

# Package ‘lgpr’

October 13, 2022

**Title** Longitudinal Gaussian Process Regression

**Version** 1.1.5

**Description** Interpretable nonparametric modeling of longitudinal data using additive Gaussian process regression. Contains functionality for inferring covariate effects and assessing covariate relevances. Models are specified using a convenient formula syntax, and can include shared, group-specific, non-stationary, heterogeneous and temporally uncertain effects. Bayesian inference for model parameters is performed using 'Stan'. The modeling approach and methods are described in detail in Timonen et al. (2021) <[doi:10.1093/bioinformatics/btab021](https://doi.org/10.1093/bioinformatics/btab021)>.

**License** GPL (>= 3)

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**LazyData** true

**Biarch** true

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**Suggests** knitr, rmarkdown, testthat, covr

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**BugReports** <https://github.com/jtimonen/lgpr/issues>

**VignetteBuilder** knitr

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lgpr-package

*The 'lgpr' package.*


---

## Description

Interpretable nonparametric modeling of longitudinal data using additive Gaussian process regression. Contains functionality for inferring covariate effects and assessing covariate relevances. Models are specified using a convenient formula syntax, and can include shared, group-specific, non-stationary, heterogeneous and temporally uncertain effects. Bayesian inference for model parameters is performed using 'Stan' ([rstan](#)). The modeling approach and methods are described in detail in [Timonen et al. \(2021\)](#).

## Core functions

Main functionality of the package consists of creating and fitting an additive GP model:

- `lgp`: Specify and fit an additive GP model with one command.
- `create_model`: Define an `lgpmodel` object.

- `sample_model`: Fit a model by sampling the posterior distribution of its parameters and create an `lgpfit` object.
- `pred`: Computing model predictions and inferred covariate effects after fitting a model.
- `relevances`: Assessing covariate relevances after fitting a model.
- `prior_pred`: Prior predictive sampling to check if your prior makes sense.

### Visualization

- `plot_pred`: Plot model predictions.
- `plot_components`: Visualize inferred model components.
- `plot_draws`: Visualize parameter draws.
- `plot_data`: Visualize longitudinal data.

### Data

The data that you wish to analyze with 'lgpr' should be in an R `data.frame` where columns correspond to measured variables and rows correspond to observations. Some functions that can help working with such data frames are:

- `new_x`: Creating new test points where the posterior distribution of any function component or sum of all components, or the posterior predictive distribution can be computed after model fitting.
- Other functions: `add_factor`, `add_factor_crossing`, `add_dis_age`, `adjusted_c_hat`.

### Vignettes and tutorials

See <https://jtimonen.github.io/lgpr-usage/index.html>. The tutorials focus on code and use cases, whereas the [Mathematical description of lgpr models](#) vignette describes the statistical models and how they can be customized in 'lgpr'.

### Citation

Run `citation("lgpr")` to get citation information.

### Feedback

Bug reports, PRs, enhancement ideas or user experiences in general are welcome and appreciated. Create an issue in Github or email the author.

### Author(s)

Juho Timonen (first.last at iki.fi)

### References

1. Timonen, J. et al. (2021). *lgpr: an interpretable non-parametric method for inferring covariate effects from longitudinal data*. *Bioinformatics*, [url](#).
2. Carpenter, B. et al. (2017). *Stan: A probabilistic programming language*. *Journal of Statistical Software* 76(1).

---

add_dis_age	<i>Easily add the disease-related age variable to a data frame</i>
-------------	--

---

**Description**

Creates the disease-related age covariate vector based on the disease initiation times and adds it to the data frame

**Usage**

```
add_dis_age(data, t_init, id_var = "id", time_var = "age")
```

**Arguments**

data	the original data frame
t_init	A named vector containing the observed initiation or onset time for each individual. The names, i.e. <code>names(t_init)</code> , should specify the individual id.
id_var	name of the id variable in data
time_var	name of the time variable in data

**Value**

A data frame with one column added. The new column will be called `dis_age`. For controls, its value will be `NaN`.

**See Also**

Other data frame handling functions: [add\\_factor\\_crossing\(\)](#), [add\\_factor\(\)](#), [adjusted\\_c\\_hat\(\)](#), [new\\_x\(\)](#), [split\(\)](#)

---

add_factor	<i>Easily add a categorical covariate to a data frame</i>
------------	---

---

**Description**

Easily add a categorical covariate to a data frame

**Usage**

```
add_factor(data, x, id_var = "id")
```

**Arguments**

data	the original data frame
x	A named vector containing the category for each individual. The names should specify the individual id.
id_var	name of the id variable in data

**Value**

A data frame with one column added. The new column will have same name as the variable passed as input x.

**See Also**

Other data frame handling functions: [add\\_dis\\_age\(\)](#), [add\\_factor\\_crossing\(\)](#), [adjusted\\_c\\_hat\(\)](#), [new\\_x\(\)](#), [split\(\)](#)

---

add\_factor\_crossing    *Add a crossing of two factors to a data frame*

---

**Description**

Add a crossing of two factors to a data frame

**Usage**

```
add_factor_crossing(data, fac1, fac2, new_name)
```

**Arguments**

data	a data frame
fac1	name of first factor, must be found in df
fac2	name of second factor, must be found in df
new_name	name of the new factor

**Value**

a data frame

**See Also**

Other data frame handling functions: [add\\_dis\\_age\(\)](#), [add\\_factor\(\)](#), [adjusted\\_c\\_hat\(\)](#), [new\\_x\(\)](#), [split\(\)](#)

---

adjusted_c_hat	<i>Set the GP mean vector, taking TMM or other normalization into account</i>
----------------	---

---

### Description

Creates the `c_hat` input for `lgp`, so that it accounts for normalization between data points in the "poisson" or "nb" observation model

### Usage

```
adjusted_c_hat(y, norm_factors)
```

### Arguments

<code>y</code>	response variable, vector of length <code>n</code>
<code>norm_factors</code>	normalization factors, vector of length <code>n</code>

### Value

a vector of length `n`, which can be used as the `c_hat` input to the `lgp` function

### See Also

Other data frame handling functions: [add\\_dis\\_age\(\)](#), [add\\_factor\\_crossing\(\)](#), [add\\_factor\(\)](#), [new\\_x\(\)](#), [split\(\)](#)

---

apply_scaling	<i>Apply variable scaling</i>
---------------	-------------------------------

---

### Description

Apply variable scaling

### Usage

```
apply_scaling(scaling, x, inverse = FALSE)
```

### Arguments

<code>scaling</code>	an object of class <a href="#">lgpscaling</a>
<code>x</code>	object to which apply the scaling (numeric)
<code>inverse</code>	whether scaling should be done in inverse direction

**Value**

a similar object as x

**See Also**

Other variable scaling functions: [create\\_scaling\(\)](#)

---

as_character	<i>Character representations of different formula objects</i>
--------------	---

---

**Description**

Character representations of different formula objects

**Usage**

```
## S4 method for signature 'lgpexpr'  
as.character(x)  
  
## S4 method for signature 'lgpterm'  
as.character(x)  
  
## S4 method for signature 'lgpformula'  
as.character(x)
```

**Arguments**

x                    an object of some S4 class

**Value**

a character representation of the object

---

create_model	<i>Create a model</i>
--------------	-----------------------

---

**Description**

See the [Mathematical description of lgpr models](#) vignette for more information about the connection between different options and the created statistical model.



**Usage**

```

create_model(
  formula,
  data,
  likelihood = "gaussian",
  prior = NULL,
  c_hat = NULL,
  num_trials = NULL,
  options = NULL,
  prior_only = FALSE,
  verbose = FALSE,
  sample_f = !(likelihood == "gaussian")
)

```

**Arguments**

formula	<p>The model formula, where</p> <ul style="list-style-type: none"> <li>• it must contain exactly one tilde (~), with response variable on the left-hand side and model terms on the right-hand side</li> <li>• terms are separated by a plus (+) sign</li> <li>• all variables appearing in formula must be found in data</li> </ul> <p>See the "Model formula syntax" section below (<a href="#">lgp</a>) for instructions on how to specify the model terms.</p>
data	<p>A data.frame where each column corresponds to one variable, and each row is one observation. Continuous covariates and the response variable must have type "numeric" and categorical covariates must have type "factor". Missing values should be indicated with NaN or NA. The response variable cannot contain missing values. Column names should not contain trailing or leading underscores.</p>
likelihood	<p>Determines the observation model. Must be either "gaussian" (default), "poisson", "nb" (negative binomial), "binomial" or "bb" (beta binomial).</p>
prior	<p>A named list, defining the prior distribution of model (hyper)parameters. See the "Defining priors" section below (<a href="#">lgp</a>).</p>
c_hat	<p>The GP mean. This should only be given if sample_f is TRUE, otherwise the GP will always have zero mean. If sample_f is TRUE, the given c_hat can be a vector of length dim(data)[1], or a real number defining a constant GP mean. If not specified and sample_f is TRUE, c_hat is set to</p> <ul style="list-style-type: none"> <li>• c_hat = mean(y), if likelihood is "gaussian",</li> <li>• c_hat = log(mean(y)) if likelihood is "poisson" or "nb",</li> <li>• c_hat = log(p/(1-p)), where p = mean(y/num_trials) if likelihood is "binomial" or "bb",</li> </ul> <p>where y denotes the response variable measurements.</p>
num_trials	<p>This argument (number of trials) is only needed when likelihood is "binomial" or "bb". Must have length one or equal to the number of data points. Setting num_trials=1 and likelihood="binomial" corresponds to Bernoulli observation model.</p>

options	<p>A named list with the following possible fields:</p> <ul style="list-style-type: none"> <li>• <code>delta</code> Amount of added jitter to ensure positive definite covariance matrices.</li> <li>• <code>vm_params</code> Variance mask function parameters (numeric vector of length 2).</li> </ul> <p>If <code>options</code> is <code>NULL</code>, default options are used. The defaults are equivalent to <code>options = list(delta = 1e-8, vm_params = c(0.025, 1))</code>.</p>
prior_only	Should likelihood be ignored? See also <a href="#">sample_param_prior</a> which can be used for any <a href="#">lgpmodel</a> , and whose runtime is independent of the number of observations.
verbose	Should some informative messages be printed?
sample_f	Determines if the latent function values are sampled (must be <code>TRUE</code> if likelihood is not "gaussian"). If this is <code>TRUE</code> , the response variable will be normalized to have zero mean and unit variance.

