Package 'lgpr'

December 4, 2019

Title Longitudinal Gaussian Process Regression

Version 0.30.4

Description Implements interpretable nonparametric analysis and
covariate selection for longitudinal data using additive
Gaussian process regression. Includes specialized non-stationary disease
effect modeling features for biomedical studies. Bayesian inference for
model parameters is performed using Stan.

License GPL (>=3)

Encoding UTF-8

LazyData true

Biarch true

Depends R (>= 3.4.0),

Imports methods,
Rcpp (>= 0.12.0),
rstan (>= 2.18.1),
rstantools (>= 2.0.0),
bayesplot (>= 1.7.0),
MASS (>= 7.3-50),
stats (>= 3.4),
ggplot2 (>= 3.1.0),
ggpubr (>= 0.2)

LinkingTo BH (>= 1.66.0),
Rcpp (>= 0.12.0),
RcppEigen (>= 0.3.3.3.0),
rstan (>= 2.18.1),
StanHeaders (>= 2.18.0)

SystemRequirements GNU make

RoxygenNote 6.1.1

Suggests knitr,
rmarkdown,
testthat,
covr

VignetteBuilder knitr

R topics documented:

lgpr-package *The 'lgpr' package.*

Description

Longitudinal Gaussian Process regression. The package features

- Additive Gaussian process modeling of longitudinal data
- Posterior inference of the model (hyper)parameters using Stan
- Computation of covariate relevances
- Specialized modeling of a non-stationary disease effect
- Functions for visualizing longitudinal data, posterior samples and model predictions
- Gaussian, Poisson, binomial or negative binomial observation models

Basic usage

- See the main function `lgp` for creating and fitting additive longitudinal GP models.
- See tutorials at `https://jtimonen.github.io/lgpr-usage/`

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References

1. Carpenter, B. et al. (2017). *Stan: A probabilistic programming language*. Journal of Statistical Software 76(1).
2. Jonah Gabry, Ben Goodrich and Martin Lysy (2019). *rstantools: Tools for Developing R Packages Interfacing with 'Stan'*. R package version 2.0.0.
3. Gabry, J. and Mahr, T. (2019). *bayesplot: Plotting for Bayesian Models*. R package version 1.7.0, http://mc-stan.org/bayesplot.
4. Stan Development Team (2019). *RStan: the R interface to Stan*. R package version 2.19.2. http://mc-stan.org/.

add_test_caseIDs *Add case IDs to test data frame*

Description

Add case IDs to test data frame

Usage

```
add_test_caseIDs(X_test, X_data)
```

Arguments

`X_test`	test data frame
`X_data`	data frame

Value

Updated X_test data frame.

`affected` *Select the affected individuals*

Description

Select the affected individuals

Usage

```
affected(object, medians.return = FALSE, threshold = 0.5)
```

Arguments

`object`	An object of class `lgpfit`.
`medians.return`	Should the medians of beta parameters also be returned?
`threshold`	A value that the median of beta has to exceed

Value

A binary vector indicating the individuals for which the disease effect is inferred to exist.

`assess_convergence` *Assess convergence of the chains*

Description

Assess convergence of the chains

Usage

```
assess_convergence(fit, skip_F_gen = TRUE)
```

Arguments

`fit`	An (incomplete) object of class `lgpfit`.
`skip_F_gen`	Should F_mean, F_var etc. be ignored

Value

A data frame with columns `c("Rhat","Bulk_ESS","Tail_ESS")`.

`average_predictions` *Average predictions over samples*

Description

Average predictions over samples

Usage

```
average_predictions(LIST)
```

Arguments

`LIST`	a list over samples

Value

a list

`check_data` *Validate the ‘data‘ input to `lgp` and resolve covariate types*

Description

Validate the ‘data‘ input to `lgp` and resolve covariate types

Usage

```
check_data(data, varInfo, verbose)
```

Arguments

`data`	the data frame that was passed to `lgp`
`varInfo`	variable type info
`verbose`	can this print some info?

Value

a list

`check_formula` *Validate the formula of* `lgp`

Description

Checks if the input ‘formula‘ to `lgp_model` are valid with the given data

Usage

```
check_formula(formula, data)
```

Arguments

`formula`	the formula that was passed to `lgp_model`
`data`	the data frame that was passed to `lgp_model`

Value

nothing

`check_hyperparameter_names` *An error message for wrong hyperparameter naming*

Description

An error message for wrong hyperparameter naming

Usage

```
check_hyperparameter_names(dist, correct)
```

Arguments

`dist`	the distribution
`correct`	the allowed hyperparameter names

Value

nothing

`check_varInfo` *Check that variable types make sense*

Description

Check that variable types make sense

Usage

```
check_varInfo(varInfo)
```

Arguments

`varInfo`	a named list

Value

nothing

`component_index_to_covariate_index` *Component index to covariate index*

Description

Component index to covariate index

Usage

```
component_index_to_covariate_index(D, idx)
```

Arguments

`D`	integer vector of length 6
`idx`	integer

Value

an integer

component_index_to_type

Component index to component type

Description

Component index to component type

Usage

```
component_index_to_type(D, idx)
```

Arguments

`D`	integer vector of length 6
`idx`	integer

Value

an integer

compute_kernel_matrices

Evaluate kernel matrices for each component

Description

Used by `compute_predictions`.

Usage

```
compute_kernel_matrices(X1, X2, kernel_info)
```

Arguments

`X1`	Covariate matrix of size `n1` x `sum(D)`.
`X2`	Covariate matrix of size `n2` x `sum(D)`.
`kernel_info`	A list of parameters and other kernel info.

Value

An array of size `n1` x `n2` x `sum(D)`.

`compute_K_beta` *Compute the multiplier matrix K_beta (to eneable heterogeneous disease effect)*

Description

Compute the multiplier matrix K_beta (to eneable heterogeneous disease effect)

Usage

```
compute_K_beta(beta, row_to_caseID_1, row_to_caseID_2)
```

Arguments

`beta`	a row vector of length `N_cases`
`row_to_caseID_1`	mapping from row index to case ID
`row_to_caseID_2`	mapping from row index to case ID

Value

a matrix

`compute_K_var_mask` *Compute the variance mask kernel matrix*

Description

Compute the variance mask kernel matrix

Usage

```
compute_K_var_mask(disAge1, disAge2, vm_params, stp, nan_replace = 0)
```

Arguments

`disAge1`	disease-related age covariate vector of length `n1`
`disAge2`	disease-related age covariate vector of length `n2`
`vm_params`	vector of two mask function parameters
`stp`	input warping steepness
`nan_replace`	value to replace nans in disAge vectors

Value

a matrix of size `n1` x `n2`

`compute_lppd` *Compute log-posterior predictive density at test points*

Description

Compute log-posterior predictive density at test points

Usage

```
compute_lppd(PRED, y_test)
```

Arguments

`PRED`	predictions
`y_test`	values of the response variable at the test points

Value

a matrix with size `n_samples` x `n_data`

`compute_noise_level` *Determine noise level*

Description

Determine noise level

Usage

```
compute_noise_level(pars, model, noise_method)
```

Arguments

`pars`	A data frame representing one parameter sample, i.e one row of `as.data.frame(stanfit)`, where stanfit is an object of class `stanfit`
`model`	An object of class `lgpmodel`
`noise_method`	Noise level estimation method.

Value

a value between 0 and 1

`compute_predicted_components`
Compute component-wise predictions at test points

Description

Used by `compute_predictions`.

Usage

```
compute_predicted_components(KK, KKs, KKss, y_data, sigma_n, DELTA)
```

Arguments

`KK`	Kernel matrices data vs. data.
`KKs`	Kernel matrices test vs. data.
`KKss`	Kernel matrices test vs. test.
`y_data`	Response variable.
`sigma_n`	Noise standard deviation parameter.
`DELTA`	Diagonal jitter that ensures pos. def. kernel.

Value

A list containing predicted means and variances.

`compute_predictions` *Compute component-wise predictions at test points*

Description

Used by `lgp_predict`.

Usage

```
compute_predictions(X_data, y_data, X_test, params, D, info, cnames, TSCL,
  handle_extra = "warning")
```

Arguments

`X_data`	Covariate matrix (data points).
`y_data`	Response variable (data points).
`X_test`	Covariate matrix (test points).
`params`	Kernel function and other hyperparameters
`D`	a vector of length 6
`info`	other model info
`cnames`	Names of the model components.
`TSCL`	time scaling function and its inverse
`handle_extra`	What to do if test data contains individuals that are not in the training data? Must be 'silent', 'warning' or 'error'.

Value

A list.

`compute_relevances` *Compute component relevances and estimate amount of noise (one MCMC sample)*

Description

Compute component relevances and estimate amount of noise (one MCMC sample)

Usage

```
compute_relevances(pars, model, method, noise_method)
```

Arguments

`pars`	A data frame representing one parameter sample, i.e one row of `as.data.frame(stanfit)`, where stanfit is an object of class `stanfit`
`model`	An object of class `lgpmodel`
`method`	Relevance determination method. Must be either `"f_mean"` or `"alpha"`.
`noise_method`	Noise level estimation method.

Value

a matrix of size `1` x `n_components` + `1`

`compute_relevances_alpha` *The alpha relevance determination method*

Description

The alpha relevance determination method

Usage

```
compute_relevances_alpha(pars, model)
```

Arguments

`pars`	A data frame representing one parameter sample, i.e one row of `as.data.frame(stanfit)`, where stanfit is an object of class `stanfit`
`model`	An object of class `lgpmodel`

Value

a vector of length `n_components`

`compute_relevances_fmean` *The f_mean relevance determination method*

Description

The f_mean relevance determination method

Usage

```
compute_relevances_fmean(pars, model)
```

Arguments

`pars`	A data frame representing one parameter sample, i.e one row of `as.data.frame(stanfit)`, where stanfit is an object of class `stanfit`
`model`	An object of class `lgpmodel`

Value

a vector of length `n_components`

`create_covariates_stan` *Create the covariate matrix that is given to stan*

Description

Create the covariate matrix that is given to stan

Usage

```
create_covariates_stan(data, varInfo, types, formula, verbose)
```

Arguments

`data`	the data frame that was passed to `lgp`
`varInfo`	original variable type info
`types`	the types returned by `check_data`
`formula`	the model formula
`verbose`	can this print some info?

