELU function

Usage

```
ngelu(x)
```

Arguments

x	The vector of values
---	----------------------

Value

$-x * \text{pnorm}(-x)$

Examples

`ngelu(2)`

<code>nhs</code>	<i>negative heavy side function</i>
------------------	-------------------------------------

Description

negative heavy side function

Usage

`nhs(x)`

Arguments

`x` The vector of values

Value

`as.integer(x < 0)`

Examples

`nhs(2)`

<code>not</code>	<i>not x</i>
------------------	--------------

Description

not x

Usage

`not(x)`

Arguments

`x` The vector of binary values

Value

1-x

Examples

not(TRUE)

nrelu	<i>negative ReLu function</i>
-------	-------------------------------

Description

negative ReLu function

Usage

nrelu(x)

Arguments

x The vector of values

Value

max(-x,0)

Examples

nrelu(2)

p0	<i>p0 polynomial term</i>
----	---------------------------

Description

p0 polynomial term

Usage

p0(x)

Arguments

x The vector of values

Value

$\log(\text{abs}(x) + \text{.Machine\$double.eps})$

Examples

$p0(2)$

p05

p05 polynomial term

Description

p05 polynomial term

Usage

$p05(x)$

Arguments

x The vector of values

Value

$(\text{abs}(x) + \text{.Machine\$double.eps})^{0.5}$

Examples

$p05(2)$

p0p0

p0p0 polynomial term

Description

p0p0 polynomial term

Usage

$p0p0(x)$

Arguments

x The vector of values

Value

$$p0(x)*p0(x)$$
Examples

$$p0p0(2)$$

p0p05

*p0p05 polynomial term***Description**

p0p05 polynomial term

Usage

$$p0p05(x)$$
Arguments

x The vector of values

Value

$$p0(x)*(abs(x)+.Machine\$double.eps)^(0.5)$$
Examples

$$p0p05(2)$$

p0p1

*p0p1 polynomial term***Description**

p0p1 polynomial term

Usage

$$p0p1(x)$$
Arguments

x The vector of values

Value
 $p0(x)*x$
Examples
 $p0p1(2)$

p0p2

p0p2 polynomial term

Description

p0p2 polynomial term

Usage
 $p0p2(x)$
Arguments

x The vector of values

Value
 $p0(x)*x^(2)$
Examples
 $p0p2(2)$

p0p3

p0p3 polynomial term

Description

p0p3 polynomial term

Usage
 $p0p3(x)$
Arguments

x The vector of values

Value

$$p0(x)*x^{(3)}$$
Examples

$$p0p3(2)$$

p0pm05

*p0pm05 polynomial term***Description**

p0pm05 polynomial term

Usage

$$p0pm05(x)$$
Arguments

x The vector of values

Value

$$p0(x)sign(x)(abs(x)+.Machine\$double.eps)^{-0.5}$$
Examples

$$p0pm05(2)$$

p0pm1

*p0pm1 polynomial terms***Description**

p0pm1 polynomial terms

Usage

$$p0pm1(x)$$
Arguments

x The vector of values

Value

$$p0(x) * (x + \text{Machine}\$\text{double.eps})^{-1}$$
Examples

$$p0pm1(2)$$

p0pm2

p0pm2 polynomial term

Description

p0pm2 polynomial term

Usage

$$p0pm2(x)$$
Arguments

x The vector of values

Value

$$p0(x) \text{sign}(x) (\text{abs}(x) + \text{Machine}\$\text{double.eps})^{-2}$$
Examples

$$p0pm2(2)$$

p2

p2 polynomial term

Description

p2 polynomial term

Usage

$$p2(x)$$
Arguments

x The vector of values

Value $x^{(2)}$ **Examples**

p2(2)

p3

p3 polynomial term

Description

p3 polynomial term

Usage

p3(x)

Arguments

x The vector of values

Value $x^{(3)}$ **Examples**

p3(2)

plot.gmjcmc

Function to plot the results, works both for results from gmjcmc and merged results from merge.results

Description

Function to plot the results, works both for results from gmjcmc and merged results from merge.results

Usage

```
## S3 method for class 'gmjcmc'
plot(x, count = "all", pop = "last", ...)
```

Arguments

x	The results to use
count	The number of features to plot, defaults to all
pop	The population to plot, defaults to last
...	Not used.