**Value**

An object of class [lgpmodel](#), containing the Stan input created based on parsing the specified formula, prior, and other options.

**See Also**

Other main functions: [draw\\_pred\(\)](#), [get\\_draws\(\)](#), [lgp\(\)](#), [pred\(\)](#), [prior\\_pred\(\)](#), [sample\\_model\(\)](#)

---

`create_model.covs_and_comps`

*Parse the covariates and model components from given data and formula*

---

**Description**

Parse the covariates and model components from given data and formula

**Usage**

```
create_model.covs_and_comps(data, model_formula, x_cont_scl, verbose)
```

**Arguments**

data	A <code>data.frame</code> where each column corresponds to one variable, and each row is one observation. Continuous covariates and the response variable must have type "numeric" and categorical covariates must have type "factor". Missing values should be indicated with <code>NaN</code> or <code>NA</code> . The response variable cannot contain missing values. Column names should not contain trailing or leading underscores.
model_formula	an object of class <a href="#">lgpformula</a>

x_cont_scl	Information on how to scale the continuous covariates. This can either be <ul style="list-style-type: none"> <li>• an existing list of objects with class <a href="#">lgpscaling</a>, or</li> <li>• NA, in which case such list is created by computing mean and standard deviation from data</li> </ul>
verbose	Should some informative messages be printed?

**Value**

parsed input to Stan and covariate scaling, and other info

**See Also**

Other internal model creation functions: [create\\_model.formula\(\)](#), [create\\_model.likelihood\(\)](#), [create\\_model.prior\(\)](#)

---

`create_model.formula` *Create a model formula*

---

**Description**

Checks if formula is in advanced format and translates if not.

**Usage**

```
create_model.formula(formula, data, verbose = FALSE)
```

**Arguments**

formula	The model formula, where <ul style="list-style-type: none"> <li>• it must contain exactly one tilde (~), with response variable on the left-hand side and model terms on the right-hand side</li> <li>• terms are separated by a plus (+) sign</li> <li>• all variables appearing in formula must be found in data</li> </ul> See the "Model formula syntax" section below ( <a href="#">lgp</a> ) for instructions on how to specify the model terms.
data	A data.frame where each column corresponds to one variable, and each row is one observation. Continuous covariates and the response variable must have type "numeric" and categorical covariates must have type "factor". Missing values should be indicated with NaN or NA. The response variable cannot contain missing values. Column names should not contain trailing or leading underscores.
verbose	Should some informative messages be printed?

**Value**

an object of class [lgpformula](#)

**See Also**

Other internal model creation functions: [create\\_model.covs\\_and\\_comps\(\)](#), [create\\_model.likelihood\(\)](#), [create\\_model.prior\(\)](#)

---

```
create_model.likelihood
```

*Parse the response variable and its likelihood model*

---

**Description**

Parse the response variable and its likelihood model

**Usage**

```
create_model.likelihood(
  data,
  likelihood,
  c_hat,
  num_trials,
  y_name,
  sample_f,
  verbose
)
```

**Arguments**

data	A data.frame where each column corresponds to one variable, and each row is one observation. Continuous covariates and the response variable must have type "numeric" and categorical covariates must have type "factor". Missing values should be indicated with NaN or NA. The response variable cannot contain missing values. Column names should not contain trailing or leading underscores.
likelihood	Determines the observation model. Must be either "gaussian" (default), "poisson", "nb" (negative binomial), "binomial" or "bb" (beta binomial).
c_hat	The GP mean. This should only be given if sample_f is TRUE, otherwise the GP will always have zero mean. If sample_f is TRUE, the given c_hat can be a vector of length dim(data)[1], or a real number defining a constant GP mean. If not specified and sample_f is TRUE, c_hat is set to <ul style="list-style-type: none"> <li>c_hat = mean(y), if likelihood is "gaussian",</li> <li>c_hat = log(mean(y)) if likelihood is "poisson" or "nb",</li> <li>c_hat = log(p/(1-p)), where p = mean(y/num_trials) if likelihood is "binomial" or "bb",</li> </ul>

where y denotes the response variable measurements.

num_trials	This argument (number of trials) is only needed when likelihood is "binomial" or "bb". Must have length one or equal to the number of data points. Setting num_trials=1 and likelihood="binomial" corresponds to Bernoulli observation model.
y_name	Name of response variable
sample_f	Determines if the latent function values are sampled (must be TRUE if likelihood is not "gaussian"). If this is TRUE, the response variable will be normalized to have zero mean and unit variance.
verbose	Should some informative messages be printed?

**Value**

a list of parsed options

**See Also**

Other internal model creation functions: [create\\_model.covs\\_and\\_comps\(\)](#), [create\\_model.formula\(\)](#), [create\\_model.prior\(\)](#)

---

create\_model.options *Parse the given modeling options*

---

**Description**

Parse the given modeling options

**Usage**

```
create_model.options(options, verbose)
```

**Arguments**

options	<p>A named list with the following possible fields:</p> <ul style="list-style-type: none"> <li>• delta Amount of added jitter to ensure positive definite covariance matrices.</li> <li>• vm_params Variance mask function parameters (numeric vector of length 2).</li> </ul> <p>If options is NULL, default options are used. The defaults are equivalent to <code>options = list(delta = 1e-8, vm_params = c(0.025, 1))</code>.</p>
verbose	Should some informative messages be printed?

**Value**

a named list of parsed options

---

`create_model.prior`      *Parse given prior*

---

**Description**

Parse given prior

**Usage**

```
create_model.prior(prior, stan_input, verbose)
```

**Arguments**

<code>prior</code>	A named list, defining the prior distribution of model (hyper)parameters. See the "Defining priors" section below ( <a href="#">lgp</a> ).
<code>stan_input</code>	a list of stan input fields
<code>verbose</code>	Should some informative messages be printed?

**Value**

a named list of parsed options

**See Also**

Other internal model creation functions: [create\\_model.covs\\_and\\_comps\(\)](#), [create\\_model.formula\(\)](#), [create\\_model.likelihood\(\)](#)

---

`create_plot_df`      *Helper function for plots*

---

**Description**

Helper function for plots

**Usage**

```
create_plot_df(object, x = "age", group_by = "id")
```

**Arguments**

<code>object</code>	model or fit
<code>x</code>	x-axis variable name
<code>group_by</code>	grouping variable name (use NULL for no grouping)

**Value**

a data frame

---

create_scaling	<i>Create a standardizing transform</i>
----------------	---

---

**Description**

Create a standardizing transform

**Usage**

```
create_scaling(x, name)
```

**Arguments**

x	variable measurements (might contain NA or NaN)
name	variable name

**Value**

an object of class `lgpscaling`

**See Also**

Other variable scaling functions: `apply_scaling()`

---

dinvgamma_stanlike	<i>Density and quantile functions of the inverse gamma distribution</i>
--------------------	---

---

**Description**

Using the same parametrization as Stan. More info [here](#).

**Usage**

```
dinvgamma_stanlike(x, alpha, beta, log = FALSE)
```

```
qinvgamma_stanlike(p, alpha, beta)
```

**Arguments**

x	point where to compute the density
alpha	positive real number
beta	positive real number
log	is log-scale used?
p	quantile (must be between 0 and 1)

**Value**

density/quantile value

**See Also**

Other functions related to the inverse-gamma distribution: [plot\\_invgamma\(\)](#), [priors](#)

---

draw_pred	<i>Draw pseudo-observations from posterior or prior predictive distribution</i>
-----------	---

---

**Description**

Draw pseudo-observations from predictive distribution. If `pred` contains draws from the component posterior (prior) distributions, then the output is draws from the posterior (prior) predictive distribution. If `pred` is not specified, then whether output draws are from prior or posterior predictive distribution depends on whether `fit` is created using the [lgp](#) option `prior_only=TRUE` or not.

**Usage**

```
draw_pred(fit, pred = NULL)
```

**Arguments**

<code>fit</code>	An object of class <a href="#">lgpfit</a> that has been created using the <a href="#">lgp</a> option <code>sample_f=TRUE</code> .
<code>pred</code>	An object of class <a href="#">Prediction</a> , containing draws of each model component. If <code>NULL</code> , this is obtained using <code>get_pred(fit)</code> .

**Value**

An array with shape  $S \times P$ , where  $S$  is the number of draws that `pred` contains and  $P$  is the length of each function draw. Each row  $s = 1, \dots, S$  of the output is one vector drawn from the predictive distribution, given parameter draw  $s$ .

**See Also**

Other main functions: [create\\_model\(\)](#), [get\\_draws\(\)](#), [lgp\(\)](#), [pred\(\)](#), [prior\\_pred\(\)](#), [sample\\_model\(\)](#)



---

example\_fit

*Quick way to create an example lgpfit, useful for debugging*


---

**Description**

Quick way to create an example lgpfit, useful for debugging

**Usage**

```
example_fit(
  formula = y ~ id + age + age | SEX + age | LOC,
  likelihood = "gaussian",
  chains = 1,
  iter = 30,
  num_indiv = 6,
  num_timepoints = 5,
  ...
)
```

**Arguments**

formula	model formula
likelihood	observation model
chains	number of chains to run
iter	number of iterations to run
num_indiv	number of individuals (data simulation)
num_timepoints	number of time points (data simulation)
...	additional arguments to <a href="#">lgp</a>

**Value**

An [lgpfit](#) object created by fitting the example model.

---

fit\_summary

*Print a fit summary.*


---

**Description**

Print a fit summary.

**Usage**

```
fit_summary(fit, ignore_pars = c("f_latent", "eta", "teff_raw", "lp_"))
```

**Arguments**

fit                    an object of class [lgpfit](#)  
 ignore\_pars        parameters and generated quantities to ignore from output

**Value**

object invisibly.

