Package 'inlabru'

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Type Package

Title Bayesian Latent Gaussian Modelling using INLA and Extensions

Version 2.5.3

URL `http://www.inlabru.org`, `https://inlabru-org.github.io/inlabru/`

BugReports `https://github.com/inlabru-org/inlabru/issues`

Description Facilitates spatial and general latent Gaussian modeling using integrated nested Laplace approximation via the INLA package (<`https://www.r-inla.org`>). Additionally, extends the GAM-like model class to more general nonlinear predictor expressions, and implements a log Gaussian Cox process likelihood for modeling univariate and spatial point processes based on ecological survey data. Model components are specified with general inputs and mapping methods to the latent variables, and the predictors are specified via general R expressions, with separate expressions for each observation likelihood model in multi-likelihood models. A prediction method based on fast Monte Carlo sampling allows posterior prediction of general expressions of the latent variables. Ecology-focused introduction in Bachl, Lindgren, Borchers, and Illian (2019) <doi:10.1111/2041-210X.13168>.

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Additional_repositories `https://inla.r-inla-download.org/R/testing`

RoxygenNote 7.2.1

Encoding UTF-8

Depends methods, R (>= 3.5), sp (>= 1.4-5), stats

Imports MatrixModels, magrittr, Matrix, patchwork, plyr, rgdal (>= 1.5.8), rgeos, rlang, utils, withr

Suggests covr, dplyr, ggmap, ggplot2, ggpolypath, graphics, INLA (>= 21.08.31), knitr, maps, maptools, mgcv, raster, RColorBrewer, rgl, rmarkdown, scales, sf, shiny, sn, spatstat.geom, spatstat.core, spatstat.data, spatstat (>= 2.0-0), sphereplot, splancs, testthat, tidyr

Config/testthat/parallel true

Config/testthat/edition 3

Collate '0_inlabru_envir.R' 'bru.covariate.R' 'bru.gof.R' 'bru.inference.R' 'bru.integration.R' 'bru.spatial.R' 'covariate.R' 'data.Poisson1_1D.R' 'data.Poisson2_1D.R' 'data.Poisson3_1D.R' 'data.gorillas.R' 'data.mexdolphin.R' 'data.mrsea.R' 'data.robins_subset.R' 'data.seals.R' 'data.shrimp.R' 'data.toygroups.R' 'deltaIC.R' 'deprecated.R' 'dsdata.R' 'dsmdata.R' 'dsmdata.tools.R' 'effect.R' 'environment.R' 'fmesher_crs.R' 'fmesher_utils.R' 'ggplot.R' 'inla.R' 'inlabru.R' 'integration.R' 'local_testthat.R' 'mappers.R' 'mesh.R' 'model.R' 'nlinla.R' 'plotsample.R' 'prediction.R' 'rgl.R' 'sampling.R' 'shapefile.R' 'spatstat.R' 'spde.R' 'stack.R' 'track_plotting.R' 'transformation.R' 'utils.R'

VignetteBuilder knitr

BuildVignettes true

LazyData false

NeedsCompilation no

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R topics documented:

`bincount` *1D LGCP bin count simulation and comparison with data*

Description

A common procedure of analyzing the distribution of 1D points is to chose a binning and plot the data's histogram with respect to this binning. This function compares the counts that the histogram calculates to simulations from a 1D log Gaussian Cox process conditioned on the number of data samples. For each bin this results in a median number of counts as well as a confidence interval. If the LGCP is a plausible model for the observed points then most of the histrogram counts (number of points within a bin) should be within the confidence intervals. Note that a proper comparison is a multiple testing problem which the function does not solve for you.