Value

No return value, just creates a plot

Examples

```
result <- gmjcmc(matrix(rnorm(600), 100), P = 2, gaussian.loglik, NULL, c("p0", "exp_dbl"))
plot(result)
```

`plot.gmjcmc_merged` *Plot a gmjcmc_merged run*

Description

Plot a gmjcmc_merged run

Usage

```
## S3 method for class 'gmjcmc_merged'
plot(x, count = "all", ...)
```

Arguments

x	The results to use
count	The number of features to plot, defaults to all
...	Not used.

Value

No return value, just creates a plot

Examples

```

result <- gmjcmc.parallel(
  runs = 1,
  cores = 1,
  list(populations = "best", complex.measure = 2, tol = 0.0000001),
  matrix(rnorm(600), 100),
  P = 2,
  gaussian.loglik,
  loglik.alpha = gaussian.loglik.alpha,
  c("p0", "exp_dbl")
)
plot(result)

```

plot.mjcmc	<i>Function to plot the results, works both for results from gmjcmc and merged results from merge.results</i>
------------	---

Description

Function to plot the results, works both for results from gmjcmc and merged results from merge.results

Usage

```

## S3 method for class 'mjcmc'
plot(x, count = "all", ...)

```

Arguments

x	The results to use
count	The number of features to plot, defaults to all
...	Not used.

Value

No return value, just creates a plot

Examples

```

result <- mjcmc(matrix(rnorm(600), 100), gaussian.loglik)
plot(result)

```

plot.mjcmc_parallel *Plot a mjcmc_parallel run*

Description

Plot a mjcmc_parallel run

Usage

```
## S3 method for class 'mjcmc_parallel'  
plot(x, count = "all", ...)
```

Arguments

x	The results to use
count	The number of features to plot, defaults to all
...	Not used.

Value

No return value, just creates a plot

Examples

```
result <- mjcmc.parallel(runs = 1, cores = 1, matrix(rnorm(600), 100), gaussian.loglik)  
plot(result)
```

pm05

pm05 polynomial term

Description

pm05 polynomial term

Usage

```
pm05(x)
```

Arguments

x	The vector of values
---	----------------------

Value

$(\text{abs}(x) + .\text{Machine}\$\text{double.eps})^{-0.5}$

Examples

pm05(2)

pm1*pm1 polynomial term*

Description

pm1 polynomial term

Usage

pm1(x)

Arguments

x The vector of values

Value $\text{sign}(x) * (\text{abs}(x) + .\text{Machine}\$\text{double.eps})^{-1}$ **Examples**

pm1(2)

pm2*pm2 polynomial term*

Description

pm2 polynomial term

Usage

pm2(x)

Arguments

x The vector of values

Value $\text{sign}(x) * (\text{abs}(x) + .\text{Machine}\$\text{double.eps})^{-2}$

Examples

```
pm2(2)
```

```
predict.gmjmc      Predict using a gmjmc result object.
```

Description

Predict using a gmjmc result object.

Usage

```
## S3 method for class 'gmjmc'
predict(object, x, link = function(x) x, quantiles = c(0.025, 0.5, 0.975), ...)
```

Arguments

object	The model to use.
x	The new data to use for the prediction, a matrix where each row is an observation.
link	The link function to use
quantiles	The quantiles to calculate credible intervals for the posterior modes (in model space).
...	Not used.

Value

A list containing aggregated predictions and per model predictions.

aggr	Aggregated predictions with mean and quantiles.
preds	A list of lists containing individual predictions per model per population in object.

Examples

```
result <- gmjmc(
  matrix(rnorm(600), 100),
  P = 2,
  gaussian.loglik,
  loglik.alpha = gaussian.loglik.alpha,
  c("p0", "exp_dbl")
)
preds <- predict(result, matrix(rnorm(600), 100))
```

predict.gjmcmc_merged

Predict using a merged gjmcmc result object.