---

GaussianPrediction-class

*An S4 class to represent analytically computed predictive distributions  
 (conditional on hyperparameters) of an additive GP model*

---

**Description**

An S4 class to represent analytically computed predictive distributions (conditional on hyperparameters) of an additive GP model

**Usage**

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

## S4 method for signature 'GaussianPrediction'
component_names(object)

## S4 method for signature 'GaussianPrediction'
num_components(object)

## S4 method for signature 'GaussianPrediction'
num_paramsets(object)

## S4 method for signature 'GaussianPrediction'
num_evalpoints(object)
```

**Arguments**

object                [GaussianPrediction](#) object for which to apply a class method.

**Methods (by generic)**

- show: Print a summary about the object.
- component\_names: Get names of components.
- num\_components: Get number of components.
- num\_paramsets: Get number of parameter combinations (different parameter vectors) using which predictions were computed.
- num\_evalpoints: Get number of points where predictions were computed.

**Slots**

- f\_comp\_mean component means
- f\_comp\_std component standard deviations
- f\_mean signal mean (on normalized scale)
- f\_std signal standard deviation (on normalized scale)
- y\_mean predictive mean (on original data scale)
- y\_std predictive standard deviation (on original data scale)
- x a data frame of points (covariate values) where the function posteriors or predictive distributions have been evaluated

**See Also**

[Prediction](#)

---

<code>get_draws</code>	<i>Extract parameter draws from <code>lgpfit</code> or <code>stanfit</code></i>
------------------------	---

---

**Description**

Uses [extract](#) with `permuted = FALSE` and `inc_warmup = FALSE`.

**Usage**

```
get_draws(object, draws = NULL, reduce = NULL, ...)
```

**Arguments**

- `object` An object of class [lgpfit](#) or `stanfit`.
- `draws` Indices of the parameter draws. `NULL` corresponds to all post-warmup draws.
- `reduce` Function used to reduce all parameter draws into one set of parameters. Ignored if `NULL`, or if `draws` is not `NULL`.
- `...` Additional arguments to `rstan::extract()`.

**Value**

The return value is always a 2-dimensional array of shape `num_param_sets x num_params`.

**See Also**

Other main functions: [create\\_model\(\)](#), [draw\\_pred\(\)](#), [lgp\(\)](#), [pred\(\)](#), [prior\\_pred\(\)](#), [sample\\_model\(\)](#)

---

get_pred	<i>Extract model predictions and function posteriors</i>
----------	--

---

**Description**

*NOTE:* It is not recommended for users to call this. Use [pred](#) instead.

**Usage**

```
get_pred(fit, draws = NULL, reduce = NULL, verbose = TRUE)
```

**Arguments**

fit	An object of class <a href="#">lgpfit</a> .
draws	Indices of parameter draws to use, or NULL to use all draws.
reduce	Reduction for parameters draws. Can be a function that is applied to reduce all parameter draws into one parameter set, or NULL (no reduction). Has no effect if draws is specified.
verbose	Should more information and a possible progress bar be printed?

**Value**

an object of class [GaussianPrediction](#) or [Prediction](#)

---

kernel	<i>Compute a kernel matrix (covariance matrix)</i>
--------	--

---

**Description**

These have STAN\_kernel\_\* counterparts. These R versions are provided for reference and are not optimized for speed. These are used when generating simulated data, and not during model inference.

**Usage**

```
kernel_eq(x1, x2, alpha = 1, ell)
kernel_ns(x1, x2, alpha = 1, ell, a)
kernel_zerohsum(x1, x2, M)
kernel_bin(x1, x2, pos_class = 0)
kernel_cat(x1, x2)
```

```
kernel_varmask(x1, x2, a, vm_params)
```

```
kernel_beta(beta, idx1_expand, idx2_expand)
```

### Arguments

x1	vector of length $n$
x2	vector of length $m$
alpha	marginal std (default = 1)
e11	lengthscale
a	steepness of the warping function rise
M	number of categories
pos_class	binary (mask) kernel function has value one if both inputs have this value, otherwise it is zero
vm_params	vector of two mask function parameters.
beta	a parameter vector (row vector) of length $N_{\text{cases}}$
idx1_expand	integer vector of length $n$
idx2_expand	integer vector of length $m$

### Value

A matrix of size  $n \times m$ .

### Functions

- `kernel_eq`: Uses the exponentiated quadratic kernel.
- `kernel_ns`: Uses the non-stationary kernel (input warping + squared exponential).
- `kernel_zerohsum`: Uses the zero-sum kernel. Here, `x1` and `x2` must be integer vectors (integers denoting different categories). Returns a binary matrix.
- `kernel_bin`: Uses the binary (mask) kernel. Here, `x1` and `x2` must be integer vectors (integers denoting different categories). Returns a binary matrix.
- `kernel_cat`: Uses the categorical kernel. Here, `x1` and `x2` must be integer vectors (integers denoting different categories). Returns a binary matrix.
- `kernel_varmask`: Computes variance mask multiplier matrix. NaN's in `x1` and `x2` will be replaced by 0.
- `kernel_beta`: Computes the heterogeneity multiplier matrix. *NOTE*: `idx_expand` needs to be given so that `idx_expand[j]-1` tells the index of the beta parameter that should be used for the  $j$ th observation. If observation  $j$  doesn't correspond to any beta parameter, then `idx_expand[j]` should be 1.

---

KernelComputer-class *An S4 class to represent input for kernel matrix computations*

---

### Description

An S4 class to represent input for kernel matrix computations

### Usage

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

## S4 method for signature 'KernelComputer'
num_components(object)

## S4 method for signature 'KernelComputer'
num_evalpoints(object)

## S4 method for signature 'KernelComputer'
num_paramsets(object)

## S4 method for signature 'KernelComputer'
component_names(object)
```

### Arguments

object            The object for which to call a class method.

### Methods (by generic)

- show: Print a summary about the object.
- num\_components: Get number of components.
- num\_evalpoints: Get number of evaluation points.
- num\_paramsets: Get number of parameter sets.
- component\_names: Get component names.

### Slots

input    Common input (for example parameter values).

K\_input    Input for computing kernel matrices between data points (N x N). A list.

Ks\_input    Input for computing kernel matrices between data and output points (P x N). A list.

Kss\_input    Input for computing kernel matrices between output points (P x P). A list, empty if  
full\_covariance=FALSE.

comp\_names    Component names (character vector).

`full_covariance` Boolean value determining if this can compute full predictive covariance matrices (or just marginal variance at each point).

`no_separate_output_points` Boolean value determining if `Ks_input` and `Kss_input` are the same thing. Using this knowledge can reduce unnecessary computations of kernel matrices.

`STREAM` external pointer (for calling 'Stan' functions)

---

lgp

*Main function of the 'lgpr' package*


---

## Description

Creates an additive Gaussian process model using `create_model` and fits it using `sample_model`. See the [Mathematical description of lgpr models](#) vignette for more information about the connection between different options and the created statistical model.

## Usage

```
lgp(
  formula,
  data,
  likelihood = "gaussian",
  prior = NULL,
  c_hat = NULL,
  num_trials = NULL,
  options = NULL,
  prior_only = FALSE,
  verbose = FALSE,
  sample_f = !(likelihood == "gaussian"),
  quiet = FALSE,
  skip_postproc = sample_f,
  ...
)
```

## Arguments

<code>formula</code>	<p>The model formula, where</p> <ul style="list-style-type: none"> <li>it must contain exactly one tilde (~), with response variable on the left-hand side and model terms on the right-hand side</li> <li>terms are separated by a plus (+) sign</li> <li>all variables appearing in formula must be found in data</li> </ul> <p>See the "Model formula syntax" section below (<a href="#">lgp</a>) for instructions on how to specify the model terms.</p>
<code>data</code>	<p>A data.frame where each column corresponds to one variable, and each row is one observation. Continuous covariates and the response variable must have type "numeric" and categorical covariates must have type "factor". Missing</p>

values should be indicated with NaN or NA. The response variable cannot contain missing values. Column names should not contain trailing or leading underscores.

likelihood	Determines the observation model. Must be either "gaussian" (default), "poisson", "nb" (negative binomial), "binomial" or "bb" (beta binomial).
prior	A named list, defining the prior distribution of model (hyper)parameters. See the "Defining priors" section below ( <a href="#">lgp</a> ).
c_hat	<p>The GP mean. This should only be given if <code>sample_f</code> is TRUE, otherwise the GP will always have zero mean. If <code>sample_f</code> is TRUE, the given <code>c_hat</code> can be a vector of length <code>dim(data)[1]</code>, or a real number defining a constant GP mean. If not specified and <code>sample_f</code> is TRUE, <code>c_hat</code> is set to</p> <ul style="list-style-type: none"> <li>• <code>c_hat = mean(y)</code>, if likelihood is "gaussian",</li> <li>• <code>c_hat = log(mean(y))</code> if likelihood is "poisson" or "nb",</li> <li>• <code>c_hat = log(p/(1-p))</code>, where <code>p = mean(y/num_trials)</code> if likelihood is "binomial" or "bb",</li> </ul> <p>where <code>y</code> denotes the response variable measurements.</p>
num_trials	This argument (number of trials) is only needed when likelihood is "binomial" or "bb". Must have length one or equal to the number of data points. Setting <code>num_trials=1</code> and <code>likelihood="binomial"</code> corresponds to Bernoulli observation model.
options	<p>A named list with the following possible fields:</p> <ul style="list-style-type: none"> <li>• <code>delta</code> Amount of added jitter to ensure positive definite covariance matrices.</li> <li>• <code>vm_params</code> Variance mask function parameters (numeric vector of length 2).</li> </ul> <p>If <code>options</code> is NULL, default options are used. The defaults are equivalent to <code>options = list(delta = 1e-8, vm_params = c(0.025, 1))</code>.</p>
prior_only	Should likelihood be ignored? See also <a href="#">sample_param_prior</a> which can be used for any <a href="#">lgpmodel</a> , and whose runtime is independent of the number of observations.
verbose	Can messages be printed during model creation? Has no effect if <code>quiet=TRUE</code> .
sample_f	Determines if the latent function values are sampled (must be TRUE if likelihood is not "gaussian"). If this is TRUE, the response variable will be normalized to have zero mean and unit variance.
quiet	Should all output messages be suppressed? You need to set also <code>refresh=0</code> if you want to suppress also the progress update messages from <a href="#">sampling</a> .
skip_postproc	Should all postprocessing be skipped? If this is TRUE, the returned <a href="#">lgpfit</a> object will likely be much smaller (if <code>sample_f=FALSE</code> ).
...	Optional arguments passed to <a href="#">sampling</a> or <a href="#">optimizing</a> .