Value

a list

`create_data_plot_df` *Create a plotting data frame for ggplot*

Description

A helper function for `plot_data`.

Usage

```
create_data_plot_df(data, hl_1, hl_2, hl_cont)
```

Arguments

`data`	a data frame
`hl_1`	highlighting by color
`hl_2`	highlighting by linestyle
`hl_cont`	highlighting continuous

Value

an extended data frame

`create_example_fit` *Create an example fit object*

Description

Create an example fit object

Usage

```
create_example_fit(N = 4, t = 10 * c(1, 2, 3, 4, 5), iter = 100,
  chains = 1)
```

Arguments

`N`	number of individuals
`t`	time points
`iter`	number of iterations
`chains`	number of chains

Value

an object of class `lgpfit`

`create_F` *Simulate latent function components for longitudinal data analysis*

Description

Simulate latent function components for longitudinal data analysis

Usage

```
create_F(X, covariates, relevances, lengthscales, X_affected, dis_fun,
  bin_kernel, steepness, vm_params, force_zeromean)
```

Arguments

`X`	input data matrix (generated by `create_X`)
`covariates`	Integer vector that defines the types of covariates (other than id and age). Different integers correspond to the following covariate types: • 0 = disease-related age • 1 = other continuous covariate • 2 = a categorical covariate that interacts with age • 3 = a categorical covariate that acts as a group offset • 4 = a categorical covariate that that acts as a group offset AND is restricted to have value 0 for controls and 1 for cases
`relevances`	Relative relevance of each component. Must have be a vector so that `length(relevances)` = 2 + `length(covariates)`. First two values define the relevance of the infividual-specific age and shared age component, respectively.
`lengthscales`	A vector so that `length(lengthscales) = 2` + `sum(covariates` `%in%` `c(0,1,2))`.
`X_affected`	which individuals are affected by the disease
`dis_fun`	A function or a string that defines the disease effect. If this is a function, that function is used to generate the effect. If `dis_fun` is "gp_vm" or "gp_ns", the disease component is drawn from a nonstationary GP prior (vm is the variance masked version of it).
`bin_kernel`	Should the binary kernel be used for categorical covariates? If this is `TRUE`, the effect will exist only for group 1.
`steepness`	Steepness of the input warping function. This is only used if the disease component is in the model.
`vm_params`	Parameters of the variance mask function. This is only needed if `useMaskedVarianceKernel` = `TRUE`.
`force_zeromean`	Should each component (excluding the disease age component) be forced to have a zero mean?

Value

a data frame FFF where one column corresponds to one additive data component

`create_predictions_plot_df1`
Create a plotting data frame for ggplot

Description

A helper function for `plot_predictions`.

Usage

```
create_predictions_plot_df1(fit, scale_f = TRUE, n_sds)
```

Arguments

`fit`	An object of class `lgpfit`.
`scale_f`	Should the predictions be scaled back to the original data scale?
`n_sds`	number of standard deviations for the uncertainty band width

Value

a data frame

`create_predictions_plot_df2`
Create a plotting data frame for ggplot

Description

A helper function for `plot_predictions`.

Usage

```
create_predictions_plot_df2(model, PRED, scale_f = TRUE, mode, n_sds)
```

Arguments

`model`	An object of class `lgpmodel`.
`PRED`	Predictions computed using `lgp_predict`.
`scale_f`	Should the predictions be scaled back to the original data scale?
`mode`	mode
`n_sds`	number of standard deviations for the uncertainty band width

Value

a data frame

`create_simdata_plot_df` *Create a plotting data frame for ggplot*

Description

A helper function for `plot_simdata_by_component`.

Usage

```
create_simdata_plot_df(simData)
```

Arguments

`simData`	An object created using `simulate_data`.

Value

a data frame

`create_stan_input` *Create input for Stan*

Description

Parses the `formula` and `data` input to `lgp_model`. Also performs many input checks.

Usage

```
create_stan_input(formula, data, prior, likelihood, varInfo, standardize,
  uncertain_effect_time, equal_effect, C_hat, DELTA, sample_F, verbose,
  variance_mask, N_trials, skip_gen_quant)
```

Arguments

`formula`	A formula of the form `y ~ x1 + x2 + x3` defining the response variable `y` and covariates `xi`. The formula must contain exatly one tilde (~), with response variable on the left-hand side and covariates on the right-hand side. Covariates should be separated by a plus (+) sign. All variables that appear in the formula must exist as columns of `data`. Note that effects of categorical covariates are by default defined as interactions with `time_variable`. If you wish to change this, see the argument `offset_vars`. The subject identifier variable cannot currently be included in `offset_vars`. If you wish to model the effect of `id_variable` as a constant offset, you can create another covariate with the same values and use it in your `formula` and `offset_vars` instead.
`data`	A data frame containing the variables given in `formula` as columns.
`prior`	A named list, defining the prior distribution of model (hyper)parameters. It is recommended to first create this using the function `prior_default`, and then possibly modify it.

`likelihood`	Determines the observation model. Must be either `"Gaussian"` (default), `"Poisson"`, `"NB"` (negative binomial) or `"binomial"`. To use Bernoulli likelihood, use `likelihood="binomial"` and set `N_trials` as a vector of ones.
`varInfo`	Variable type info.
`standardize`	Should the response variable be standardized?
`uncertain_effect_time`	Do we wish to model uncertainty in the disease effect time?
`equal_effect`	Is the disease effect assumed to be equally strong for all diseased individuals?
`C_hat`	The constant GP mean. By default this is NULL, and set to • `C_hat = 0`, if `likelihood` is `"Gaussian"`, because with Gaussian likelihood the response variable is by default centered to have zero mean. • `C_hat = log(mean(y))` if `likelihood` is `"Poisson"` or `"NB"`, • `C_hat = log(p/(1-p))`, where `p = mean(y/N_trials)` if `likelihood` is `"binomial"` Above, `y` denotes the response variable.
`DELTA`	the amount of added jitter to ensure positive definiteness of the kernel
`sample_F`	Determines if the function values are be sampled (must be `TRUE` if likelihood is not `"Gaussian"`).
`verbose`	Should more verbose output be printed?
`variance_mask`	Should a variance mask be used to force disease component variance to zero before disease onset?
`N_trials`	This argument (number of trials) is only needed when likelihood is binomial. Must have length one or equal to number of data points. Setting `N_trials=1` corresponds to Bernoulli observation model.
`skip_gen_quant`	If this is true, the generated quantities block of Stan is skipped.

Value

A list containing the data to be given to `rstan::sampling`, some info about preprocessing and all the information about scaling the inputs and response, and updated variable type info.

`create_test_points` *Create a matrix of test points*

Description

Create a matrix of test points

Usage

```
create_test_points(object, t_test)
```

Arguments

`object`	An object of class `lgpmodel` or `lgpfit`
`t_test`	Test time points (will be same for each individual).

Value

A data frame.

create_X *Simulate an input data frame X*

Description

Simulate an input data frame X

Usage

```
create_X(N, covariates, names, n_categs, t_data, t_jitter, t_effect_range,
  continuous_info, verbose)
```

Arguments

`N`	Number of individuals.
`covariates`	Integer vector that defines the types of covariates (other than id and age). If not given, only the id and age covariates are created. Different integers correspond to the following covariate types: • 0 = disease-related age • 1 = other continuous covariate • 2 = a categorical covariate that interacts with age • 3 = a categorical covariate that acts as a group offset • 4 = a categorical covariate that that acts as a group offset AND is restricted to have value 0 for controls and 1 for cases
`names`	Covariate names.
`n_categs`	An integer vector defining the number of categories for each categorical covariate, so that `length(n_categs)` equals to the number of 2's and 3's in the `covariates` vector.
`t_data`	Measurement times.
`t_jitter`	Standard deviation of the jitter added to the given measurement times.
`t_effect_range`	Time interval from which the disease effect times are sampled uniformly. Alternatively, This can any function that returns the (possibly randomly generated) real disease effect time for one individual.
`continuous_info`	Info for generating continuous covariates. Must be a list containing fields `lambda` and `mu`, which have length 3. The continuous covariates are generated so that `x <-sin(a*t + b) + c`, where • `t <-seq(0,2*pi,length.out = k)` • `a <-mu[1] + lambda[1]*stats::runif(1)` • `b <-mu[2] + lambda[2]*stats::runif(1)` • `c <-mu[3] + lambda[3]*stats::runif(1)`
`verbose`	verbosity mode

Value

`list(X,onsets,par_cont)`

create_X_star *Create X_star*

Description

Create X_star

Usage

```
create_X_star(X, D, t_test, SCL, X_notnan)
```

Arguments

X	covariate matrix
D	covariate type information
t_test	Test time points (will be same for each individual).
SCL	time scaling function and its inverse
X_notnan	indicates where X_diseaseAge is not NaN

Value

A data frame.

create_y *Generate noisy observations*

Description

Generate noisy observations

Usage

```
create_y(noise_type, f, snr, phi, N_trials)
```

Arguments

noise_type	Either "Gaussian", "Poisson", NB" (negative binomial) or "binomial".
f	The underlying signal.
snr	The desired signal-to-noise ratio. This argument is valid only with noise_type = "Gaussian".
phi	The dispersion parameter for negative binomial data. The variance is g + g^2/phi.
N_trials	The number of trials parameter for binomial data.

Value

A list out, where

- out$g is f mapped through an inverse link function and
- out$y is the noisy response variable.