Usage

```
bincount(
  result,
  predictor,
  observations,
  breaks,
  nint = 20,
  probs = c(0.025, 0.5, 0.975),
  ...
)
```

Arguments

`result`	A result object from a `bru()` or `lgcp()` call
`predictor`	A formula describing the prediction of a 1D LGCP via `predict()`.
`observations`	A vector of observed values
`breaks`	A vector of bin boundaries
`nint`	Number of integration points per bin. Increase this if the bins are wide and
`probs`	numeric vector of probabilities with values in `[0,1]`
`...`	arguments passed on to `predict.bru()`

Value

An `data.frame` with a ggplot attribute ggp

Examples

```
## Not run:
if (require(ggplot2)) {
  # Load a point pattern
  data(Poisson2_1D)

  # Take a look at the point (and frequency) data

  ggplot(pts2) +
   geom_histogram(aes(x = x), binwidth = 55 / 20, boundary = 0, fill = NA, color = "black") +
    geom_point(aes(x), y = 0, pch = "|", cex = 4) +
    coord_fixed(ratio = 1)

  # Fit an LGCP model
  x <- seq(0, 55, length = 50)
  mesh1D <- inla.mesh.1d(x, boundary = "free")
  mdl <- x ~ spde1D(x, model = inla.spde2.matern(mesh1D)) + Intercept(1)
  fit.spde <- lgcp(mdl, pts2, domain = list(x = c(0, 55)))

  # Calculate bin statistics
  bc <- bincount(
    result = fit.spde,
    observations = pts2,
```

```
    breaks = seq(0, max(pts2), length = 12),
    predictor = x ~ exp(spde1D + Intercept)
  )


  # Plot them!
  attributes(bc)$ggp
}

## End(Not run)
```

---

bru *Convenient model fitting using (iterated) INLA*

Description

This method is a wrapper for `INLA::inla` and provides multiple enhancements.

- Easy usage of spatial covariates and automatic construction of inla projection matrices for (spatial) SPDE models. This feature is accessible via the `components` parameter. Practical examples on how to use spatial data by means of the components parameter can also be found by looking at the lgcp function's documentation.
- Constructing multiple likelihoods is straight forward. See like for more information on how to provide additional likelihoods to `bru` using the `...` parameter list.
- Support for non-linear predictors. See example below.
- Log Gaussian Cox process (LGCP) inference is available by using the `cp` family or (even easier) by using the lgcp function.

Usage

```
bru(components = ~Intercept(1), ..., options = list(), .envir = parent.frame())

bru_rerun(result, options = list())
```

Arguments

`components`	A `formula`-like specification of latent components. Also used to define a default linear additive predictor. See `component()` for details.
`...`	Likelihoods, each constructed by a calling `like()`, or named parameters that can be passed to a single `like()` call. Note that all the arguments will be evaluated before calling `like()` in order to detect if they are `like` objects. This means that special arguments that need to be evaluated in the context of `response_data` or `data` (such as Ntrials) may will only work that way in direct calls to `like()`.
`options`	A bru_options options object or a list of options passed on to `bru_options()`
`.envir`	Environment for component evaluation (for when a non-formula specification is used)
`result`	A previous estimation object of class `bru`

Details

- `bru_rerun` Continue the optimisation from a previously computed estimate.

Value

bru returns an object of class "bru". A `bru` object inherits from `INLA::inla` (see the inla documentation for its properties) and adds additional information stored in the `bru_info` field.

Author(s)

Fabian E. Bachl <`bachlfab@gmail.com`>

Examples

```
if (bru_safe_inla(multicore = FALSE)) {

  # Simulate some covariates x and observations y
  input.df <- data.frame(x = cos(1:10))
  input.df <- within(input.df, y <- 5 + 2 * x + rnorm(10, mean = 0, sd = 0.1))

  # Fit a Gaussian likelihood model
  fit <- bru(y ~ x + Intercept, family = "gaussian", data = input.df)

  # Obtain summary
  fit$summary.fixed
}


if (bru_safe_inla(multicore = FALSE)) {

  # Alternatively, we can use the like() function to construct the likelihood:

  lik <- like(family = "gaussian", formula = y ~ x + Intercept, data = input.df)
  fit <- bru(~ x + Intercept(1), lik)
  fit$summary.fixed
}

# An important addition to the INLA methodology is bru's ability to use
# non-linear predictors. Such a predictor can be formulated via like()'s
# \code{formula} parameter. The z(1) notation is needed to ensure that
# the z component should be interpreted as single latent variable and not
# a covariate:

if (bru_safe_inla(multicore = FALSE)) {
  z <- 2
  input.df <- within(input.df, y <- 5 + exp(z) * x + rnorm(10, mean = 0, sd = 0.1))
  lik <- like(
    family = "gaussian", data = input.df,
    formula = y ~ exp(z) * x + Intercept
  )
  fit <- bru(~ z(1) + Intercept(1), lik)
```

```
  # Check the result (z posterior should be around 2)
  fit$summary.fixed
}
```