**Value**

Returns an object of the S4 class [lgpfit](#).



### Model formula syntax

There are two ways to define the model formula:

- Using a common [formula](#)-like syntax, like in  $y \sim \text{age} + \text{age} | \text{id} + \text{sex}$ . Terms can consist of a single variable, such as `age`, or an interaction of two variables, such as `age | id`. In single-variable terms, the variable can be either continuous (numeric) or categorical (factor), whereas in interaction terms the variable on the left-hand side of the vertical bar (`|`) has to be continuous and the one on the right-hand side has to be categorical. Formulae specified using this syntax are translated to the advanced format so that
  - single-variable terms become `gp(x)` if variable `x` is numeric and `zs(x)` if `x` is a factor
  - interaction terms `x | z` become `gp(x)*zs(z)`
- Using the advanced syntax, like in  $y \sim \text{gp}(\text{age}) + \text{gp}(\text{age}) * \text{zs}(\text{id}) + \text{het}(\text{id}) * \text{gp\_vm}(\text{disAge})$ . This creates [lgprhs](#) objects, which consist of [lgpterms](#), which consist of [lgpexprs](#). This approach must be used if creating nonstationary, heterogeneous or temporally uncertain components.

Either one of the approaches should be used and they should not be mixed.

### Defining priors

The prior argument must be a named list, like `list(alpha=student_t(4), wrp=igam(30, 10))`. See examples in tutorials. Possible allowed names are

- "alpha" = component magnitude parameters
- "ell" = component lengthscale parameters
- "wrp" = input warping steepness parameters
- "sigma" = noise magnitude (Gaussian obs. model)
- "phi" = inv. overdispersion (negative binomial obs. model)
- "gamma" = overdispersion (beta-binomial obs. model)
- "beta" = heterogeneity parameters
- "effect\_time" = uncertain effect time parameters
- "effect\_time\_info" = additional options for the above

See [priors](#) for functions that can be used to define the list elements. If a parameter of a model is not given in this list, a default prior will be used for it.

### When to not use default priors

It is not recommended to use default priors blindly. Rather, priors should be specified according to the knowledge about the problem at hand, as in any Bayesian analysis. In `lgpr` this is especially important when

- Using a non-Gaussian likelihood or otherwise setting `sample_f = TRUE`. In this case the response variable is not normalized, so the scale on which the data varies must be taken into account when defining priors of the signal magnitude parameters `alpha` and possible noise parameters (`sigma`, `phi`, `gamma`). Also it should be checked if `c_hat` is set in a sensible way.

- Using a model that contains a `gp_ns(x)` or `gp_vm(x)` expression in its formula. In this case the corresponding covariate `x` is not normalized, and the prior for the input warping steepness parameter `wrp` must be set according to the expected width of the window in which the non-stationary effect of `x` occurs. By default, the width of this window is about 36, which has been set assuming that the unit of `x` is months.

### See Also

Other main functions: [create\\_model\(\)](#), [draw\\_pred\(\)](#), [get\\_draws\(\)](#), [pred\(\)](#), [prior\\_pred\(\)](#), [sample\\_model\(\)](#)

---

<code>lgpexpr-class</code>	<i>An S4 class to represent an lgp expression</i>
----------------------------	---

---

### Description

An S4 class to represent an lgp expression

### Slots

`covariate` name of a covariate  
`fun` function name

### See Also

See [operations](#) for performing arithmetics on [lgprhs](#), [lgpterm](#) and [lgpexpr](#) objects.

---

<code>lgpfit-class</code>	<i>An S4 class to represent the output of the lgp function</i>
---------------------------	--

---

### Description

An S4 class to represent the output of the lgp function

### Usage

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

## S4 method for signature 'lgpfit'
component_names(object)

## S4 method for signature 'lgpfit'
postproc(object, verbose = TRUE)

## S4 method for signature 'lgpfit'
```

```

contains_postproc(object)

## S4 method for signature 'lgpfit'
clear_postproc(object)

## S4 method for signature 'lgpfit'
get_model(object)

## S4 method for signature 'lgpfit'
get_stanfit(object)

## S4 method for signature 'lgpfit'
is_f_sampled(object)

## S4 method for signature 'lgpfit,missing'
plot(x, y)

```

### Arguments

object	The object for which to apply a class method.
verbose	Can the method print any messages?
x	an <a href="#">lgpfit</a> object to visualize
y	unused argument

### Methods (by generic)

- `show`: Print information and summary about the fit object.
- `component_names`: Get names of model components.
- `postproc`: Apply postprocessing. Returns an updated [lgpfit](#) object (copies data).
- `contains_postproc`: Check if object contains postprocessing information.
- `clear_postproc`: Returns an updated (copies data) [lgpfit](#) object without any postprocessing information.
- `get_model`: Get the stored [lgpmodel](#) object. Various properties of the returned object can be accessed as explained in the documentation of [lgpmodel](#).
- `get_stanfit`: Get the stored [stanfit](#) object. Various properties of the returned object can be accessed or plotted as explained [here](#) or in the documentation of [stanfit](#).
- `is_f_sampled`: Determine if inference was done by sampling the latent signal  $f$  (and its components).
- `plot`: Visualize parameter draws using [plot\\_draws](#).

### Slots

<code>stan_fit</code>	An object of class <code>stanfit</code> .
<code>model</code>	An object of class <code>lgpmodel</code> .
<code>num_draws</code>	Total number of parameter draws.
<code>postproc_results</code>	A named list containing possible postprocessing results.

**See Also**

For extracting parameter draws, see [get\\_draws](#), or the `rstan` methods for `stanfit` objects.

For more detailed plotting functions, see [plot\\_draws](#), [plot\\_beta](#), [plot\\_warp](#), [plot\\_effect\\_times](#)

---

`lgpformula-class`      *An S4 class to represent an lgp formula*

---

**Description**

An S4 class to represent an lgp formula

**Slots**

`terms` an object of class [lgprhs](#)

`y_name` name of the response variable

`call` original formula call

**See Also**

See [operations](#) for performing arithmetics on [lgprhs](#), [lgpterm](#) and [lgpexpr](#) objects.

---

`lgpmodel-class`      *An S4 class to represent an additive GP model*

---

**Description**

An S4 class to represent an additive GP model

**Usage**

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

```
## S4 method for signature 'lgpmodel'
parameter_info(object, digits = 3)
```

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

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

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

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

**Arguments**

object	The object for which to apply a class method.
digits	number of digits to show for floating point numbers

**Methods (by generic)**

- show: Print information and summary about the object. Returns object invisibly.
- parameter\_info: Get a parameter summary (bounds and priors). Returns a data.frame.
- component\_info: Get a data frame with information about each model component.
- covariate\_info: Get covariate information.
- component\_names: Get names of model components.
- is\_f\_sampled: Determine if inference of the model requires sampling the latent signal  $f$  (and its components).

**Slots**

formula	An object of class <a href="#">lgpformula</a>
data	The original unmodified data.
stan_input	The data to be given as input to <code>rstan::sampling</code>
var_names	List of variable names grouped by type.
var_scalings	A named list with fields <ul style="list-style-type: none"> <li>• <code>y</code> - Response variable normalization function and its inverse operation. Must be an <a href="#">lgp-scaling</a> object.</li> <li>• <code>x_cont</code> - Continuous covariate normalization functions and their inverse operations. Must be a named list with each element is an <a href="#">lgpscaling</a> object.</li> </ul>
var_info	A named list with fields <ul style="list-style-type: none"> <li>• <code>x_cat_levels</code> - Names of the levels of categorical covariates before converting from factor to numeric.</li> </ul>
info	Other info in text format.
sample_f	Whether the signal $f$ is sampled or marginalized.
full_prior	Complete prior information.

---

lgprhs-class

*An S4 class to represent the right-hand side of an lgp formula*


---

**Description**

An S4 class to represent the right-hand side of an lgp formula

**Slots**

summands a list of one or more [lgpterms](#)

**See Also**

See [operations](#) for performing arithmetics on [lgprhs](#), [lgpterm](#) and [lgpexpr](#) objects.

---

lgpscaling-class	<i>An S4 class to represent variable scaling</i>
------------------	--

---

**Description**

An S4 class to represent variable scaling

**Slots**

loc original location (mean)  
 scale original scale (standard deviation)  
 var\_name variable name

---

lgpsim-class	<i>An S4 class to represent a data set simulated using the additive GP formalism</i>
--------------	--

---

**Description**

An S4 class to represent a data set simulated using the additive GP formalism

**Usage**

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

## S4 method for signature 'lgpsim,missing'
plot(x, y, ...)
```

**Arguments**

object	an <a href="#">lgpsim</a> object
x	an <a href="#">lgpsim</a> object to plot
y	not used
...	optional arguments passed to <a href="#">plot_sim</a>

**Methods (by generic)**

- show: Show summary of object.
- plot: Plot the data and generating process. For more information see [plot\\_sim](#).

**Slots**

`data` the actual data

`response` name of the response variable in the data

`components` the drawn function components

`kernel_matrices` the covariance matrices for each gp

`info` A list with fields

- `par_ell` the used lengthscale parameters
- `par_cont` the parameters used to generate the continuous covariates
- `p_signal` signal proportion

`effect_times` A list with fields

- `true` possible true effect times that generate the disease effect
- `observed` possible observed effect times

---

<code>lgp<code>term</code>-class</code>	<i>An S4 class to represent one formula term</i>
---	--

---

**Description**

An S4 class to represent one formula term

**Slots**

`factors` a list of at most two [lgp`exprs`](#)

**See Also**

See [operations](#) for performing arithmetics on [lgp`rhs`](#), [lgp`term`](#) and [lgp`expr`](#) objects.