`disease_effect` *Draw disease component from a parametric form*

Description

Draw disease component from a parametric form

Usage

```
disease_effect(X_id, X_disAge, dis_fun)
```

Arguments

`X_id`	the id covariate
`X_disAge`	the diseaseAge covariate
`dis_fun`	the disease age effect function

Value

a vector

`drawCategorical` *Indepedently draw categorical variables for each individual*

Description

Indepedently draw categorical variables for each individual

Usage

```
drawCategorical(N, k, v)
```

Arguments

`N`	number of individuals
`k`	number of timepoints
`v`	vector of numbers of different categories

Value

a matrix of size `N` x `D`, where `D <-length(v)`

`drawContinuous` *Indepedently draw continuous variables for each individual*

Description

Indepedently draw continuous variables for each individual

Usage

```
drawContinuous(N, k, D, mu, lambda)
```

Arguments

`N`	number of individuals
`k`	number of timepoints
`D`	number of variables
`mu`	a vector of length 3
`lambda`	a vector of length 3

Value

a matrix of size `N` x `D`

`drawLatentComponents` *Draw realizations of multivariate normals*

Description

Draw realizations of multivariate normals

Usage

```
drawLatentComponents(KK)
```

Arguments

`KK`	3D matrix where `KK[,,j]` is the `j`th kernel matrix

Value

a matrix `FFF`

`drawMeasurementTimes` *Draw the age covariate*

Description

Draw the age covariate

Usage

```
drawMeasurementTimes(N, t_data, t_jitter)
```

Arguments

`N`	number of individuals
`t_data`	a vector of length `k`
`t_jitter`	Standard deviation of the jitter added to the given measurement times.

Value

a vector of length `N*k`

`extract_t_effect_samples` *Extract samples of T_effect*

Description

Extract samples of T_effect

Usage

```
extract_t_effect_samples(fit)
```

Arguments

`fit`	an object of class `lgpfit`

Value

a matrix

full_model *Create a full model with all covariates included*

Description

Create a full model with all covariates included

Usage

```
full_model(data, ...)
```

Arguments

data	a data frame
...	additional parameters to lgp_model

Value

a ggplot object

full_model_formula *Get formula of a full model with all covariates included*

Description

Get formula of a full model with all covariates included

Usage

```
full_model_formula(data)
```

Arguments

data	a data frame, where the response variable is the last column

Value

a formula

`get_case_ids` *Get case ids in original data*

Description

Get case ids in original data

Usage

```
get_case_ids(fit)
```

Arguments

`fit`	an object of class `lgpfit`

Value

a character vector

`get_case_row_mappings` *Create case ID to rows and back mappings*

Description

Create mappings

- from case ID to data rows (caseID_to_rows, caseID_nrows)
- from row number to case ID (row_to_caseID)

Usage

```
get_case_row_mappings(X_notnan, X_id, only_R2C = FALSE)
```

Arguments

`X_notnan`	binary vector indicating if diseaseAge is available for that measurement
`X_id`	the id covariate in X
`only_R2C`	should this return only the rows-to-caseID mapping

Value

a list

`get_diseased_info` *Get some variables related to diseased individuals*

Description

Get some variables related to diseased individuals

Usage

```
get_diseased_info(D, X, X_notnan, uncertain_effect_time, equal_effect,
  TSCL)
```

Arguments

`D`	an integer vector of length 6
`X`	the design matrix
`X_notnan`	a binary vector of length n
`uncertain_effect_time`	Boolean value
`equal_effect`	Boolean value
`TSCL`	time scaling function and its inverse

Value

a list

`get_function_components_from_df` *Get values of function components at data points, for one MCMC sample*

Description

Get values of function components at data points, for one MCMC sample

Usage

```
get_function_components_from_df(pars, model)
```

Arguments

`pars`	A data frame representing one parameter sample, i.e one row of `as.data.frame(stanfit)`, where stanfit is an object of class `stanfit`
`model`	An object of class `lgpmodel`

Value

A matrix of size `n_data` x `n_components+2`

`get_function_components_from_df_all` *Get values of function components at data points*

Description

Get values of function components at data points

Usage

```
get_function_components_from_df_all(df, model)
```

Arguments

`df`	A `stanfit` object as data frame, obtained as `as.data.frame(stanfit)`
`model`	An object of class `lgpmodel`

Value

An array of size `n_samples` x `n_data` x `n_components+2`

`get_g_from_f` *Get signal on data scale from process f*

Description

Get signal on data scale from process f

Usage

```
get_g_from_f(f, model)
```

Arguments

`f`	A vector
`model`	an object of class `lgpmodel`

Value

A vector g

`get_model_dims` *Get some dimension variables that the Stan model needs as input*

Description

Get some dimension variables that the Stan model needs as input

Usage

```
get_model_dims(X, D)
```

Arguments

`X`	the design matrix
`D`	a vector of length 6

Value

a list

`get_obs_onset_times` *Extract observed disease onset times from diseaseAge covariate vector*

Description

Extract observed disease onset times from diseaseAge covariate vector

Usage

```
get_obs_onset_times(id, age, disAge)
```

Arguments

`id`	the id covariate, vector of length `n`
`age`	the age covariate, vector of length `n`
`disAge`	the observed disease-related age covariate, vector of length `n`

Value

vector of observed onset times

`get_onset_info` *Get disease onset info*

Description

This returns

- a vector of observed onsets
- mapping from case ID to average sampling interval before the observed disease onset

Usage

```
get_onset_info(D, X, MAPS, TSCL)
```

Arguments

`D`	an integer vector of length 6
`X`	the design matrix
`MAPS`	mappings created by `get_case_row_mappings`
`TSCL`	time scaling function and its inverse

Value

two vectors of length `N_cases`

`get_pkg_description` *Get lgpr version description*

Description

Get lgpr version description

Usage

```
get_pkg_description()
```

Value

package description

`get_predicted` *A helper function*

Description

A helper function

Usage

```
get_predicted(fit)
```

Arguments

`fit`	An (incomplete) object of class `lgpfit`.

Value

a list

`get_prior_params` *Get prior parameters*

Description

Get prior parameters

Usage

```
get_prior_params(dist, add_correct)
```

Arguments

`dist`	the distribution
`add_correct`	additional correct parameter names

Value

a hyperparameter vector of length 2

`get_prior_type` *A dictionary from distribution names to integer encoding*

Description

A dictionary from distribution names to integer encoding

Usage

```
get_prior_type(type)
```

Arguments

`type`	type of the distribution as a string

Value

an integer

`get_response` *Get the (scaled) response variable*

Description

Gets and possibly scales the response variable.

Usage

```
get_response(data, varInfo, standardize, LH)
```

Arguments

`data`	the data frame given as input to `lgp`
`varInfo`	variable type info
`standardize`	should the response be standardized to unit variance and zero mean
`LH`	likelihood as integer

Value

a list with the (scaled) response variable

`get_runtime` *Get average runtime of a chain*

Description

Get average runtime of a chain

Usage

```
get_runtime(object)
```

Arguments

`object`	An object of class `lgpfit`.

Value

Average runtimes for warmup and sampling

`get_stan_model` *Get main stan model of the package*

Description

Get main stan model of the package

Usage

```
get_stan_model()
```

Value

an object of class stanmodel

`get_transform_type` *A dictionary from transform names to integer encoding*

Description

A dictionary from transform names to integer encoding

Usage

```
get_transform_type(type)
```

Arguments

`type`	Type of the transform as a string. Allowed arguments are "none" or "square". If NULL, "none" is used.

Value

an integer (0, 1 or 2)

`hyperparam_estimate` *Get a posterior estimate of model (hyper)parameters*

Description

Get a posterior estimate of model (hyper)parameters

Usage

```
hyperparam_estimate(object, type = "mean")
```

Arguments

`object`	An (incomplete) object of class `lgpfit`.
`type`	Must be "mean", "median", or "map".

Value

a data frame

`hyperparam_samples` *Get a set of model (hyper)parameter samples*

Description

Get a set of model (hyper)parameter samples

Usage

```
hyperparam_samples(object, samples = NULL)
```

Arguments

`object`	An (incomplete) object of class `lgpfit`.
`samples`	Sample indices. If NULL, all samples are taken.

Value

a data frame

`idx_to_cont_index` *Component index to how manyth continuous covariate it is*

Description

Component index to how manyth continuous covariate it is

Usage

```
idx_to_cont_index(D, idx)
```

Arguments

`D`	integer vector of length 6
`idx`	an integer

Value

an integer

`kernel_bin` *Compute a binary kernel matrix*

Description

Compute a binary kernel matrix

Usage

```
kernel_bin(x1, x2 = NULL, alpha = 1, pos_class = 1)
```

Arguments

`x1`	(integer) vector of length n
`x2`	(integer) vector of length m
`alpha`	marginal std (default = 1)
`pos_class`	the positive class label

Value

A kernel matrix of size n x m

`kernel_ns` *Compute a nonstationary kernel matrix using input warping*

Description

Compute a nonstationary kernel matrix using input warping

Usage

```
kernel_ns(x1, x2 = NULL, alpha = 1, ell, a, b, c, nan_replace = 0)
```

Arguments

`x1`	vector of length n
`x2`	vector of length m
`alpha`	marginal std (default = 1)
`ell`	lengthscale in the warped space
`a`	steepness of the warping function rise
`b`	location of the effective time window
`c`	maximum range
`nan_replace`	the value to use for replacing NaN values

Value

A kernel matrix of size n x m

`kernel_se` *Compute a squared exponential kernel matrix*

Description

Compute a squared exponential kernel matrix

Usage

```
kernel_se(x1, x2, alpha = 1, ell = 1)
```

Arguments

`x1`	vector of length n
`x2`	vector of length m
`alpha`	marginal std (default = 1)
`ell`	lengthscale (default = 1)

Value

A kernel matrix of size n x m

kernel_zerosum *Compute a zeros-sum kernel matrix*

Description

Compute a zeros-sum kernel matrix

Usage

```
kernel_zerosum(x1, x2, M, alpha = 1)
```

Arguments

x1	(integer) vector of length n
x2	(integer) vector of length m
M	number of categories
alpha	marginal std (default = 1)

Value

A (binary) kernel matrix of size n x m

lgp *The main function of the ‘lgpr‘ package*

Description

This is a wrapper for both `lgp_model` and `lgp_fit`. It first creates an `lgpmodel` object and then fits the model, finally returning an `lgpfit` object. Note that the covariate types are automatically inferred from the given `data`. If you wish to change these, see the arguments

- `id_variable`
- `time_variable`
- `disAge_variable`
- `continuous_vars` and
- `categorical_vars`.