Description

Predict using a merged gjmcmc result object.

Usage

```
## S3 method for class 'gjmcmc_merged'
predict(object, x, link = function(x) x, quantiles = c(0.025, 0.5, 0.975), ...)
```

Arguments

object	The model to use.
x	The new data to use for the prediction, a matrix where each row is an observation.
link	The link function to use
quantiles	The quantiles to calculate credible intervals for the posterior modes (in model space).
...	Not used.

Value

A list containing aggregated predictions and per model predictions.

aggr	Aggregated predictions with mean and quantiles.
preds	A list of lists containing individual predictions per model per population in object.

Examples

```
result <- gjmcmc.parallel(
  runs = 1,
  cores = 1,
  list(populations = "best", complex.measure = 2, tol = 0.0000001),
  matrix(rnorm(600), 100),
  P = 2,
  gaussian.loglik,
  loglik.alpha = gaussian.loglik.alpha,
  c("p0", "exp_dbl")
)
preds <- predict(result, matrix(rnorm(600), 100))
```

```
predict.gjmcmc_parallel
```

Predict using a gjmcmc result object from a parallel run.

Description

Predict using a gjmcmc result object from a parallel run.

Usage

```
## S3 method for class 'gjmcmc_parallel'
predict(object, x, link = function(x) x, quantiles = c(0.025, 0.5, 0.975), ...)
```

Arguments

object	The model to use.
x	The new data to use for the prediction, a matrix where each row is an observation.
link	The link function to use
quantiles	The quantiles to calculate credible intervals for the posterior modes (in model space).
...	Additional arguments to pass to merge_results.

Value

A list containing aggregated predictions and per model predictions.

aggr	Aggregated predictions with mean and quantiles.
preds	A list of lists containing individual predictions per model per population in object.

Examples

```
result <- gjmcmc.parallel(
  runs = 1,
  cores = 1,
  list(populations = "best", complex.measure = 2, tol = 0.0000001),
  matrix(rnorm(600), 100),
  P = 2,
  gaussian.loglik,
  loglik.alpha = gaussian.loglik.alpha,
  c("p0", "exp_dbl")
)
preds <- predict(result$results, matrix(rnorm(600), 100))
```

predict.mjcmc *Predict using a mjcmc result object.*

Description

Predict using a mjcmc result object.

Usage

```
## S3 method for class 'mjcmc'
predict(object, x, link = function(x) x, quantiles = c(0.025, 0.5, 0.975), ...)
```

Arguments

object	The model to use.
x	The new data to use for the prediction, a matrix where each row is an observation.
link	The link function to use
quantiles	The quantiles to calculate credible intervals for the posterior modes (in model space).
...	Not used.

Value

A list containing aggregated predictions.

mean	Mean of aggregated predictions.
quantiles	Quantiles of aggregated predictions.

Examples

```
result <- mjcmc(matrix(rnorm(600), 100), gaussian.loglik)
preds <- predict(result, matrix(rnorm(500), 100))
```

predict.mjcmc_parallel
Predict using a mjcmc result object from a parallel run.

Description

Predict using a mjcmc result object from a parallel run.

Usage

```
## S3 method for class 'mjcmc_parallel'
predict(object, x, link = function(x) x, quantiles = c(0.025, 0.5, 0.975), ...)
```

Arguments

object	The model to use.
x	The new data to use for the prediction, a matrix where each row is an observation.
link	The link function to use
quantiles	The quantiles to calculate credible intervals for the posterior modes (in model space).
...	Not used.

Value

A list containing aggregated predictions.

mean	Mean of aggregated predictions.
quantiles	Quantiles of aggregated predictions.