---

<code>model<code>_summary</code></code>	<i>Print a model summary.</i>
---	-------------------------------

---

**Description**

Print a model summary.

**Usage**

```
model_summary(object, digits = 3)
```

```
param_summary(object, digits = 3)
```

**Arguments**

object	a model or fit
digits	number of digits to round floats to

**Value**

object invisibly.

---

new_x	<i>Create prediction points</i>
-------	---------------------------------

---

**Description**

Replaces a continuous variable `x` in the data frame, and possibly another continuous variable `x_ns` derived from it, with new values, for each level of a grouping factor (usually `id`)

**Usage**

```
new_x(data, x_values, group_by = "id", x = "age", x_ns = NULL)
```

**Arguments**

<code>data</code>	A data frame. Can also be an <a href="#">lgpfit</a> or <a href="#">lgpmodel</a> object, in which case data is extracted from it.
<code>x_values</code>	the values of <code>x</code> to set for each individual
<code>group_by</code>	name of the grouping variable, must be a factor in <code>data</code> (or use <code>group_by=NA</code> to create a dummy grouping factor which has only one value)
<code>x</code>	of the variable along which to extend, must be a numeric in <code>data</code>
<code>x_ns</code>	of a nonstationary variable derived from <code>x</code> , must be a numeric in <code>data</code>

**Value**

a data frame containing the following columns

- all factors in the original data
- `x`
- `x_ns` (unless it is `NULL`)

**See Also**

Other data frame handling functions: [add\\_dis\\_age\(\)](#), [add\\_factor\\_crossing\(\)](#), [add\\_factor\(\)](#), [adjusted\\_c\\_hat\(\)](#), [split\(\)](#)



---

operations

*Operations on formula terms and expressions*

---

### Description

Operations on formula terms and expressions

### Usage

```
## S4 method for signature 'lgprhs,lgprhs'  
e1 + e2
```

```
## S4 method for signature 'lgpterm,lgpterm'  
e1 + e2
```

```
## S4 method for signature 'lgprhs,lgpterm'  
e1 + e2
```

```
## S4 method for signature 'lgpterm,lgpterm'  
e1 * e2
```

### Arguments

e1	The first sum, term or expression
e2	The second sum, term or expression

### Value

The behaviour and return type depend on the types of e1 and e2. You can

- sum (+) two [lgprhs](#)'s to yield an [lgprhs](#)
- sum (+) two [lgpterm](#)'s to yield an [lgprhs](#)
- sum (+) an [lgprhs](#) and an [lgpterm](#) to yield an [lgprhs](#)
- multiply (\*) two [lgpterm](#)'s to yield an [lgpterm](#)

---

plot\_api\_c

*Plot a generated/fit model component*

---

## Description

Data frames specified in arguments `df`, and `df_err` must have a format where

- The first column is the grouping factor (usually `id`).
- The second column is the x-axis variable (usually `age`).
- The third column is the coloring factor. If name of the third column is `NA`, coloring is not done.
- A column named `y` must contain the y-axis variable (not for `df_err`).
- A column named `lower` (`upper`) must contain the lower (`upper`) bound of error bar (only for `df_err`).
- The posterior draw using which the fit has been computed can be specified with a factor named `_draw_` (only for `df`).

## Usage

```
plot_api_c(  
  df,  
  df_err = NULL,  
  alpha = 1,  
  alpha_err = 0.2,  
  no_err = FALSE,  
  no_line = FALSE  
)
```

## Arguments

<code>df</code>	a data frame
<code>df_err</code>	a data frame
<code>alpha</code>	line opacity
<code>alpha_err</code>	ribbon opacity
<code>no_err</code>	hide error bar even when it would normally be plotted?
<code>no_line</code>	hide line even when it would normally be plotted?

## Value

A `ggplot` object.

## See Also

Other internal plot API functions: [plot\\_api\\_g\(\)](#)

---

plot_api_g	<i>Plot longitudinal data and/or model fit so that each subject/group has their own panel</i>
------------	---

---

### Description

Data frames specified in arguments `df_data`, `df_signal`, `df_fit`, and `df_fit_err` must have a format where

- the first column is the grouping factor (usually id)
- the second column is the x-axis variable (usually age)
- a column named `y` must contain the y-axis variable (not for `df_fit_err`)
- a column named `lower` (`upper`) must contain the lower (`upper`) bound of error bar (only for `df_fit_err`)
- a column named `draw` must be a factor that specifies the posterior draw using which the fit has been computed (only for `df_fit`)

### Usage

```
plot_api_g(
  df_data,
  df_signal = NULL,
  df = NULL,
  df_err = NULL,
  teff_signal = NULL,
  teff_obs = NULL,
  i_test = NULL,
  color_signal = color_palette(2)[1],
  color = color_palette(2)[2],
  color_err = colorset("red", "light_highlight"),
  color_vlines = colorset("gray", "mid_highlight"),
  alpha = 1,
  alpha_err = 0.5,
  nrow = NULL,
  ncol = NULL,
  y_transform = function(x) x
)
```

### Arguments

<code>df_data</code>	A data frame containing the observations.
<code>df_signal</code>	A data frame containing the true signal. Omitted if <code>NULL</code> .
<code>df</code>	A data frame containing the model fit, or a list of data frames. The list version can be used for example so that each list element corresponds to the fit computed using one parameter draw. Omitted if <code>NULL</code> .

df_err	A data frame containing error bars. Omitted if NULL. Must be NULL if df_fit is a list.
teff_signal	A named vector containing true effect times used to generate the signal. Omitted if NULL.
teff_obs	A named vector containing observed effect times. Omitted if NULL.
i_test	Indices of test points.
color_signal	Line color for true signal.
color	Line color for model fit.
color_err	Color of the error ribbon.
color_vlines	Two line colors for vertical lines (true and obs. effect time).
alpha	Line opacity for model fit.
alpha_err	Opacity of the error ribbon.
nrow	number of rows, an argument for <a href="#">facet_wrap</a>
ncol	number of columns, an argument for <a href="#">facet_wrap</a>
y_transform	A function to be applied to the third column of df_data.

**Value**

A [ggplot](#) object.

**See Also**

Other internal plot API functions: [plot\\_api\\_c\(\)](#)

---

plot_components	<i>Visualize all model components</i>
-----------------	---------------------------------------

---

**Description**

This calls [plot\\_f](#) for all model components.

**Usage**

```
plot_components(
  fit,
  pred = NULL,
  group_by = "id",
  t_name = "age",
  MULT_STD = 2,
  verbose = TRUE,
  draws = NULL,
  reduce = function(x) base::mean(x),
  color_by = NA,
  no_err = FALSE,
```

```

    ylim = NULL,
    draw = TRUE,
    nrow = NULL,
    ncol = NULL,
    gg_add = NULL,
    x = NULL,
    ...
)

```

### Arguments

fit	An object of class <a href="#">lgpfit</a> .
pred	An object of class <a href="#">GaussianPrediction</a> or <a href="#">Prediction</a> . If pred=NULL, the <code>pred</code> function is called with the given <code>reduce</code> and <code>draws</code> arguments.
group_by	name of the grouping variable (use <code>group_by=NA</code> to avoid grouping)
t_name	name of the x-axis variable
MULT_STD	a multiplier for standard deviation
verbose	Can this print any messages?
draws	Only has effect if <code>pred=NULL</code> .
reduce	Only has effect if <code>pred=NULL</code> .
color_by	Names of coloring factors. Can have length 1 or equal to the number of components. See the <code>color_by</code> argument of <a href="#">plot_f</a> .
no_err	Should the error ribbons be skipped even though they otherwise would be shown? Can have length 1 or equal to number of components + 1. See the <code>no_err</code> argument of <a href="#">plot_api_c</a> .
ylim	a vector of length 2 (upper and lower y-axis limits), or NULL
draw	if this is TRUE, the plot grid is drawn using <a href="#">arrangeGrob</a>
nrow	number of grid rows
ncol	number of grid columns
gg_add	additional ggplot object to add to each plot
x	Deprecated argument. This is now taken from the <code>pred</code> object to ensure compatibility.
...	additional arguments to <a href="#">plot_api_c</a>

### Value

a list of ggplot objects invisibly

### See Also

Other main plot functions: [plot\\_draws\(\)](#), [plot\\_pred\(\)](#)

---

`plot_data`*Vizualizing longitudinal data*

---

**Description**

Vizualizing longitudinal data

**Usage**

```
plot_data(  
  data,  
  x_name = "age",  
  y_name = "y",  
  group_by = "id",  
  facet_by = NULL,  
  color_by = NULL,  
  highlight = NULL,  
  main = NULL,  
  sub = NULL  
)
```

**Arguments**

<code>data</code>	A data frame.
<code>x_name</code>	Name of x-axis variable.
<code>y_name</code>	Name of the y-axis variable.
<code>group_by</code>	Name of grouping variable (must be a factor).
<code>facet_by</code>	Name of the faceting variable (must be a factor).
<code>color_by</code>	Name of coloring variable (must be a factor).
<code>highlight</code>	Value of category of the <code>group_by</code> variable that is highlighted. Can only be used if <code>color_by</code> is NULL.
<code>main</code>	main plot title
<code>sub</code>	plot subtitle

**Value**a `ggplot` object

---

plot_draws	<i>Visualize the distribution of parameter draws</i>
------------	--

---

### Description

Visualize the distribution of parameter draws

### Usage

```
plot_draws(
  fit,
  type = "intervals",
  regex_pars = c("alpha", "ell", "wrp", "sigma", "phi", "gamma"),
  ...
)
```

```
plot_beta(fit, type = "dens", verbose = TRUE, ...)
```

```
plot_warp(
  fit,
  num_points = 300,
  window_size = 48,
  color = colorset("red", "dark"),
  alpha = 0.5
)
```

```
plot_effect_times(fit, type = "areas", verbose = TRUE, ...)
```

### Arguments

fit	an object of class <a href="#">lgpfit</a>
type	plot type, allowed options are "intervals", "dens", "areas", and "trace"
regex_pars	regex for parameter names to plot
...	additional arguments for the bayesplot function <a href="#">mcmc_intervals</a> , <a href="#">mcmc_dens</a> , <a href="#">mcmc_areas</a> or <a href="#">mcmc_trace</a>
verbose	Can any output be printed?
num_points	number of plot points
window_size	width of time window
color	line color
alpha	line alpha