Usage

```
lgp(formula, data, likelihood = "Gaussian", prior = prior_default(),
  uncertain_effect_time = FALSE, equal_effect = TRUE,
  id_variable = "id", time_variable = "age", disAge_variable = NULL,
  continuous_vars = NULL, categorical_vars = NULL,
  offset_vars = NULL, C_hat = NULL, DELTA = 1e-08, sample_F = NULL,
  parallel = FALSE, skip_postproc = FALSE, threshold = 0.95,
  variance_mask = TRUE, N_trials = NULL, relevance_method = "f_mean",
  verbose = FALSE, ...)
```

Arguments

`formula`	A formula of the form `y ~ x1 + x2 + x3` defining the response variable `y` and covariates `xi`. The formula must contain exatly one tilde (~), with response variable on the left-hand side and covariates on the right-hand side. Covariates should be separated by a plus (+) sign. All variables that appear in the formula must exist as columns of `data`. Note that effects of categorical covariates are by default defined as interactions with `time_variable`. If you wish to change this, see the argument `offset_vars`. The subject identifier variable cannot currently be included in `offset_vars`. If you wish to model the effect of `id_variable` as a constant offset, you can create another covariate with the same values and use it in your `formula` and `offset_vars` instead.
`data`	A data frame containing the variables given in `formula` as columns.
`likelihood`	Determines the observation model. Must be either `"Gaussian"` (default), `"Poisson"`, `"NB"` (negative binomial) or `"binomial"`. To use Bernoulli likelihood, use `likelihood="binomial"` and set `N_trials` as a vector of ones.
`prior`	A named list, defining the prior distribution of model (hyper)parameters. It is recommended to first create this using the function `prior_default`, and then possibly modify it.
`uncertain_effect_time`	Do we wish to model uncertainty in the disease effect time?
`equal_effect`	Is the disease effect assumed to be equally strong for all diseased individuals?
`id_variable`	Name of the unique subject identifier variable (default = `"id"`).
`time_variable`	Name of the time variable (default = `"age"`).
`disAge_variable`	Name of the disease-related age variable. If NULL (default), this will be chosen to be `"diseaseAge"`, if such covariate is found in the data.
`continuous_vars`	Names of other continuous covariates. If `NULL`, the remaining covariates that have floating point values are interpreted as continuous.
`categorical_vars`	Names of categorical covariates that interact with the time variable. If `NULL` (default), the remaining covariates that have integer values are interpreted as categorical.
`offset_vars`	Names of the categorical covariates that are treated as time-independent group offsets. If `NULL` (default), no variables are interpreted as such covariates.
`C_hat`	The constant GP mean. By default this is NULL, and set to • `C_hat = 0`, if `likelihood` is `"Gaussian"`, because with Gaussian likelihood the response variable is by default centered to have zero mean. • `C_hat = log(mean(y))` if `likelihood` is `"Poisson"` or `"NB"`, • `C_hat = log(p/(1-p))`, where `p = mean(y/N_trials)` if `likelihood` is `"binomial"` Above, `y` denotes the response variable.
`DELTA`	the amount of added jitter to ensure positive definiteness of the kernel
`sample_F`	Determines if the function values are be sampled (must be `TRUE` if likelihood is not `"Gaussian"`).
`parallel`	Determines if the chain will be run in parallel (`default = FALSE`). If `TRUE`, then Stan is run by first defining `options(mc.cores = parallel::detectCores())`.

`skip_postproc`	In this mode the postprocessing after running Stan is skipped.
`threshold`	Component selection threshold for relevance sum.
`variance_mask`	Should a variance mask be used to force disease component variance to zero before disease onset?
`N_trials`	This argument (number of trials) is only needed when likelihood is binomial. Must have length one or equal to number of data points. Setting `N_trials=1` corresponds to Bernoulli observation model.
`relevance_method`	Component relevance determination method. Must be either `"f_mean"` or `"alpha"`.
`verbose`	Should more verbose output be printed?
`...`	Optional arguments passed to `rstan::sampling`, for example `iter`, `chains` or `control`. See `sampling` for the possible arguments.

Value

An object of class `lgpfit`.

`lgpfit-class` *An S4 class to represent the output of the* `lgp_fit` *function*

Description

An S4 class to represent the output of the `lgp_fit` function

Slots

`stan_fit` The `stanfit` object returned by `rstan::sampling`.

`model` The `lgpmodel` object returned by `lgp_model`.

`relevances` Inferred component relevances.

`selection` Component selection info.

`pkg_version` Package version number.

`diagnostics` A data frame with columns `c("Rhat","Bulk_ESS","Tail_ESS")`.

`lgpmodel-class` *An S4 class to represent an lgp model*

Description

An S4 class to represent an lgp model

Slots

`data` The original unmodified data frame.

`stan_dat` The data to be given as input to `rstan::sampling`.

`scalings` Preprocessing scaling functions and their inverse operations.

`info` Model info.

`lgp_component_names` *Get names of model components*

Description

Get names of model components

Usage

```
lgp_component_names(stan_dat)
```

Arguments

`stan_dat`	The data that was passed to `rstan::sampling`

Value

names of model components

`lgp_covariate_names` *Get names of model covariates*

Description

Get names of model covariates

Usage

```
lgp_covariate_names(stan_dat)
```

Arguments

`stan_dat`	The data that was passed to `rstan::sampling`

Value

names of model components

lgp_fit *Fit an lgp model*

Description

Samples the posterior of an additive Gaussian process regression model using rstan.

Usage

```
lgp_fit(model, threshold = 0.95, parallel = FALSE,
  skip_postproc = FALSE, relevance_method = "f_mean",
  verbose = FALSE, ...)
```

Arguments

model	An object of class lgpmodel.
threshold	Component selection threshold for relevance sum.
parallel	Determines if the chain will be run in parallel (default = FALSE). If TRUE, then Stan is run by first defining options(mc.cores = parallel::detectCores()).
skip_postproc	In this mode the postprocessing after running Stan is skipped.
relevance_method	Component relevance determination method. Must be either "f_mean" or "alpha".
verbose	should some output be printed?
...	Optional arguments passed to rstan::sampling, for example iter, chains or control. See sampling for the possible arguments.

Value

An object of class lgpfit.

See Also

For the possible additional arguments, see sampling. For creating the lgpmodel input, see lgp_model.

lgp_model *Create an lgp model*

Description

Creates an object of class lgpmodel

Usage

```
lgp_model(formula, data, likelihood = "Gaussian",
  prior = prior_default(), uncertain_effect_time = FALSE,
  equal_effect = TRUE, C_hat = NULL, DELTA = 1e-08,
  sample_F = NULL, id_variable = "id", time_variable = "age",
  disAge_variable = NULL, continuous_vars = NULL,
  categorical_vars = NULL, offset_vars = NULL, variance_mask = TRUE,
  N_trials = NULL, skip_gen_quant = FALSE, verbose = FALSE)
```

Arguments

`formula`	A formula of the form `y ~ x1 + x2 + x3` defining the response variable `y` and covariates `xi`. The formula must contain exatly one tilde (~), with response variable on the left-hand side and covariates on the right-hand side. Covariates should be separated by a plus (+) sign. All variables that appear in the formula must exist as columns of `data`. Note that effects of categorical covariates are by default defined as interactions with `time_variable`. If you wish to change this, see the argument `offset_vars`. The subject identifier variable cannot currently be included in `offset_vars`. If you wish to model the effect of `id_variable` as a constant offset, you can create another covariate with the same values and use it in your `formula` and `offset_vars` instead.
`data`	A data frame containing the variables given in `formula` as columns.
`likelihood`	Determines the observation model. Must be either `"Gaussian"` (default), `"Poisson"`, `"NB"` (negative binomial) or `"binomial"`. To use Bernoulli likelihood, use `likelihood="binomial"` and set `N_trials` as a vector of ones.
`prior`	A named list, defining the prior distribution of model (hyper)parameters. It is recommended to first create this using the function `prior_default`, and then possibly modify it.
`uncertain_effect_time`	Do we wish to model uncertainty in the disease effect time?
`equal_effect`	Is the disease effect assumed to be equally strong for all diseased individuals?
`C_hat`	The constant GP mean. By default this is NULL, and set to • `C_hat = 0`, if `likelihood` is `"Gaussian"`, because with Gaussian likelihood the response variable is by default centered to have zero mean. • `C_hat = log(mean(y))` if `likelihood` is `"Poisson"` or `"NB"`, • `C_hat = log(p/(1-p))`, where `p = mean(y/N_trials)` if `likelihood` is `"binomial"` Above, `y` denotes the response variable.
`DELTA`	the amount of added jitter to ensure positive definiteness of the kernel
`sample_F`	Determines if the function values are be sampled (must be `TRUE` if likelihood is not `"Gaussian"`).
`id_variable`	Name of the unique subject identifier variable (default = `"id"`).
`time_variable`	Name of the time variable (default = `"age"`).
`disAge_variable`	Name of the disease-related age variable. If NULL (default), this will be chosen to be `"diseaseAge"`, if such covariate is found in the data.
`continuous_vars`	Names of other continuous covariates. If `NULL`, the remaining covariates that have floating point values are interpreted as continuous.
`categorical_vars`	Names of categorical covariates that interact with the time variable. If `NULL` (default), the remaining covariates that have integer values are interpreted as categorical.
`offset_vars`	Names of the categorical covariates that are treated as time-independent group offsets. If `NULL` (default), no variables are interpreted as such covariates.
`variance_mask`	Should a variance mask be used to force disease component variance to zero before disease onset?

`N_trials`	This argument (number of trials) is only needed when likelihood is binomial. Must have length one or equal to number of data points. Setting `N_trials=1` corresponds to Bernoulli observation model.
`skip_gen_quant`	If this is true, the generated quantities block of Stan is skipped.
`verbose`	Should more verbose output be printed?

Value

An object of class `lgpmodel`.

See Also

For fitting the model, see `lgp_fit`.