Examples

```
result <- mjcmc.parallel(runs = 1, cores = 1, matrix(rnorm(600), 100), gaussian.loglik)
preds <- predict(result, matrix(rnorm(500), 100))
```

print.feature	<i>Print method for "feature" class</i>
---------------	---

Description

Print method for "feature" class

Usage

```
## S3 method for class 'feature'
print(x, dataset = FALSE, alphas = FALSE, labels = FALSE, round = FALSE, ...)
```

Arguments

x	An object of class "feature"
dataset	Set the regular covariates as columns in a dataset
alphas	Print a "?" instead of actual alphas to prepare the output for alpha estimation
labels	Should the covariates be named, or just referred to as their place in the data.frame.
round	Should numbers be rounded when printing? Default is FALSE, otherwise it can be set to the number of decimal places.
...	Not used.

Value

String representation of a feature

Examples

```
result <- gmjcmc(matrix(rnorm(600), 100), P = 2, gaussian.loglik, NULL, c("p0", "exp_db1"))
print(result$populations[[1]][1])
```

relu	<i>ReLU function</i>
------	----------------------

Description

ReLU function

Usage

```
relu(x)
```

Arguments

x The vector of values

Value

max(x,0)

Examples

```
relu(2)
```

set.transforms	<i>Set the transformations option for GMJMCMC (Genetically Modified MJMCMC), this is also done when running the algorithm, but this function allows for it to be done manually.</i>
----------------	---

Description

Set the transformations option for GMJMCMC (Genetically Modified MJMCMC), this is also done when running the algorithm, but this function allows for it to be done manually.

Usage

```
set.transforms(transforms)
```

Arguments

transforms The vector of non-linear transformations

Value

No return value, just sets the gmjcmc-transformations option

Examples

```
set.transforms(c("p0", "p1"))
```

sigmoid

Sigmoid function

Description

Sigmoid function

Usage

```
sigmoid(x)
```

Arguments

x The vector of values

Value

The sigmoid of x

Examples

```
sigmoid(2)
```

sin_deg	<i>Sine function for degrees</i>
---------	----------------------------------

Description

Sine function for degrees

Usage

sin_deg(x)

Arguments

x The vector of values in degrees

Value

The sine of x

Examples

sin_deg(0)

sqrt	<i>Square root function</i>
------	-----------------------------

Description

Square root function

Usage

sqrt(x)

Arguments

x The vector of values

Value

The square root of the absolute value of x

Examples

sqrt(4)

string.population *Function to get a character representation of a list of features*

Description

Function to get a character representation of a list of features

Usage

```
string.population(x, round = 2)
```

Arguments

x	A list of feature objects
round	Rounding precision for parameters of the features

Value

A matrix of character representations of the features of a model.

Examples

```
result <- gmjcmc(matrix(rnorm(600), 100), P = 2, gaussian.loglik, NULL, c("p0", "exp_dbl"))
string.population(result$populations[[1]])
```

string.population.models *Function to get a character representation of a list of models*

Description

Function to get a character representation of a list of models

Usage

```
string.population.models(features, models, round = 2, link = "I")
```

Arguments

features	A list of feature objects on which the models are build
models	A list of model objects
round	Rounding precision for parameters of the features
link	The link function to use, as a string

Value

A matrix of character representations of a list of models.

Examples

```
result <- gjmcmc(matrix(rnorm(600), 100), P = 2, gaussian.loglik, NULL, c("p0", "exp_dbl"))
string.population.models(result$populations[[2]], result$models[[2]])
```

summary.gjmcmc	<i>Function to print a quick summary of the results</i>
----------------	---

Description

Function to print a quick summary of the results

Usage

```
## S3 method for class 'gjmcmc'
summary(object, pop = "last", tol = 1e-04, labels = FALSE, effects = NULL, ...)
```

Arguments

object	The results to use
pop	The population to print for, defaults to last
tol	The tolerance to use as a threshold when reporting the results.
labels	Should the covariates be named, or just referred to as their place in the data.frame.
effects	Quantiles for posterior modes of the effects across models to be reported, if either effects are NULL or if labels are NULL, no effects are reported.
...	Not used.

Value

A data frame containing the following columns:

feats.strings	Character representation of the features ordered by marginal probabilities.
marg.probs	Marginal probabilities corresponding to the ordered feature strings.