### Value

a ggplot object or list of them

**Functions**

- `plot_draws`: visualizes the distribution of any set of model parameters (defaults to kernel hyperparameters and possible observation model parameters)
- `plot_beta`: visualizes the distribution of the individual-specific disease effect magnitude parameter draws
- `plot_warp`: visualizes the input warping function for different draws of the warping steepness parameter
- `plot_effect_times`: visualizes the input warping function for different parameter draws

**See Also**

Other main plot functions: [plot\\_components\(\)](#), [plot\\_pred\(\)](#)

---

<code>plot_inputwarp</code>	<i>Visualize input warping function with several steepness parameter values</i>
-----------------------------	---

---

**Description**

Visualize input warping function with several steepness parameter values

**Usage**

```
plot_inputwarp(wrp, x, color = colorset("red", "dark"), alpha = 0.5)
```

**Arguments**

<code>wrp</code>	a vector of values of the warping steepness parameter
<code>x</code>	a vector of input values
<code>color</code>	line color
<code>alpha</code>	line alpha

**Value**

a ggplot object



---

`plot_invgamma`*Plot the inverse gamma-distribution pdf*

---

**Description**

Plot the inverse gamma-distribution pdf

**Usage**

```
plot_invgamma(  
  alpha,  
  beta,  
  by = 0.01,  
  log = FALSE,  
  IQR = 0.95,  
  return_quantiles = FALSE,  
  linecolor = colorset("red", "dark"),  
  fillcolor = colorset("red", "mid")  
)
```

**Arguments**

<code>alpha</code>	positive real number
<code>beta</code>	positive real number
<code>by</code>	grid size
<code>log</code>	is log-scale used?
<code>IQR</code>	inter-quantile range width
<code>return_quantiles</code>	should this return a list
<code>linecolor</code>	line color
<code>fillcolor</code>	fill color

**Value**

a ggplot object

**See Also**

Other functions related to the inverse-gamma distribution: [dinvgamma\\_stanlike\(\)](#), [priors](#)

plot\_pred

*Visualizing model predictions or inferred covariate effects***Description**

- Function draws at data points can be visualized using plot\_pred. If the pred argument is NULL, it is computed using the [pred](#) function with x=NULL.
- The total signal f or any of its additive components can be plotted using plot\_f.

**Usage**

```
plot_pred(
  fit,
  pred = NULL,
  group_by = "id",
  t_name = "age",
  MULT_STD = 2,
  verbose = TRUE,
  draws = NULL,
  reduce = function(x) base::mean(x),
  x = NULL,
  ...
)
```

```
plot_f(
  fit,
  pred = NULL,
  group_by = "id",
  t_name = "age",
  MULT_STD = 2,
  verbose = TRUE,
  draws = NULL,
  reduce = function(x) base::mean(x),
  comp_idx = NULL,
  color_by = NA,
  x = NULL,
  ...
)
```

**Arguments**

fit	An object of class <a href="#">lgpfit</a> .
pred	An object of class <a href="#">GaussianPrediction</a> or <a href="#">Prediction</a> . If pred=NULL, the <a href="#">pred</a> function is called with the given reduce and draws arguments.
group_by	name of the grouping variable (use group_by=NA to avoid grouping)
t_name	name of the x-axis variable

MULT_STD	a multiplier for standard deviation
verbose	Can this print any messages?
draws	Only has effect if pred=NULL.
reduce	Only has effect if pred=NULL.
x	Deprecated argument. This is now taken from the pred object to ensure compatibility.
...	additional arguments to <a href="#">plot_api_g</a> or <a href="#">plot_api_c</a>
comp_idx	Index of component to plot. The total sum is plotted if this is NULL.
color_by	name of coloring factor

**Value**

a [ggplot](#) object

**See Also**

Other main plot functions: [plot\\_components\(\)](#), [plot\\_draws\(\)](#)

---

plot_sim	<i>Visualize an lgpsim object (simulated data)</i>
----------	--

---

**Description**

Visualize an lgpsim object (simulated data)

**Usage**

```
plot_sim(
  simdata,
  group_by = "id",
  x_name = "age",
  h_name = "h",
  y_name = "y",
  comp_idx = NULL,
  color_by = NA,
  verbose = TRUE,
  ...
)
```

**Arguments**

<code>simdata</code>	an object of class <code>lgpsim</code>
<code>group_by</code>	grouping factor
<code>x_name</code>	name of x-axis variable
<code>h_name</code>	name of the signal in <code>simdata\$components</code> ("h" or "f")
<code>y_name</code>	name of response variable
<code>comp_idx</code>	Possible index of a component to be shown. If this is NULL, the data and total signal are shown.
<code>color_by</code>	coloring factor
<code>verbose</code>	should some information be printed?
<code>...</code>	additional arguments to <code>plot_api_g</code> or <code>plot_api_c</code>

**Value**

a `ggplot` object

---

ppc

*Graphical posterior predictive checks*

---

**Description**

Graphical posterior predictive checks

**Usage**

```
ppc(fit, data = NULL, fun = default_ppc_fun(fit), verbose = TRUE, ...)
```

**Arguments**

<code>fit</code>	An object of class <code>lgpfit</code> that can be created with <code>sample_f=TRUE</code> .
<code>data</code>	the original data frame (deprecated argument with no effect, now obtained from fit object)
<code>fun</code>	bayesplot function name
<code>verbose</code>	Can this print any messages?
<code>...</code>	additional arguments passed to the default <code>pp_check</code> method in bayesplot

**Value**

a `ggplot` object

**See Also**

Introduction to graphical posterior predictive checks: [here](#). Prior predictive check can be done by calling `prior_pred` and then `bayesplot::pp_check()`.

**Description**

- If `fit` is for a model that marginalizes the latent signal `f` (i.e. `is_f_sampled(fit)` is `FALSE`), this computes the analytic conditional posterior distributions of each model component, their sum, and the conditional predictive distribution. All these are computed for each (hyper)parameter draw (defined by `draws`), or other parameter set (obtained by a reduction defined by `reduce`). Results are stored in a [GaussianPrediction](#) object which is then returned.
- If `fit` is for a model that samples the latent signal `f` (i.e. `is_f_sampled(fit)` is `TRUE`), this will extract these function samples, compute their sum, and a version of the sum `f` that is transformed through the inverse link function. If `x` is not `NULL`, the function draws are extrapolated to the points specified by `x` using kernel regression. Results are stored in a [Prediction](#) object which is then returned.

**Usage**

```
pred(
  fit,
  x = NULL,
  reduce = function(x) base::mean(x),
  draws = NULL,
  verbose = TRUE,
  STREAM = get_stream(),
  c_hat_pred = NULL,
  force = FALSE,
  debug_kc = FALSE
)
```

**Arguments**

<code>fit</code>	An object of class <a href="#">lgpfit</a> .
<code>x</code>	A data frame of points where function posterior distributions and predictions should be computed or sampled. The function <a href="#">new_x</a> provides an easy way to create it. If this is <code>NULL</code> , the data points are used.
<code>reduce</code>	Reduction for parameters draws. Can be a function that is applied to reduce all parameter draws into one parameter set, or <code>NULL</code> (no reduction). Has no effect if <code>draws</code> is specified.
<code>draws</code>	Indices of parameter draws to use, or <code>NULL</code> to use all draws.
<code>verbose</code>	Should more information and a possible progress bar be printed?
<code>STREAM</code>	External pointer. By default obtained with <code>rstan::get_stream()</code> .
<code>c_hat_pred</code>	This is only used if the latent signal <code>f</code> was sampled. This input contains the values added to the sum <code>f</code> before passing through inverse link function. Must be a vector with length equal to the number of prediction points. If original

	c_hat was constant, then c_hat_pred can be ignored, in which case this will by default use the same constant.
force	This is by default FALSE to prevent unintended large computations that might crash R or take forever. Set it to TRUE try computing no matter what.
debug_kc	If this is TRUE, this only returns a <a href="#">KernelComputer</a> object that is created internally. Meant for debugging.

**Value**

An object of class [GaussianPrediction](#) or [Prediction](#).

**See Also**

Other main functions: [create\\_model\(\)](#), [draw\\_pred\(\)](#), [get\\_draws\(\)](#), [lgp\(\)](#), [prior\\_pred\(\)](#), [sample\\_model\(\)](#)

---

Prediction-class	<i>An S4 class to represent prior or posterior draws from an additive function distribution.</i>
------------------	--

---

**Description**

An S4 class to represent prior or posterior draws from an additive function distribution.