`lgp_predict` *Compute predictions for a fitted model*

Description

Compute predictions for a fitted model. Only possible for models with Gaussian likelihood.

Usage

```
lgp_predict(fit, X_test, samples = "map", print_progress = TRUE,
  print_params = FALSE)
```

Arguments

`fit`	An object of class `lgpfit`.
`X_test`	The test points where the predictions should be computed.
`samples`	The predictions can be computed either by using only the posterior mean (`samples="mean"`), median (`samples="median"`), or MAP (`samples="map"`) parameters, or for all parameter samples (`samples="all"`). This can also be a set of indices, for example `samples=c(1:10)` gives predictions for the parameter samples 1...10.
`print_progress`	Should progress be printed (if there is more than one sample)?
`print_params`	Should the parameter values be printed? (only works if `samples` is mean or median.)

Value

A list.

See Also

- For creating an `lgpfit` object, see `lgp_fit`.
- For creating an `lgpmodel` object, see `lgp_model`.

lgp_test *Compute predictions and log-posterior predictive density at test points*

Description

This is a convenience function that wraps lgp_predict, compute_lppd and plot_posterior_y.

Usage

```
lgp_test(fit, test_data, plot = FALSE, verbose = TRUE,
  samples = "mean")
```

Arguments

fit	an object of class lgpfit
test_data	a test data matrix
plot	should this return also a plot of the data and predictions?
verbose	Should this print progress?
samples	Sample indices or a keyword "mean", "median", "map", or "all".

Value

a ggplot object or lppd

likelihood_as_int *Convert likelihood string to Stan encoding*

Description

Convert likelihood string to Stan encoding

Usage

```
likelihood_as_int(likelihood)
```

Arguments

likelihood	a string

Value

an integer

`likelihood_as_str` *Convert the Stan likelihood encoding to a string*

Description

Convert the Stan likelihood encoding to a string

Usage

```
likelihood_as_str(LH)
```

Arguments

`LH`	an integer

Value

a string

`log_gaussian_density` *Compute log-density for gaussian distribution*

Description

Compute log-density for gaussian distribution

Usage

```
log_gaussian_density(x, mu, s2)
```

Arguments

`x`	point x
`mu`	mean
`s2`	variance

Value

a number

`matrix_to_df` *Matrix to data frame without editing column names*

Description

Matrix to data frame without editing column names

Usage

```
matrix_to_df(M)
```

Arguments

`M`	a matrix

Value

a data frame

`model_info` *Get model info*

Description

Get model info

Usage

```
model_info(object, print = TRUE)
```

Arguments

`object`	an object of class `lgpmodel` or `lgpfit`
`print`	should this print the info?

Value

the info as a string

`nameComponents` *Create names for all components based on covariate names and types*

Description

Create names for all components based on covariate names and types

Usage

```
nameComponents(types, names)
```

Arguments

`types`	vector of covariate types
`names`	names of the covariates

Value

a vector of component names

`onsetsToDiseaseAge` *Compute the disease-related ages*

Description

Compute the disease-related ages

Usage

```
onsetsToDiseaseAge(onsets, age, k)
```

Arguments

`onsets`	true disease effect times, a vector of length `N`
`age`	the age covariate, a vector of length `N*k`
`k`	number of measurements per individual

Value

the diseaseAge covariate, a vector of length `N*k`

parse_prior_distribution

Turn a list describing a prior distribution into vectors to be given to Stan

Description

Turn a list describing a prior distribution into vectors to be given to Stan

Usage

```
parse_prior_distribution(dist, add_correct = NULL)
```

Arguments

`dist`	a list with field type, and possibly others
`add_correct`	additional correct parameter names

Value

a list with two vectors to be given to Stan

parse_prior_t_effect

Turn a list describing an effect time distribution into things to be given to Stan

Description

Turn a list describing an effect time distribution into things to be given to Stan

Usage

```
parse_prior_t_effect(dist, N_cases, T_observed, T_last, UNCRT)
```

Arguments

`dist`	This is `prior$effect`, where `prior` is an argument of `lgp_model`
`N_cases`	number of case individuals
`T_observed`	observed disease onsets / initiation times
`T_last`	last time point for each diseased individual
`UNCRT`	0 or 1

Value

a list with things to be given to Stan

`plot,lgpfit,ANY-method` *Visualize a fitted ‘lgpfit‘ object*

Description

Visualize a fitted ‘lgpfit‘ object

Usage

```
## S4 method for signature 'lgpfit,ANY'
plot(fit, x = 1, y = 1, color_scheme = "red")
```

Arguments

`fit`	an object of class `lgpfit`
`x`	does nothing
`y`	does nothing
`color_scheme`	bayesplot color scheme

Value

a ggplot object

`plot_beta` *Visualize posterior samples of individual-specific disease effect magnitude parameters*

Description

Can only be used if the disease effect was modeled heterogeneously.

Usage

```
plot_beta(fit, color_scheme = "red", threshold = 0.5)
```

Arguments

`fit`	An object of class `lgpfit`.
`color_scheme`	Name of bayesplot color scheme.
`threshold`	Threshold for median.

Value

a ggplot object

`plot_component` *Helper function for plotting one component*

Description

Helper function for plotting one component

Usage

```
plot_component(MMM, SSS, model, idx, time_is_xvar, linealpha, linetype,
  fill_alpha, X_test, marker, sum_highlight, viridis_option)
```

Arguments

`MMM`	a n array of size n_samples x n_data x n_components
`SSS`	a n array of size n_samples x n_data x n_components
`model`	an object of class 'lgpmodel'
`idx`	Index of component to be plotted.
`time_is_xvar`	is the time variable the x-axis variable
`linealpha`	line alpha
`linetype`	line type
`fill_alpha`	fill alpha for geom_ribbons
`X_test`	optional matrix of test points
`marker`	point type
`sum_highlight`	name of a categorical covariate to be highlighted
`viridis_option`	the option argument of `ggplot2::scale_colour_viridis_c` by colour in the sum plot

Value

a ggplot object

`plot_components` *Helper function for plotting components*

Description

Helper function for plotting components

Usage

```
plot_components(MMM, SSS, model, time_is_xvar, X_test = NULL,
  sum_highlight = NULL, linealpha = 1, linetype = 1,
  fill_alpha = 0.3, marker = NULL, ncol = NULL, nrow = NULL,
  legend = NULL, labels = NULL, ylim = NULL, font_size = 9,
  theme = ggplot2::theme_linedraw(), legend_dir = "horizontal",
  xlabel = NULL, ylabel = " ", viridis_option = "viridis",
  return_list = FALSE)
```

Arguments

`MMM`	a n array of size n_samples x n_data x n_components
`SSS`	a n array of size n_samples x n_data x n_components
`model`	an object of class 'lgpmodel'
`time_is_xvar`	is the time variable the x-axis variable
`X_test`	optional matrix of test points
`sum_highlight`	name of a categorical covariate to be highlighted
`linealpha`	line alpha
`linetype`	line type
`fill_alpha`	fill alpha for geom_ribbons
`marker`	point type
`ncol`	number of plot columns
`nrow`	number of plot rows
`legend`	legend argument for ggarrange, use "none" to remove legends
`labels`	labels argument for ggarrange
`ylim`	y axis limits
`font_size`	font size for plots
`theme`	ggplot theme
`legend_dir`	direction of legend
`xlabel`	x-axis label
`ylabel`	y-axis label
`viridis_option`	the option argument of `ggplot2::scale_colour_viridis_c` by colour in the sum plot
`return_list`	should this return a list of ggplot objects instead of doing ggarrange

Value

an object returned by ggpubr::ggarrange or list

`plot_components_posterior` *Visualize inferred components*

Description

Visualize inferred components

Usage

```
plot_components_posterior(fit, subsamples = NULL, time_is_xvar = TRUE,
  PRED = NULL, marker = NULL, sample_idx = 1, n_sd = 2, ...)
```

Arguments

`fit`	An object of class `lgpfit`.
`subsamples`	How many samples to plot. If this is NULL, average over all samples is plotted. If this is "all", all samples are plotted.
`time_is_xvar`	is the time variable the x-axis variable in all subplots?
`PRED`	object returned by `lgp_predict`
`marker`	point type
`sample_idx`	Which sample to plot.
`n_sd`	number of standard deviations (ribbon width)
`...`	additional arguments for `plot_components`

Value

an object returned by ggpubr::ggarrange or a list of ggplot2 objects

---

`plot_components_posterior_sub1`

Helper for `plot_components_posterior`

Description

Helper for `plot_components_posterior`

Usage

```
plot_components_posterior_sub1(fit, subsamples, time_is_xvar, marker, ...)
```

Arguments

`fit`	An object of class `lgpfit`.
`subsamples`	How many samples to plot. If this is NULL, average over all samples is plotted. If this is "all", all samples are plotted.
`time_is_xvar`	is the time variable the x-axis variable in all subplots?
`marker`	point type
`...`	additional arguments for `plot_components`

Value

an object returned by ggpubr::ggarrange or a list

---

plot_components_posterior_sub2

Helper for plot_components_posterior

Description

Helper for plot_components_posterior

Usage

```
plot_components_posterior_sub2(fit, PRED, sample_idx, time_is_xvar, n_sd,
  ...)
```

Arguments

fit	An object of class lgpfit.
PRED	object returned by lgp_predict
sample_idx	Which sample to plot.
time_is_xvar	is the time variable the x-axis variable in all subplots?
n_sd	number of standard deviations (ribbon width)
...	additional arguments for plot_components

Value

an object returned by ggpubr::ggarrange or a list

---

plot_components_simdata

Visualize the components of a simulated data set

Description

Visualize the components of a simulated data set

Usage

```
plot_components_simdata(simData, time_is_xvar = TRUE, marker = 16, ...)
```

Arguments

simData	simulated data object (list)
time_is_xvar	is the time variable the x-axis variable in all subplots?
marker	point marker
...	additional arguments for plot_components

Value

an object returned by ggpubr::ggarrange or list

`plot_data`	*A spaghetti plot of longitudinal data.*

Description

A spaghetti plot of longitudinal data.