Examples

```
result <- gjmcmc(matrix(rnorm(600), 100), P = 2, gaussian.loglik, NULL, c("p0", "exp_dbl"))
summary(result)
```

`summary.gmjcmc_merged`*Function to print a quick summary of the results*

Description

Function to print a quick summary of the results

Usage

```
## S3 method for class 'gmjcmc_merged'  
summary(object, tol = 1e-04, labels = FALSE, effects = NULL, ...)
```

Arguments

<code>object</code>	The results to use
<code>tol</code>	The tolerance to use as a threshold when reporting the results.
<code>labels</code>	Should the covariates be named, or just referred to as their place in the data.frame.
<code>effects</code>	Quantiles for posterior modes of the effects across models to be reported, if either effects are NULL or if labels are NULL, no effects are reported.
<code>...</code>	Not used.

Value

A data frame containing the following columns:

<code>feats.strings</code>	Character representation of the features ordered by marginal probabilities.
<code>marg.probs</code>	Marginal probabilities corresponding to the ordered feature strings.

Examples

```
result <- gmjcmc.parallel(  
  runs = 1,  
  cores = 1,  
  list(populations = "best", complex.measure = 2, tol = 0.0000001),  
  matrix(rnorm(600), 100),  
  P = 2,  
  gaussian.loglik,  
  loglik.alpha = gaussian.loglik.alpha,  
  c("p0", "exp_dbl")  
)  
summary(result)
```

```
summary.mjmc      Function to print a quick summary of the results
```

Description

Function to print a quick summary of the results

Usage

```
## S3 method for class 'mjmc'
summary(object, tol = 1e-04, labels = FALSE, effects = NULL, ...)
```

Arguments

object	The results to use
tol	The tolerance to use as a threshold when reporting the results.
labels	Should the covariates be named, or just referred to as their place in the data.frame.
effects	Quantiles for posterior modes of the effects across models to be reported, if either effects are NULL or if labels are NULL, no effects are reported.
...	Not used.

Value

A data frame containing the following columns:

feats.strings	Character representation of the covariates ordered by marginal probabilities.
marg.probs	Marginal probabilities corresponding to the ordered feature strings.

Examples

```
result <- mjmc(matrix(rnorm(600), 100), gaussian.loglik)
summary(result)
```

```
summary.mjmc_parallel      Function to print a quick summary of the results
```

Description

Function to print a quick summary of the results

Usage

```
## S3 method for class 'mjmc_parallel'
summary(object, tol = 1e-04, labels = FALSE, effects = NULL, ...)
```

Arguments

object	The results to use
tol	The tolerance to use as a threshold when reporting the results.
labels	Should the covariates be named, or just referred to as their place in the data.frame.
effects	Quantiles for posterior modes of the effects across models to be reported, if either effects are NULL or if labels are NULL, no effects are reported.
...	Not used.

Value

A data frame containing the following columns:

feats.strings	Character representation of the covariates ordered by marginal probabilities.
marg.probs	Marginal probabilities corresponding to the ordered feature strings.

Examples

```
result <- mjmcmc.parallel(runs = 1, cores = 1, matrix(rnorm(600), 100), gaussian.loglik)
summary(result)
```

to23

To the 2.3 power function

Description

To the 2.3 power function

Usage

```
to23(x)
```

Arguments

x	The vector of values
---	----------------------

Value

$x^{2.3}$

Examples

```
to23(2)
```

to25

To 2.5 power

Description

To 2.5 power

Usage

to25(x)

Arguments

x The vector of values

Value

$x^{(2.5)}$

Examples

to25(2)

to35

To 3.5 power

Description

To 3.5 power

Usage

to35(x)

Arguments

x The vector of values

Value

$x^{(3.5)}$

Examples

to35(2)

to72 *To the 7/2 power function*

Description

To the 7/2 power function

Usage

to72(x)

Arguments

x The vector of values

Value

$x^{(7/2)}$

Examples

to72(2)

root *Cube root function*

Description

Cube root function

Usage

root(x)

Arguments

x The vector of values

Value

The cube root of x

Examples

root(27)

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