**Usage**

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

## S4 method for signature 'Prediction'
component_names(object)

## S4 method for signature 'Prediction'
num_components(object)

## S4 method for signature 'Prediction'
num_paramsets(object)

## S4 method for signature 'Prediction'
num_evalpoints(object)
```

**Arguments**

object      [Prediction](#) object for which to apply a class method.

**Methods (by generic)**

- show: Print a summary about the object.
- component\_names: Get names of components.
- num\_components: Get number of components.
- num\_paramsets: Get number of parameter combinations (different parameter vectors) using which predictions were computed.
- num\_evalpoints: Get number of points where predictions were computed.

**Slots**

f\_comp component draws

f signal draws

h predictions (signal draws + scaling factor  $\hat{c}$ , transformed through inverse link function)

x a data frame of points (covariate values) where the functions/predictions have been evaluated/sampled  
 extrapolated Boolean value telling if the function draws are original MCMC draws or if they have been created by extrapolating such draws.

**See Also**

[GaussianPrediction](#)

---

priors

*Prior definitions*

---

**Description**

These use the same parametrizations as defined in the 'Stan' documentation. See the docs for [gamma](#) and [inverse gamma](#) distributions.

**Usage**

uniform(square = FALSE)

normal(mu, sigma, square = FALSE)

student\_t(nu, square = FALSE)

gam(shape, inv\_scale, square = FALSE)

igam(shape, scale, square = FALSE)

log\_normal(mu, sigma, square = FALSE)

bet(a, b)

**Arguments**

square	is prior for a square-transformed parameter?
mu	mean
sigma	standard deviation
nu	degrees of freedom
shape	shape parameter (alpha)
inv_scale	inverse scale parameter (beta)
scale	scale parameter (beta)
a	shape parameter
b	shape parameter

**Value**

a named list

**See Also**

Other functions related to the inverse-gamma distribution: [dinvgamma\\_stanlike\(\)](#), [plot\\_invgamma\(\)](#)

**Examples**

```
# Log-normal prior
log_normal(mu = 1, sigma = 1)

# Cauchy prior
student_t(nu = 1)

# Exponential prior with rate = 0.1
gam(shape = 1, inv_scale = 0.1)

# Create a similar priors as in LongP (Cheng et al., 2019)
# Not recommended, because a lengthscale close to 0 is possible.
a <- log(1) - log(0.1)
log_normal(mu = 0, sigma = a / 2) # for continuous lengthscale
student_t(nu = 4) # for interaction lengthscale
igam(shape = 0.5, scale = 0.005, square = TRUE) # for sigma
```

---

prior\_pred

*Prior (predictive) sampling*

---

**Description**

These functions take an [lgpmodel](#) object, and

- `prior_pred` samples from the prior predictive distribution of the model
- `sample_param_prior` samples only its parameter prior using [sampling](#)



**Usage**

```
prior_pred(
  model,
  verbose = TRUE,
  quiet = FALSE,
  refresh = 0,
  STREAM = get_stream(),
  ...
)

sample_param_prior(model, verbose = TRUE, quiet = FALSE, ...)
```

**Arguments**

model	An object of class <a href="#">lgpmodel</a> .
verbose	Should more information and a possible progress bar be printed?
quiet	This forces verbose to be FALSE. If you want to suppress also the output from Stan, give the additional argument refresh=0.
refresh	Argument for <a href="#">sampling</a> .
STREAM	External pointer. By default obtained with <code>rstan::get_stream()</code> .
...	Additional arguments for <a href="#">sampling</a> .

**Value**

- `prior_pred` returns a list with components
  - `y_draws`: A matrix containing the prior predictive draws as rows. Can be passed to `bayesplot::pp_check()` for graphical prior predictive checking.
  - `pred_draws`: an object of class [Prediction](#), containing prior draws of each model component and their sum
  - `param_draws`: a `stanfit` object of prior parameter draws (obtained by calling `sample_param_prior` internally)
- `sample_param_prior` returns an object of class [stanfit](#)

**See Also**

Other main functions: [create\\_model\(\)](#), [draw\\_pred\(\)](#), [get\\_draws\(\)](#), [lgp\(\)](#), [pred\(\)](#), [sample\\_model\(\)](#)

---

prior_to_num	<i>Convert given prior to numeric format</i>
--------------	--

---

**Description**

Convert given prior to numeric format

**Usage**

```
prior_to_num(desc)
```

**Arguments**

desc            Prior description as a named list, containing fields

- dist - Distribution name. Must be one of 'uniform', 'normal', 'student-t', 'gamma', 'inv-gamma', 'log-normal' (case-insensitive)
- square - Is the prior for a square-transformed parameter.

Other list fields are interpreted as hyperparameters.

**Value**

a named list of parsed options

---

read\_proteomics\_data    *Function for reading the built-in proteomics data*

---

**Description**

Function for reading the built-in proteomics data

**Usage**

```
read_proteomics_data(parentDir = NULL, protein = NULL, verbose = TRUE)
```

**Arguments**

parentDir        Path to local parent directory for the data. If this is NULL, data is downloaded from <https://github.com/jtimonen/lgpr-usage/tree/master/data/proteomics>.

protein          Index or name of protein.

verbose          Can this print some output?

**Value**

a data.frame

---

relevances	<i>Assess component relevances</i>
------------	------------------------------------

---

**Description**

Assess component relevances

**Usage**

```
relevances(fit, reduce = function(x) base::mean(x), verbose = TRUE, ...)
```

**Arguments**

fit	an object of class <code>lgpfit</code>
reduce	a function to apply to reduce the relevances given each parameter draw into one value
verbose	Can this print any messages?
...	currently has no effect

**Value**

a named vector with length equal to `num_comps + 1`

---

s4_generics	<i>S4 generics for <code>lgpfit</code>, <code>lgpmodel</code>, and other objects</i>
-------------	--

---

**Description**

S4 generics for `lgpfit`, `lgpmodel`, and other objects

**Usage**

```
parameter_info(object, digits)
component_info(object)
covariate_info(object)
component_names(object)
get_model(object)
is_f_sampled(object)
get_stanfit(object)
```

```

postproc(object, ...)
contains_postproc(object)
clear_postproc(object)
num_paramsets(object)
num_evalpoints(object)
num_components(object)

```

### Arguments

<code>object</code>	object for which to apply the generic
<code>digits</code>	number of digits to show
<code>...</code>	additional optional arguments to pass

### Value

- `parameter_info` returns a data frame with one row for each parameter and columns for parameter name, parameter bounds, and the assigned prior
- `component_info` returns a data frame with one row for each model component, and columns encoding information about model components
- `covariate_info` returns a list with names `continuous` and `categorical`, with information about both continuous and categorical covariates
- `component_names` returns a character vector with component names
- `get_model` for `lgpfit` objects returns an `lgpmodel`
- `is_f_sampled` returns a logical value
- `get_stanfit` returns a `stanfit` (rstan)
- `postproc` applies postprocessing and returns an updated `lgpfit`
- `clear_postproc` removes postprocessing information and returns an updated `lgpfit`
- `num_paramsets`, `num_evalpoints` and `num_components` return an integer

### Functions

- `parameter_info`: Get parameter information (priors etc.).
- `component_info`: Get component information.
- `covariate_info`: Get covariate information.
- `component_names`: Get component names.
- `get_model`: Get `lgpmodel` object.
- `is_f_sampled`: Determine if signal `f` is sampled or marginalized.
- `get_stanfit`: Extract `stanfit` object.

- `postproc`: Perform postprocessing.
- `contains_postproc`: Determine if object contains postprocessing information.
- `clear_postproc`: Clear postprocessing information (to reduce size of object).
- `num_paramsets`: Get number of parameter sets.
- `num_evalpoints`: Get number of points where posterior is evaluated.
- `num_components`: Get number of model components.

### See Also

To find out which methods have been implemented for which classes, see [lgpfit](#), [lgpmodel](#), [Prediction](#) and [GaussianPrediction](#).

---

sample_model	<i>Fitting a model</i>
--------------	------------------------

---

### Description

- `sample_model` takes an [lgpmodel](#) object and fits it using [sampling](#).
- `optimize_model` takes an [lgpmodel](#) object and fits it using [optimizing](#).

### Usage

```
sample_model(
  model,
  verbose = TRUE,
  quiet = FALSE,
  skip_postproc = is_f_sampled(model),
  ...
)

optimize_model(model, ...)
```

### Arguments

<code>model</code>	An object of class <a href="#">lgpmodel</a> .
<code>verbose</code>	Can messages be printed?
<code>quiet</code>	Should all output messages be suppressed? You need to set also <code>refresh=0</code> if you want to suppress also the progress update messages from <a href="#">sampling</a> .
<code>skip_postproc</code>	Should all postprocessing be skipped? If this is TRUE, the returned <a href="#">lgpfit</a> object will likely be much smaller (if <code>sample_f=FALSE</code> ).
<code>...</code>	Optional arguments passed to <a href="#">sampling</a> or <a href="#">optimizing</a> .

**Value**

- `sample_model` returns an object of class `lgpfit` containing the parameter draws, the original model object, and possible postprocessing results. See documentation of `lgpfit` for more information.
- `optimize_model` directly returns the list returned by `optimizing`. See its documentation for more information.

**See Also**

Other main functions: `create_model()`, `draw_pred()`, `get_draws()`, `lgp()`, `pred()`, `prior_pred()`

---

select

*Select relevant components*

---

**Description**

- `select` performs strict selection, returning either TRUE or FALSE for each component.
- `select.integrate` is like `select`, but instead of a fixed threshold, computes probabilistic selection by integrating over a threshold density.
- `select_freq` performs the selection separately using each parameter draw and returns the frequency at which each component was selected.
- `select_freq.integrate` is like `select_freq`, but instead of a fixed threshold, computes probabilistic selection frequencies by integrating over a threshold density.

**Usage**

```
select(fit, reduce = function(x) base::mean(x), threshold = 0.95, ...)
```

```
select_freq(fit, threshold = 0.95, ...)
```

```
select.integrate(
  fit,
  reduce = function(x) base::mean(x),
  p = function(x) stats::dbeta(x, 100, 5),
  h = 0.01,
  verbose = TRUE,
  ...
)
```

```
select_freq.integrate(
  fit,
  p = function(x) stats::dbeta(x, 100, 5),
  h = 0.01,
  verbose = TRUE,
  ...
)
```

**Arguments**

fit	An object of class <code>lgpfit</code> .
reduce	The reduce argument for <a href="#">relevances</a> .
threshold	Threshold for relevance sum. Must be a value between 0 and 1.
...	Additional arguments to <a href="#">relevances</a> .
p	A threshold density over interval [0,1].
h	A discretization parameter for computing a quadrature.
verbose	Should this show a progress bar?

**Value**

See description.

---

show	<i>Printing formula object info using the show generic</i>
------	--

---

**Description**

Printing formula object info using the show generic

**Usage**

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

## S4 method for signature 'lgprhs'
show(object)

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

**Arguments**

object	an object of some S4 class
--------	----------------------------

**Value**

the object invisibly

sim.create\_f

*Simulate latent function components for longitudinal data analysis***Description**

Simulate latent function components for longitudinal data analysis

**Usage**