Usage

```
plot_data(data, highlight = NULL, response = "y", id_variable = "id",
  time_variable = "age", psize = 2, lwd = 0.5, title = NULL)
```

Arguments

`data`	A data frame.
`highlight`	Name of a covariate to be highlighted with color, or id of a subject to be highlighted.
`response`	Name of the response variable.
`id_variable`	Name of id variable.
`time_variable`	Name of time variable.
`psize`	point size
`lwd`	line width
`title`	additional string added to title

Value

a ggplot object

`plot_data_hl_cat`	*A spaghetti plot of longitudinal data, highlighting a categorical covariate.*

Description

A spaghetti plot of longitudinal data, highlighting a categorical covariate.

Usage

```
plot_data_hl_cat(data, highlight = NULL, response = "y",
  id_variable = "id", time_variable = "age", psize = 2, lwd = 0.5)
```

Arguments

`data`	A data frame.
`highlight`	Name of a categorical covariate to be highlighted with color.
`response`	Name of the response variable.
`id_variable`	Name of id variable.
`time_variable`	Name of time variable.
`psize`	point size
`lwd`	line width

Value

a ggplot object

---

plot_data_hl_cont *A spaghetti plot of longitudinal data, highlighting a continuous covariate.*

Description

A spaghetti plot of longitudinal data, highlighting a continuous covariate.

Usage

```
plot_data_hl_cont(data, highlight = NULL, response = "y",
  id_variable = "id", time_variable = "age", psize = 2, lwd = 0.5,
  colgrad = ggplot2::scale_colour_gradient2())
```

Arguments

`data`	A data frame.
`highlight`	Name of a continuous covariate to be highlighted with color.
`response`	Name of the response variable.
`id_variable`	Name of id variable.
`time_variable`	Name of time variable.
`psize`	point size
`lwd`	line width
`colgrad`	color gradient

Value

a ggplot object

---

plot_data_hl_disease *A spaghetti plot of longitudinal data, highlighting based on disease group.*

Description

A spaghetti plot of longitudinal data, highlighting based on disease group.

Usage

```
plot_data_hl_disease(data, highlight = "diseaseAge", response = "y",
  id_variable = "id", time_variable = "age", psize = 2, lwd = 0.5)
```

Arguments

`data`	A data frame.
`highlight`	Name of the disease-related age variable.
`response`	Name of the response variable.
`id_variable`	Name of id variable.
`time_variable`	Name of time variable.
`psize`	point size
`lwd`	line width

Value

a ggplot object

`plot_data_hl_individual` *A spaghetti plot of longitudinal data, highlighting one individual.*

Description

A spaghetti plot of longitudinal data, highlighting one individual.

Usage

```
plot_data_hl_individual(data, highlight = 1, response = "y",
  id_variable = "id", time_variable = "age", psize = 2, lwd = 0.5)
```

Arguments

`data`	A data frame.
`highlight`	Number indicating the individual to highlight.
`response`	Name of the response variable.
`id_variable`	Name of id variable.
`time_variable`	Name of time variable.
`psize`	point size
`lwd`	line width

Value

a ggplot object

plot_data_plain *A spaghetti plot of longitudinal data without highlighting.*

Description

A spaghetti plot of longitudinal data without highlighting.

Usage

```
plot_data_plain(data, response = "y", id_variable = "id",
  time_variable = "age", psize = 2, lwd = 0.5)
```

Arguments

`data`	A data frame.
`response`	Name of the response variable.
`id_variable`	Name of id variable.
`time_variable`	Name of time variable.
`psize`	point size
`lwd`	line width

Value

a ggplot object

plot_effect_times *Visualize posterior uncertainty in the disease effect times*

Description

Can only be used if the uncertainty of effect time was modeled.

Usage

```
plot_effect_times(fit, color_scheme = "red", prob = 1,
  prob_outer = 1, point_est = "none")
```

Arguments

`fit`	An object of class `lgpfit`.
`color_scheme`	Name of bayesplot color scheme.
`prob`	Inner interval
`prob_outer`	Outer interval
`point_est`	Point estimate type

Value

a ggplot object

plot_inputwarp — *Visualize the input warping function for different parameter samples*

Description

Visualize the input warping function for different parameter samples

Usage

```
plot_inputwarp(fit, p = 300, color_scheme = "red", b = 0, c = 1)
```

Arguments

`fit`	An object of class `lgpfit`.
`p`	number of plot points
`color_scheme`	Name of bayesplot color scheme.
`b`	location of the effective time window (default = 0)
`c`	maximum range (default = 1)

Value

a ggplot object

plot_posterior_f — *Plot posterior of f*

Description

This is a wrapper for `plot_posterior_predictions`.

Usage

```
plot_posterior_f(fit, PRED = NULL, plot_uncertainty = TRUE,
  data_marker = 16, n_sds = 2, ...)
```

Arguments

`fit`	An object of class `lgpfit`.
`PRED`	Predictions computed using `lgp_predict`.
`plot_uncertainty`	Should an uncertainty ribbon be plotted?
`data_marker`	pch for data points
`n_sds`	number of standard deviations for the uncertainty band width
`...`	additional arguments to `plot_posterior_predictions`

Value

a ggplot object

plot_posterior_predictions

Plot posterior of f or predictive distribution for y

Description

Plot posterior of f or predictive distribution for y

Usage

```
plot_posterior_predictions(fit, mode, PRED = NULL,
  color_scheme = "red", color_scheme_t_effect = "gray", alpha = 0.5,
  alpha_line = 1, alpha2 = 0.5, plot_uncertainty = TRUE,
  title = NULL, ylim = NULL, plot_obs_onset = FALSE,
  plot_t_effect_samples = FALSE, ypos_dens = NULL, test_data = NULL,
  color_test = "deepskyblue2", pch_test = 21, size_test = 2,
  error_bar = FALSE, n_sds = 2, reference_times = NULL,
  post_t_effect_stat = "none", original_y_scale = TRUE,
  data_color = "black", data_marker = 21, ons_linetypes = c(1, 2, 3),
  ons_linecolors = c("black", "red", "gray50"))
```

Arguments

`fit`	An object of class `lgpfit`.
`mode`	Must be either "posterior" or "predictive".
`PRED`	Predictions computed using `lgp_predict`.
`color_scheme`	Name of bayesplot color scheme or a list with fieds 'dark' and 'light'.
`color_scheme_t_effect`	color scheme name for effect time density plotting
`alpha`	Ribbon fill opacity.
`alpha_line`	Line opacity.
`alpha2`	alpha of t_onset density
`plot_uncertainty`	Should an uncertainty ribbon be plotted?
`title`	optional prefix to plot title
`ylim`	y axis limits
`plot_obs_onset`	should the observed disease onset/initiation time be plotted by a vertical line
`plot_t_effect_samples`	should a distribution of sampled effect times be plotted
`ypos_dens`	y-position of the density plot
`test_data`	Test data frame
`color_test`	test point color
`pch_test`	test point marker
`size_test`	test point size
`error_bar`	should uncertainty be plotted using error bars instead of a ribbon

`n_sds`	number of standard deviations for the uncertainty band width
`reference_times`	reference onset times
`post_t_effect_stat`	statistic computed from effect time samples (mean or median)
`original_y_scale`	should the predictions be scaled back to original data scale
`data_color`	data marker color
`data_marker`	data marker type
`ons_linetypes`	onset line types
`ons_linecolors`	onset line colors

Value

a ggplot object

`plot_posterior_y` *Plot posterior predictive distribution*

Description

This is a wrapper for `plot_posterior_predictions`.

Usage

```
plot_posterior_y(fit, PRED, uncertainty = "ribbon", test_data = NULL,
  data_marker = 16, n_sds = 2, ...)
```

Arguments

`fit`	An object of class `lgpfit`.
`PRED`	Predictions computed using `lgp_predict`.
`uncertainty`	Either "none", "ribbon" or "errorbar".
`test_data`	Test data set.
`data_marker`	pch for data points
`n_sds`	number of standard deviations for the uncertainty band width
`...`	additional arguments to `plot_posterior_predictions`

Value

a ggplot object

plot_predictions_add_onsets

Add disease onset / effect times to predictions plot

Description

NOTE: currently assumes that diseased individuals come first.

Usage

```
plot_predictions_add_onsets(fit, h, plot_obs_onset, plot_t_effect_samples,
  idvar, timevar, ypos_dens, color_scheme_t_effect, reference_times,
  post_t_effect_stat, linetypes = c(1, 2, 3), linecolors = c("black",
  "red", "gray50"), alpha2 = 1)
```

Arguments

`fit`	An object of class `lgpfit`.
`h`	a ggplot object
`plot_obs_onset`	a boolean value
`plot_t_effect_samples`	a boolean value
`idvar`	id variable name
`timevar`	time variable name
`ypos_dens`	y position of the estimated onset density
`color_scheme_t_effect`	color scheme
`reference_times`	reference onset times
`post_t_effect_stat`	statistic computed from effect time samples
`linetypes`	onset line types
`linecolors`	onset line colors
`alpha2`	alpha parameter

Value

a modified ggplot object

`plot_predictions_options` *Do input checks and set options for plotting predictions*

Description

Do input checks and set options for plotting predictions

Usage

```
plot_predictions_options(fit, color_scheme, original_y_scale, PRED,
  test_data, color_scheme_t_effect, mode, n_sds)
```

Arguments

`fit`	An object of class `lgpfit`.
`color_scheme`	Name of bayesplot color scheme.
`original_y_scale`	Boolean value.
`PRED`	Predictions computed using `lgp_predict`.
`test_data`	test data
`color_scheme_t_effect`	Another color scheme.
`mode`	mode
`n_sds`	number of standard deviations for the uncertainty band width

Value

a list

`plot_relevances` *Barplot of covariate relevances*

Description

Barplot of covariate relevances

Usage

```
plot_relevances(object, violin = FALSE, color_scheme = "red", ...)
```

Arguments

`object`	an object of class `lgpfit`
`violin`	Should a violin plot be used instead of a boxplot
`color_scheme`	bayesplot color scheme name
`...`	Additional arguments to `ggplot2::geom_boxplot` or `ggplot2::geom_violin`.