`bru_call_options` *Additional bru options*

Description

Construct a `bru_options` object including the default and global options, and converting deprecated option names.

Usage

```
bru_call_options(...)
```

Arguments

`...`	Options passed on to `as.bru_options()`

Author(s)

Finn Lindgren <`finn.lindgren@gmail.com`>

Examples

```
opts <- bru_call_options()

# Print them:
opts
```

`bru_compute_linearisation` *Compute inlabru model linearisation information*

Description

Compute inlabru model linearisation information

Usage

```
bru_compute_linearisation(...)

## S3 method for class 'component'
bru_compute_linearisation(
  cmp,
  model,
  lhood_expr,
  data,
  state,
  A,
  effects,
  pred0,
  allow_latent,
  allow_combine,
  eps,
  ...
)

## S3 method for class 'bru_like'
bru_compute_linearisation(lhood, model, data, state, A, eps, ...)

## S3 method for class 'bru_like_list'
bru_compute_linearisation(lhoods, model, state, A, eps = 1e-05, ...)

## S3 method for class 'bru_model'
bru_compute_linearisation(model, lhoods, state, A, ...)
```

Arguments

`...`	Parameters passed on to other methods
`cmp`	A bru_component object
`model`	A `bru_model` object
`lhood_expr`	A predictor expression
`data`	Input data
`state`	The state information, as a list of named vectors
`A`	A-matrix information: • For `bru_component`: Precomputed A-matrix for the component • For `bru_like`: A list of named A-matrices for the components in the likelihood for the component • For `bru_like_list`: A list, where each element is a list of named A-matrices.
`effects`	• For `bru_component`: Precomputed effect list for all components involved in the likelihood expression
`pred0`	Precomputed predictor for the given state

`allow_latent`	logical. If `TRUE`, the latent state of each component is directly available to the predictor expression, with a `_latent` suffix.
`allow_combine`	logical; If `TRUE`, the predictor expression may involve several rows of the input data to influence the same row.
`eps`	The finite difference step size
`lhood`	A `bru_like` object
`lhoods`	A `bru_like_list` object

`bru_fill_missing` *Fill in missing values in Spatial grids*

Description

Computes nearest-available-value imputation for missing values in space

Usage

```
bru_fill_missing(
  data,
  where,
  values,
  layer = NULL,
  selector = NULL,
  batch_size = 500
)
```

Arguments

`data`	A SpatialPointsDataFrame, SpatialPixelsDataFrame, or a SpatialGridDataFrame containg data to use for filling
`where`	A, matrix, data.frame, or SpatialPoints or SpatialPointsDataFrame, containing the locations of the evaluated values
`values`	A vector of values to be filled in where `is.na(values)` is `TRUE`
`layer, selector`	Specifies what data column or columns from which to extract data, see `component()` for details.
`batch_size`	Size of nearest-neighbour calculation blocks, to limit the memory and computational complexity.