```
sim.create_f(
  X,
  covariates,
  relevances,
  lengthscales,
  X_affected,
  dis_fun,
  bin_kernel,
  steepness,
  vm_params,
  force_zeromean
)
```

**Arguments**

X	input data matrix (generated by <a href="#">sim.create_x</a> )
covariates	Integer vector that defines the types of covariates (other than id and age). Different integers correspond to the following covariate types: <ul style="list-style-type: none"> <li>• 0 = disease-related age</li> <li>• 1 = other continuous covariate</li> <li>• 2 = a categorical covariate that interacts with age</li> <li>• 3 = a categorical covariate that acts as a group offset</li> <li>• 4 = a categorical covariate that that acts as a group offset AND is restricted to have value 0 for controls and 1 for cases</li> </ul>
relevances	Relative relevance of each component. Must have be a vector so that $\text{length}(\text{relevances}) = 2 + \text{length}(\text{covariates})$ . First two values define the relevance of the individual-specific age and shared age component, respectively.
lengthscales	A vector so that $\text{length}(\text{lengthscales}) = 2 + \text{sum}(\text{covariates} \%in\% c(0, 1, 2))$ .
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 <code>dis_fun</code> 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 component

---

sim.create_x	<i>Create an input data frame X for simulated data</i>
--------------	--

---

**Description**

Create an input data frame X for simulated data

**Usage**

```
sim.create_x(
  N,
  covariates,
  names,
  n_categs,
  t_data,
  t_jitter,
  t_effect_range,
  continuous_info
)
```

**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: <ul style="list-style-type: none"> <li>• 0 = disease-related age</li> <li>• 1 = other continuous covariate</li> <li>• 2 = a categorical covariate that interacts with age</li> <li>• 3 = a categorical covariate that acts as a group offset</li> <li>• 4 = a categorical covariate that that acts as a group offset AND is restricted to have value 0 for controls and 1 for cases</li> </ul>

names	Covariate names.
n_categs	An integer vector defining the number of categories for each categorical covariate, so that <code>length(n_categs)</code> equals to the number of 2's and 3's in the covariates vector.
t_data	Measurement times (same for each individual, unless <code>t_jitter &gt; 0</code> in which case they are perturbed).
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 <code>lambda</code> and <code>mu</code> , which have length 3. The continuous covariates are generated so that $x \leftarrow \sin(a*t + b) + c$ , where <ul style="list-style-type: none"> <li>• <code>t &lt;- seq(0, 2*pi, length.out = k)</code></li> <li>• <code>a &lt;- mu[1] + lambda[1]*stats::runif(1)</code></li> <li>• <code>b &lt;- mu[2] + lambda[2]*stats::runif(1)</code></li> <li>• <code>c &lt;- mu[3] + lambda[3]*stats::runif(1)</code></li> </ul>

**Value**

a list

---

sim.create_y	<i>Simulate noisy observations</i>
--------------	------------------------------------

---

**Description**

Simulate noisy observations

**Usage**

```
sim.create_y(noise_type, f, snr, phi, gamma, N_trials)
```

**Arguments**

noise_type	Either "gaussian", "poisson", "nb" (negative binomial), "binomial", or "bb" (beta-binomial).
f	The underlying signal.
snr	The desired signal-to-noise ratio. This argument is valid only when <code>noise_type</code> is "gaussian".
phi	The inverse overdispersion parameter for negative binomial data. The variance is $g + g^2/\phi$ .
gamma	The dispersion parameter for beta-binomial data.
N_trials	The number of trials parameter for binomial data.

**Value**

A list out, where

- `out$h` is `f` mapped through an inverse link function (times `N_trials` if `noise_type` is binomial or beta-binomial)
- `out$y` is the noisy response variable.

---

sim.kernels

*Compute all kernel matrices when simulating data*

---

**Description**

Compute all kernel matrices when simulating data

**Usage**

```
sim.kernels(
  X,
  types,
  lengthscales,
  X_affected,
  bin_kernel,
  useMaskedVarianceKernel,
  steepness,
  vm_params
)
```

**Arguments**

<code>X</code>	covariates
<code>types</code>	vector of covariate types, so that <ul style="list-style-type: none"> <li>• 1 = ID</li> <li>• 2 = age</li> <li>• 3 = diseaseAge</li> <li>• 4 = other continuous covariate</li> <li>• 5 = a categorical covariate that interacts with age</li> <li>• 6 = a categorical covariate that acts as an offset</li> </ul>
<code>lengthscales</code>	vector of lengthscales
<code>X_affected</code>	which individuals are affected by the disease
<code>bin_kernel</code>	whether or not binary (mask) kernel should be used for categorical covariates (if not, the zerosum kernel is used)
<code>useMaskedVarianceKernel</code>	should the masked variance kernel be used for drawing the disease component
<code>steepness</code>	steepness of the input warping function
<code>vm_params</code>	parameters of the variance mask function

**Value**

a 3D array

---

simulate_data	<i>Generate an artificial longitudinal data set</i>
---------------	---

---

**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_cats = 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,
  gamma = 0.2,
  N_affected = round(N/2),
  t_effect_range = "auto",
  t_observed = "after_0",
  c_hat = 0,
  dis_fun = "gp_warp_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,
  force_zeromean = TRUE
)
```

**Arguments**

N	Number of individuals.
t_data	Measurement times (same for each individual, unless t_jitter > 0 in which case they are perturbed).
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 $\text{length}(\text{relevances}) = 2 + \text{length}(\text{covariates})$ . First two values define the relevance of the individual-specific age and shared age component, respectively.
n_categs	An integer vector defining the number of categories for each categorical covariate, so that $\text{length}(\text{n\_categs})$ 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 $\text{length}(\text{lengthscales}) = 2 + \text{sum}(\text{covariates} \%in\% c(0, 1, 2))$ .
f_var	variance of f
noise_type	Either "gaussian", "poisson", "nb" (negative binomial), "binomial", or "bb" (beta-binomial).
snr	The desired signal-to-noise ratio. This argument is valid only when noise_type is "gaussian".
phi	The inverse overdispersion parameter for negative binomial data. The variance is $g + g^2/\text{phi}$ .
gamma	The dispersion parameter for beta-binomial data.
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 $x \leftarrow \sin(a*t + b) + c$ , where <ul style="list-style-type: none"> <li>• <math>t \leftarrow \text{seq}(0, 2*\pi, \text{length.out} = k)</math></li> <li>• <math>a \leftarrow \text{mu}[1] + \text{lambda}[1]*\text{stats}::\text{runif}(1)</math></li> <li>• <math>b \leftarrow \text{mu}[2] + \text{lambda}[2]*\text{stats}::\text{runif}(1)</math></li> <li>• <math>c \leftarrow \text{mu}[3] + \text{lambda}[3]*\text{stats}::\text{runif}(1)</math></li> </ul>
N_trials	The number of trials parameter for binomial data.
force_zeromean	Should each component (excluding the disease age component) be forced to have a zero mean?

**Value**

An object of class `lgpsim`.

**Examples**

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

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

---

split

*Split data into training and test sets*

---

**Description**

- `split_by_factor` splits according to given factor
- `split_within_factor` splits according to given data point indices within the same level of a factor
- `split_within_factor_random` selects k points from each level of a factor uniformly at random as test data
- `split_random` splits uniformly at random
- `split_data` splits according to given data rows

**Usage**

```

split_by_factor(data, test, var_name = "id")

split_within_factor(data, idx_test, var_name = "id")

split_within_factor_random(data, k_test = 1, var_name = "id")

split_random(data, p_test = 0.2, n_test = NULL)

split_data(data, i_test, sort_ids = TRUE)

```

**Arguments**

data	a data frame
test	the levels of the factor that will be used as test data
var_name	name of a factor in the data
idx_test	indices point indices with the factor
k_test	desired number of test data points per each level of the factor
p_test	desired proportion of test data
n_test	desired number of test data points (if NULL, p_test is used to compute this)
i_test	test data row indices
sort_ids	should the test indices be sorted into increasing order

**Value**

a named list with names train, test, i\_train and i\_test

**See Also**

Other data frame handling functions: [add\\_dis\\_age\(\)](#), [add\\_factor\\_crossing\(\)](#), [add\\_factor\(\)](#), [adjusted\\_c\\_hat\(\)](#), [new\\_x\(\)](#)

---

testdata\_001

*A very small artificial test data, used mostly for unit tests*


---

**Description**

A very small artificial test data, used mostly for unit tests

**Usage**

```
testdata_001
```

**Format**

A data frame with 24 rows and 6 variables:

**id** individual id, a factor with levels: 1, 2, 3, 4

**age** age

**dis\_age** disease-related age

**blood** a continuous variable

**sex** a factor with 2 levels: Male, Female

**y** a continuous variable

**See Also**

Other built-in datasets: [testdata\\_002](#)

---

testdata\_002

*Medium-size artificial test data, used mostly for tutorials*

---

**Description**

Medium-size artificial test data, used mostly for tutorials

**Usage**

```
testdata_002
```

**Format**

A data frame with 96 rows and 6 variables:

**id** individual id, a factor with levels: 01-12

**age** age

**diseaseAge** disease-related age

**sex** a factor with 2 levels: Male, Female

**group** a factor with 2 levels: Case, Control

**y** a continuous variable

**See Also**

[read\\_proteomics\\_data](#)

Other built-in datasets: [testdata\\_001](#)



---

validate	<i>Validate S4 class objects</i>
----------	----------------------------------

---

**Description**

Validate S4 class objects

**Usage**

```
validate_lgpexpr(object)
validate_lgpformula(object)
validate_lgpscaling(object)
validate_lgpfit(object)
validate_GaussianPrediction(object)
validate_Prediction(object)
```

**Arguments**

object            an object to validate

**Value**

TRUE if valid, otherwise reasons for invalidity

---

var_mask	<i>Variance masking function</i>
----------	----------------------------------

---

**Description**

Variance masking function

**Usage**

```
var_mask(x, stp)
```

**Arguments**

x                    a vector of length  $n$   
 stp                  a positive real number (steepness of mask function)

**Value**

a vector of length  $n$

**See Also**

Other kernel utility functions: [warp\\_input\(\)](#)

---

warp\_input

*Input warping function*

---

**Description**

Input warping function

**Usage**

```
warp_input(x, a)
```

**Arguments**

x	a vector of length $n$
a	steepness of the warping function rise

**Value**

a vector of warped inputs  $w(x)$ , length  $n$

**See Also**

Other kernel utility functions: [var\\_mask\(\)](#)

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