Value

a ggplot object

`plot_samples` *Visualize the distribution of the model parameter samples*

Description

This is a wrapper for functions in the `bayesplot` package.

Usage

```
plot_samples(object, pars = character(), regex_pars = character(),
  type = "intervals", prob = 0.5, prob_outer = 0.9,
  color_scheme = "red", point_est = "median", binwidth = NULL,
  transformations = list(), off_diag_args = list(size = 1),
  facet_args = list())
```

Arguments

`object`	An object of class `lgpfit`.
`pars`	parameter names
`regex_pars`	regex for parameter names
`type`	Visualization type. Must be either `"dens"`, `"areas"`, `"intervals"`(default) or `"hist"`.
`prob`	inner interval
`prob_outer`	outer interval
`color_scheme`	See different color schemes in the `bayesplot` package.
`point_est`	the point estimate type
`binwidth`	width of histogram bins if `type = "hist"`
`transformations`	the parameter transformations
`off_diag_args`	Additional argument list for the pairs plot.
`facet_args`	additional facetting arguments

Value

a ggplot object

plot_simdata — *Plot a simulated longitudinal data set for each individual separately*

Description

Plot a simulated longitudinal data set for each individual separately

Usage

```
plot_simdata(simData, linecolor = "gray50", nrow = NULL, ncol = NULL,
  i_test = NULL, color_point = "black", color_test = "steelblue2",
  signal_name = "signal", y_transform = function(x) {     x })
```

Arguments

simData	a list returned by simulate_data
linecolor	line color
nrow	an argument for ggplot2::facet_wrap
ncol	an argument for ggplot2::facet_wrap
i_test	test point indices
color_point	data point color
color_test	test point color
signal_name	name of signal
y_transform	function to transform the data y

Value

a ggplot object

See Also

For plotting each component separately, see plot_components_simdata

postproc — *Finalize the lgpfit object after sampling*

Description

Finalize the lgpfit object after sampling

Usage

```
postproc(fit, threshold = 0.95, relevance_method = "f_mean",
  verbose = FALSE)
```

Arguments

`fit`	An (incomplete) object of class `lgpfit`.
`threshold`	Threshold for relevance sum. Must be a value between 0 and 1.
`relevance_method`	Component relevance determination method. Must be either `"f_mean"` or `"alpha"`.
`verbose`	Should some output be printed?

Value

An updated object of class `lgpfit`.

`postproc_relevances` *Compute component relevances and estimate amount of noise (one MCMC sample)*

Description

Compute component relevances and estimate amount of noise (one MCMC sample)

Usage

```
postproc_relevances(fit, relevance_method = "f_mean",
  noise_method = "SSE", verbose = FALSE)
```

Arguments

`fit`	An (incomplete) object of class `lgpfit`.
`relevance_method`	Component relevance determination method. Must be either `"f_mean"` or `"alpha"`.
`noise_method`	Noise level determination method. Currently must be `"SSE"`.
`verbose`	Should some output be printed?

Value

An updated object of class `lgpfit`.

`predict_preproc` *Preprocess some things before computing predictions*

Description

This is a helper function for `lgp_predict`.

Usage

```
predict_preproc(fit, X_test, samples)
```

Arguments

`fit`	An object of class `lgpfit`.
`X_test`	The test points where the predictions should be computed.
`samples`	The samples argument to `lgp_predict`

`PRED_to_arrays` *PRED object to arrays*

Description

PRED object to arrays

Usage

```
PRED_to_arrays(PRED)
```

Arguments

`PRED`	an object returned by `lgp_predict`

Value

a list containing two arrays

`print_prior` *Human-readable description of a specified prior*

Description

Print human-readable info about the prior specification that was used or will be used

Usage

```
print_prior(object)
```

Arguments

`object`	An object of class `lgpfit` or a valid prior argument for the ‘lgp‘ function.

Value

nothing

`prior_default` *Create the default prior*

Description

Create the default prior

Usage

```
prior_default(sigma_alpha = 1)
```

Arguments

`sigma_alpha`	Sigma parameter of the student-t distribution for all alpha.

Value

A list defining a valid `prior` argument for the `lgp` function.

`prior_LonGP` *Create a similar default prior as in* `LonGP` *(Cheng et. al, 2019)*

Description

Not recommended, because a lengthscale close to 0 is possible.

Usage

```
prior_LonGP()
```

Value

A list defining a valid `prior` argument for the `lgp_model` function.

`prior_stan_to_readable` *Human-readable information about the priors in the Stan data object*

Description

Human-readable information about the priors in the Stan data object

Usage

```
prior_stan_to_readable(stan_dat)
```

Arguments

`stan_dat`	The list that is passed as data to `rstan::sampling`.

Value

Info as a string.

`prior_statement` *Human-readable prior statement*

Description

Human-readable prior statement

Usage

```
prior_statement(parname, TYP, P, dist, row_change = TRUE)
```

Arguments

`parname`	parameter name
`TYP`	two integers
`P`	three real numbers
`dist`	list of distribution names
`row_change`	should a newline be last character?

Value

Sampling statement as a string.

`prior_to_stan` *Get priors as a format that can be input to Stan*

Description

Get priors as a format that can be input to Stan

Usage

```
prior_to_stan(D, prior, HMGNS, UNCRT, N_cases, T_observed, T_last)
```

Arguments

`D`	an integer vector of length 6
`prior`	The `prior` argument supplied to `lgp()`.
`HMGNS`	Is diseaseAge assumed to have a homogenous effect (1) or not (0)?
`UNCRT`	Boolean value, is uncertainty of disease onset modeled?
`N_cases`	number of case individuals
`T_observed`	observed disease onsets
`T_last`	last time point for each diseased individual

Value

a list with all things related to priors that Stan needs

`repvec` *Repeat a vector as a rows of an array*

Description

Repeat a vector as a rows of an array

Usage

```
repvec(v, n)
```

Arguments

`v`	a vector of length `m`
`n`	number of times to repeat

Value

returns an array of size `n` x `m`

rtgeom — *Sample from the 'truncated geometric' distribution*

Description

Sample from the 'truncated geometric' distribution

Usage

```
rtgeom(s, p, n = 1)
```

Arguments

`s`	an integer
`p`	a number between 0 and 1
`n`	number of samples

Value

an integer from the interval 1...n

scaleRelevances — *Scale the effect sizes*

Description

Scale the effect sizes

Usage

```
scaleRelevances(FFF, relevances, force_zeromean, i_skip)
```

Arguments

`FFF`	matrix where one column corresponds to one additive data component
`relevances`	the desired variance of each component (column)
`force_zeromean`	Should each component (excluding the disease age component) be forced to have a zero mean.
`i_skip`	induces of components for which the zero-mean forcing is skipped

Value

a new matrix `FFF`

`selection` *Selection of relevant components*

Description

Selection of relevant components

Usage

```
selection(object, threshold = 0.95)
```

Arguments

`object`	An object of class `lgpfit`.
`threshold`	Threshold for relevance sum. Must be a value between 0 and 1.

Value

A named list

`selection_fixed_threshold` *Select relevant components*

Description

Select relevant components

Usage

```
selection_fixed_threshold(rel, threshold)
```

Arguments

`rel`	a named vector of component relevances
`threshold`	value between 0 and 1

Value

indices of selected components (including "noise" always)

selection_prob — *Probabilistic selection of relevant components*

Description

Probabilistic selection of relevant components

Usage

```
selection_prob(object, p = function(x) {     stats::dbeta(x, 100, 5) },
  h = 0.01, show_progbar = FALSE)
```

Arguments

`object`	An object of class `lgpfit`.
`p`	a function defining a density over interval [0,1]
`h`	discretization parameter for computing a quadrature
`show_progbar`	Should this show a progress bar?

Value

Selection probabilities for each component

selection_prob_fixed_threshold — *Selection probabilities using a fixed threshold*

Description

Selection probabilities using a fixed threshold

Usage

```
selection_prob_fixed_threshold(relevances, threshold)
```

Arguments

`relevances`	The `relevances$samples` slot of an `lgpfit` object.
`threshold`	value between 0 and 1

Value

proportion of times each component was selected

`selection_prob_plot` *Plot of probabilistic selection of relevant components*

Description

Plot of probabilistic selection of relevant components

Usage

```
selection_prob_plot(PROB, H, P)
```

Arguments

`PROB`	computed probabilities at points H
`H`	a grid on interval [0,1]
`P`	threshold probability distribution evaluated at H

Value

a ggplot object

`set_C_hat` *Set C_hat (Non-gaussian observation models)*

Description

Set C_hat (Non-gaussian observation models)

Usage

```
set_C_hat(C_hat, response, LH, N_trials)
```

Arguments

`C_hat`	the C_hat argument given as input to `lgp`
`response`	response variable
`LH`	likelihood as int
`N_trials`	the N_trials data (binomial likelihood)

Value

a real number

`set_N_cat` *Count numbers of different categories for each categorical variable*

Description

Count numbers of different categories for each categorical variable

Usage

```
set_N_cat(X, D)
```

Arguments

`X`	the design matrix
`D`	a vector of length 6

Value

a numeric vector

`set_N_trials` *Set N_trials (binomial and Bernoulli observation models)*

Description

Set N_trials (binomial and Bernoulli observation models)

Usage

```
set_N_trials(N_trials, response, LH)
```

Arguments

`N_trials`	the N_trials argument given as input to `lgp`
`response`	response variable
`LH`	likelihood as int

Value

a numeric vector

show,lgpfit-method *Show a summary of results of the* `lgp` *function*

Description

Show a summary of results of the `lgp` function

Usage

```
## S4 method for signature 'lgpfit'
show(object)
```

Arguments

`object`	an object of class `lgpfit`

Value

nothing

show,lgpmodel-method *Show a summary of an* `lgpmodel`

Description

Show a summary of an `lgpmodel`

Usage

```
## S4 method for signature 'lgpmodel'
show(object)
```

Arguments

`object`	an object of class `lgpmodel`

Value

nothing

simdata_colnames_pretty — *Simulated data column names in a prettier form*

Description

Simulated data column names in a prettier form

Usage

```
simdata_colnames_pretty(cn)
```

Arguments

cn	column names

Value

names of model components

simulate_data — *Generate an artificial longitudinal data set*

Description

Generate an artificial longitudinal data set.