Value

An infilled vector of values

Examples

```
## Not run:
if (bru_safe_inla()) {
  points <-
    sp::SpatialPointsDataFrame(
      matrix(1:6, 3, 2),
      data = data.frame(val = c(NA, NA, NA))
    )
  input_coord <- expand.grid(x = 0:7, y = 0:7)
  input <-
    sp::SpatialPixelsDataFrame(
      input_coord,
      data = data.frame(val = as.vector(input_coord$y))
    )
  points$val <- bru_fill_missing(input, points, points$val)
  print(points)

  # To fill in missing values in a grid:
  print(input$val[c(3, 30)])
  input$val[c(3, 30)] <- NA # Introduce missing values
  input$val <- bru_fill_missing(input, input, input$val)
  print(input$val[c(3, 30)])
}

## End(Not run)
```

`bru_forward_transformation` *Transformation tools*

Description

Tools for transforming between N(0,1) variables and other distributions in predictor expressions

Usage

```
bru_forward_transformation(qfun, x, ..., tail.split. = 0)

bru_inverse_transformation(pfun, x, ..., tail.split. = NULL)
```

Arguments

`qfun`	A quantile function object, such as `qexp`
`x`	Values to be transformed
`...`	Distribution parameters passed on to the `qfun` and `pfun` functions

`tail.split.`	For x-values larger than `tail.split.`, upper quantile calculations are used internally, and for smaller values lower quantile calculations are used. This can avoid lack of accuracy in the distribution tails. If `NULL`, forward calculations split at 0, and inverse calculations use lower tails only, potentially losing accuracy in the upper tails.
`pfun`	A CDF function object, such as `pexp`

Value

- For `bru_forward_transformation`, a numeric vector
- For `bru_inverse_transformation`, a numeric vector

Examples

```
## Not run:
if (interactive()) {
  # EXAMPLE1
}

## End(Not run)
```

`bru_log_reset` *inlabru log message methods*

Description

Resets the inlabru log object

Retrieve, add, and/or print log messages

Usage

```
bru_log_reset()

bru_log_get(pretty = FALSE)

bru_log_message(
  ...,
  domain = NULL,
  appendLF = TRUE,
  verbosity = 1,
  allow_verbose = TRUE,
  verbose = NULL,
  verbose_store = NULL
)

bru_log(txt, verbose = NULL)

bru_log_active(activation = NULL)
```

Arguments

`pretty`	logical; If `TRUE`, return a single string with the log messages separated and terminated by line feeds, suitable for `cat(...)`. If `FALSE`, return the raw log as a vector of strings, suitable for `cat(..., sep = "\n")`. Default: `FALSE`
`...`	Zero or more objects passed on to `base::.makeMessage()`
`domain`	Domain for translations, passed on to `base::.makeMessage()`
`appendLF`	logical; whether to add a newline to the message. Only used for verbose output.
`verbosity`	numeric value describing the verbosity level of the message
`allow_verbose`	Whether to allow verbose output. Must be set to FALSE until the options object has been initialised.
`verbose`	logical; if `TRUE`, print the log message on screen with `message(txt)`. Default: `bru_options_get("bru_verbose")`
`verbose_store`	Same as `verbose`, but controlling what messages are stored in the global log object. Can be controlled via the `bru_verbose_store` with `bru_options_set()`.
`txt`	character; log message.
`activation`	logical; whether to activate (`TRUE`) or deactivate (`FALSE`) the inlabru logging system. Default: NULL, to keep the current activation state

Details

`bru_log_reset()` clears the log contents.

- `bru_log_message` DETAILS

The log message is stored if the log is active, see `bru_log_active()`

Value

`bru_log_get` RETURN_VALUE

- `bru_log_message` OUTPUT_DESCRIPTION

`bru_log` invisibly returns the added log message.

`bru_log_active` returns the previous activation state

Author(s)

Fabian E. Bachl <`bachlfab@gmail.com`> and Finn Lindgren <`finn.lindgren@gmail.com`>

Examples

```
## Not run:
if (interactive()) {
  # EXAMPLE1
}

## End(Not run)
```

```
## Not run:
if (interactive()) {
  # EXAMPLE1
}

## End(Not run)
code_runner <- function() {
  oa <- bru_log_active(TRUE)
  on.exit(bru_log_active(oa))
  bru_log("Test message")
}
bru_log_active()
code_runner()
cat(bru_log_get())
bru_log_active()
```

`bru_make_stack` *Build an inla data stack from linearisation information*

Description

Combine linearisation for multiple likelihoods

Usage

```
bru_make_stack(...)

## S3 method for class 'bru_like'
bru_make_stack(lhood, lin, idx, ...)

## S3 method for class 'bru_like_list'
bru_make_stack(lhoods, lin, idx, ...)
```

Arguments

`...`	Arguments passed on to other methods
`lhood`	A `bru_like` object
`lin`	Linearisation information • For `.bru_like`, a linearisation information list with elements `A` and `offset` • For `.bru_like_list`, a list of linearisation information lists
`idx`	Output from `evaluate_index(...)`
`lhoods`	A `bru_like_list` object

`bru_mapper` *Methods for* `bru_mapper` *objects*

Description

Methods for `bru_mapper` objects

Usage

```
bru_mapper(...)

ibm_n(mapper, inla_f = FALSE, ...)

ibm_values(mapper, inla_f = FALSE, ...)

ibm_amatrix(mapper, input, inla_f = FALSE, ...)

ibm_inla_subset(mapper, ...)

ibm_valid_input(mapper, input, inla_f = FALSE, ...)

## Default S3 method:
bru_mapper(mapper, new_class = NULL, methods = NULL, ...)

## Default S3 method:
ibm_inla_subset(mapper, ...)

## S3 method for class 'inla.mesh'
bru_mapper(mesh, ...)

## S3 method for class 'inla.mesh.1d'
bru_mapper(mesh, indexed = NULL, ...)

bru_mapper_index(n = 1L, ...)

bru_mapper_linear(...)

bru_mapper_matrix(labels, ...)

bru_mapper_factor(values, factor_mapping, ...)

bru_mapper_offset(...)

bru_mapper_multi(mappers, ...)

bru_mapper_collect(mappers, hidden = FALSE, ...)
```

```
bru_mapper_harmonics(
  order = 1,
  scaling = 1,
  intercept = TRUE,
  interval = c(0, 1),
  ...
)
```

Arguments

`...`	Arguments passed on to other methods
`mapper`	A mapper S3 object, normally inheriting from `bru_mapper`. For the default `bru_mapper` method, a list that will be converted to a `bru_mapper` object by adding class information and (optional) methods.
`inla_f`	logical; when `TRUE` in `ibm_n`, `ibm_values`, and `ibm_amatrix` methods, these must result in values compatible with `INLA::f(...)` an specification and corresponding `INLA::inla.stack(...)` constructions. Implementations do not normally need to do anything different, except for mappers of the type needed for hidden multicomponent models such as "bym2", which can be handled by `bru_mapper_collect`.
`input`	The values for which to produce validity information
`new_class`	If non-`NULL`, this is added at the front of the class definition
`methods,`	optional `list` of named method definitions; See Details.
`mesh`	An `inla.mesh.1d` or `inla.mesh.2d` object to use as a mapper
`indexed`	logical; If `TRUE`, the `ibm_values()` output will be the integer indexing sequence for the latent variables (needed for `spde` models). If `FALSE`, the knot locations are returned (useful as an interpolator for `rw2` models and similar). Default: `NULL`, to force user specification of this parameter
`n`	Size of a model for `bru_mapper_index`
`labels`	Column labels for matrix mappings
`values`	Input values calculated by `input_eval.bru_input()`
`factor_mapping`	character; selects the type of factor mapping. • `'contrast'` for leaving out the first factor level. • `'full'` for keeping all levels.
`mappers`	A list of `bru_mapper` objects
`hidden`	`logical`, set to `TRUE` to flag that the mapper is to be used as a first level input mapper for `INLA::f()` in a model that requires making only the first mapper visible to `INLA::f()` and `INLA::inla.stack()`, such as for "bym2" models, as activated by the `inla_f` argument to `ibm_n`, `ibm_values`, and `ibm_amatrix`. Set to `FALSE` to always access the full mapper, e.g. for `rgeneric` models
`order`	For `bru_mapper_harmonics`, specifies the maximum `cos`/`sin` order. (Default 1)
`scaling`	For `bru_mapper_harmonics`, specifies an optional vector of scaling factors of length `intercept` + `order`, or a common single scalar.