Usage

```
simulate_data(N, t_data, covariates = c(), names = NULL,
  relevances = c(1, 1, rep(1, length(covariates))), n_categs = rep(2,
  sum(covariates %in% c(2, 3))), t_jitter = 0, lengthscales = rep(12,
  2 + sum(covariates %in% c(0, 1, 2))), f_var = 1,
  noise_type = "Gaussian", snr = 3, phi = 1,
  N_affected = round(N/2), t_effect_range = "auto",
  t_observed = "after_0", C_hat = 0, dis_fun = "gp_vm",
  bin_kernel = FALSE, steepness = 0.5, vm_params = c(0.025, 1),
  continuous_info = list(mu = c(pi/8, pi, -0.5), lambda = c(pi/8, pi,
  1)), N_trials = 1, verbose = FALSE, force_zeromean = TRUE)
```

Arguments

N	Number of individuals.
t_data	Measurement times.
covariates	Integer vector that defines the types of covariates (other than id and age). If not given, only the id and age covariates are created. Different integers correspond to the following covariate types: • 0 = disease-related age • 1 = other continuous covariate

- 2 = a categorical covariate that interacts with age
- 3 = a categorical covariate that acts as a group offset
- 4 = a categorical covariate that that acts as a group offset AND is restricted to have value 0 for controls and 1 for cases

`names`	Covariate names.
`relevances`	Relative relevance of each component. Must have be a vector so that `length(relevances) = 2 + length(covariates)`. First two values define the relevance of the infividual-specific age and shared age component, respectively.
`n_categs`	An integer vector defining the number of categories for each categorical covariate, so that `length(n_categs)` equals to the number of 2's and 3's in the `covariates` vector.
`t_jitter`	Standard deviation of the jitter added to the given measurement times.
`lengthscales`	A vector so that `length(lengthscales) = 2 + sum(covariates %in% c(0,1,2))`.
`f_var`	variance of f
`noise_type`	Either "Gaussian", "Poisson", NB" (negative binomial) or "binomial".
`snr`	The desired signal-to-noise ratio. This argument is valid only with `noise_type = "Gaussian"`.
`phi`	The dispersion parameter for negative binomial data. The variance is g + g^2/phi.
`N_affected`	Number of diseased individuals that are affected by the disease. This defaults to the number of diseased individuals. This argument can only be given if `covariates` contains a zero.
`t_effect_range`	Time interval from which the disease effect times are sampled uniformly. Alternatively, This can any function that returns the (possibly randomly generated) real disease effect time for one individual.
`t_observed`	Determines how the disease effect time is observed. This can be any function that takes the real disease effect time as an argument and returns the (possibly randomly generated) observed onset/initiation time. Alternatively, this can be a string of the form `"after_n"` or `"random_p"` or `"exact"`.
`C_hat`	A constant added to f
`dis_fun`	A function or a string that defines the disease effect. If this is a function, that function is used to generate the effect. If `dis_fun` is "gp_vm" or "gp_ns", the disease component is drawn from a nonstationary GP prior (vm is the variance masked version of it).
`bin_kernel`	Should the binary kernel be used for categorical covariates? If this is `TRUE`, the effect will exist only for group 1.
`steepness`	Steepness of the input warping function. This is only used if the disease component is in the model.
`vm_params`	Parameters of the variance mask function. This is only needed if `useMaskedVarianceKernel = TRUE`.
`continuous_info`	Info for generating continuous covariates. Must be a list containing fields `lambda` and `mu`, which have length 3. The continuous covariates are generated so that `x <-sin(a*t + b) + c`, where

- `t <-seq(0,2*pi,length.out = k)`

	• a <-mu[1] + lambda[1]*stats::runif(1) • b <-mu[2] + lambda[2]*stats::runif(1) • c <-mu[3] + lambda[3]*stats::runif(1)
`N_trials`	The number of trials parameter for binomial data.
`verbose`	verbosity mode
`force_zeromean`	Should each component (excluding the disease age component) be forced to have a zero mean?

Value

A list `out`, where

- `out$data` is a data frame containing the actual data and
- `out$components` contains more points for smoother visualizations of the generating process.
- `out$onsets` contains the real disease effect times
- `out$p_signal` proportion of variance explained by signal

Examples

```
# Generate Gaussian data
dat <- simulate_data(N = 4, t_data = c(6,12,24,36,48), snr = 3)

# Generate negative binomially distributed count data
dat <- simulate_data(N = 6, t_data = seq(2, 10, by = 2), noise_type = "NB", phi = 2)
```

`simulate_kernels` *Compute all kernel matrices when simulating data*

Description

Compute all kernel matrices when simulating data

Usage

```
simulate_kernels(X, types, lengthscales, X_affected, bin_kernel,
  useMaskedVarianceKernel, steepness, vm_params)
```

Arguments

`X`	covariates
`types`	vector of covariate types, so that • 1 = ID • 2 = age • 3 = diseaseAge • 4 = other continuous covariate • 5 = a categorical covariate that interacts with age • 6 = a categorical covariate that acts as an offset
`lengthscales`	vector of lengthscales

`X_affected`	which individuals are affected by the disease
`bin_kernel`	whether or not binary (mask) kernel should be used for categorical covariates
`useMaskedVarianceKernel`	should the masked variance kernel be used for drawing the disease component
`steepness`	steepness of the input warping function
`vm_params`	parameters of the variance mask function

Value

a 3D array

`sim_check_covariates` *Input check for the covariates-related arguments of* `simulate_data`

Description

Input check for the covariates-related arguments of `simulate_data`

Usage

```
sim_check_covariates(covariates, relevances, names, n_cat)
```

Arguments

`covariates`	argument to `simulate_data`
`relevances`	argument to `simulate_data`
`names`	argument to `simulate_data`
`n_cat`	the `n_categs` argument to `simulate_data`

Value

the covariate names

`sim_data_to_observed` *Real generated disease ages to observed ones*

Description

Real generated disease ages to observed ones

Usage

```
sim_data_to_observed(dat, t_observed)
```

Arguments

`dat`	data frame
`t_observed`	Determines how the disease onset is observed. See documentation of `simulate_data`.

Value

a new data frame and observed onsets

`sim_generate_names` *Generate names for covariates*

Description

Generate names for covariates

Usage

```
sim_generate_names(covariates)
```

Arguments

`covariates`	vector of covariate types

Value

covariate names

`sim_parse_t_obs` *Parse the t_observed argument of* `simulate_data`

Description

Parse the t_observed argument of `simulate_data`

Usage

```
sim_parse_t_obs(t_observed)
```

Arguments

`t_observed`	a string

Value

a list with a name and number

split_data — *Split data into training and test data according to given row indices*

Description

Split data into training and test data according to given row indices

Usage

```
split_data(data, i_test, sort_ids = TRUE)
```

Arguments

`data`	a data frame
`i_test`	test data row indices
`sort_ids`	should the test indices be sorted into increasing order

Value

a `list(train,test)`

split_data_by_id — *Split data into training and test data according to given individuals*

Description

Split data into training and test data according to given individuals

Usage

```
split_data_by_id(data, test_ids, id_variable = "id")
```

Arguments

`data`	a data frame
`test_ids`	test data individual identifiers
`id_variable`	name of id variable

Value

a `list(train,test)`

`split_data_by_timepoint` *Split data into training and test data according to time point indices*

Description

Split data into training and test data according to time point indices

Usage

```
split_data_by_timepoint(data, test_idx, id_variable = "id",
  time_variable = "age")
```

Arguments

`data`	a data frame
`test_idx`	indices of test time points
`id_variable`	name of id variable
`time_variable`	name of time variable

Value

a `list(train,test)`

`split_data_random` *Split data into training and test data randomly*

Description

Split data into training and test data randomly

Usage

```
split_data_random(data, p_test = 0.1, n_test = NULL)
```

Arguments

`data`	a data frame
`p_test`	desired proportion of test data
`n_test`	desired number of test data points (if NULL, p_test is used to compute this)

Value

a `list(train,test)`

`split_data_random_each` *Split data into training and test data by selecting randomly k points from each individual*

Description

Split data into training and test data by selecting randomly k points from each individual

Usage

```
split_data_random_each(data, n_test = 1, id_variable = "id",
  time_variable = "age")
```

Arguments

`data`	a data frame
`n_test`	desired number of test data points per individual
`id_variable`	name of id variable
`time_variable`	name of time variable

Value

a `list(train,test)`

`standardize_inputs` *Standardize continuous input variables in X*

Description

Standardize continuous input variables in X

Usage

```
standardize_inputs(X, D)
```

Arguments

`X`	the design matrix
`D`	the covariate types, a vector of length 6

Value

updated X and info about scaling

`stan_input_X_and_D` *Predictor covariates and types to Stan input*

Description

Reorders covariates and takes only those that are needed

Usage

```
stan_input_X_and_D(data, varInfo, types, formula, verbose)
```

Arguments

`data`	a data frame containing the covariates
`varInfo`	original variable type info
`types`	types of the covariates
`formula`	model formula
`verbose`	can this print some info?

Value

X and needed types and updated varInfo

`validate_prior` *Validate prior by sampling the signal and noise from it*

Description

Validate prior by sampling the signal and noise from it

Usage

```
validate_prior(model, chains = 4, iter = 1000, parallel = FALSE)
```

Arguments

`model`	An object of class `lgpmodel`.
`chains`	how many chains are used to sample from the prior
`iter`	for how many iterations are the chains run
`parallel`	should the chains be run in parallel?

Value

An object of class `lgpfit` and random samples of both ‘f‘ and ‘y‘.

`warp_input` *Warp inputs*

Description

Warp inputs

Usage

```
warp_input(t, a, b, c)
```

Arguments

`t`	a vector
`a`	steepness of the rise
`b`	location of the effective time window
`c`	maximum range

Value

a vector of warped inputs `w(t)`

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