`intercept`	logical; For `bru_mapper_harmonics`, if `TRUE`, the first basis function is a constant. (Default `TRUE`)
`interval`	numeric length-2 vector specifying a domain interval. Default `c(0, 1)`.

Details

- `bru_mapper` Generic mapper S3 constructor. See below for details of the default constructor that can be used to define new mappers in user code.
- `ibm_n` Generic. Implementations must return the size of the latent vector being mapped to.
- `ibm_values` Generic. Implementations must return a vector that would be interpretable by an `INLA::f(..., values = ...)` specification. The exception is the method for `bru_mapper_multi`, that returns a multi-column data frame
- `ibm_amatrix` Generic. Implementations must return a (sparse) matrix of size `NROW(input)` (except for the `bru_mapper_multi` and `bru_mapper_collect` methods, that require `list()` inputs, and the input size is determined by the combined inputs) by `ibm_n(mapper, inla_f = FALSE)`. The `inla_f=TRUE` argument should only affect the allowed type of input format.
- `ibm_inla_subset` Generic. Implementations must return a logical vector of `TRUE/FALSE` for the subset such that, given the full A matrix and values output, `A[, subset, drop = FALSE]` and `values[subset]` (or `values[subset, , drop = FALSE]` for data.frame values) are equal to the `inla_f = TRUE` version of A and values. The default method uses the `ibm_values` output to construct the subset indexing.
- `ibm_valid_input` Generic. Implementations must return a logical vector of length `NROW(input)` (or for `bru_mapper_multi` and `bru_mapper_collect` a list of such vectors)
- `bru_mapper.default` adds the "bru_mapper" class and `new_class` to an object. If provided, mapper method functions are added to an environment `.envir` in the object. The generic methods `ibm_n`, `ibm_n_inla`, `ibm_values`, `ibm_values_inla`, `ibm_amatrix`, `ibm_amatrix_inla`, `ibm_valid_input`, and `ibm_valid_input_inla` look for these functions first, and otherwise call `UseMethod()`. This is an alternative to using `.S3method()` to register the methods, e.g. `.S3method("ibm_amatrix", "my_mapper_class", ibm_amatrix.my_mapper_class)`.
- The default `ibm_inla_subset` method uses the `ibm_values` output to construct the inla subset indexing, passing extra arguments such as `multi` on to the methods (this means it supports both regular vector values and `multi=1` data.frame values).
- `bru_mapper_multi` constructs a kronecker product mapping
- `bru_mapper_collect` constructs concatenated collection mapping
- `bru_mapper_harmonics` constructs a mapper for `cos`/`sin` functions of orders 1 (if `intercept` is `TRUE`, otherwise 0) through `order`. The total number of basis functions is `intercept + 2 * order`.

  Optionally, each order can be given a non-unit scaling, via the `scaling` vector, of length `intercept + order`. This can be used to give an effective spectral prior. For example, let

```
scaling = 1 / (1 + (0:4)^2)
A1 = bru_mapper_harmonics(order = 4)
u1 <- A1 %*% rnorm(9, sd = scaling)
```

Then, with

```
A2 = bru_mapper_harmonics(order = 4, scaling = scaling)
u2 = A2 %*% rnorm(9)
```

the stochastic properties of `u1` and `u2` will be the same, with `scaling^2` determining the variance for each frequency contribution.

The period for the first order harmonics is shifted and scaled to match `interval`.

See Also

bru_mapper_methods for specific method implementations.

Examples

```
mapper <- bru_mapper_index(5)
ibm_amatrix(mapper, c(1, 3, 4, 5, 2))
```

`bru_mapper_methods` *Implementation methods for mapper objects*

Description

A `bru_mapper` sub-class implementation must provide an `ibm_matrix()` method. If the model size 'n' and definition values 'values' are stored in the object itself, default methods are available (see Details). Otherwise the `ibm_n()` and `ibm_values()` methods also need to be provided.

Usage

```
## Default S3 method:
ibm_n(mapper, inla_f = FALSE, ...)

## Default S3 method:
ibm_values(mapper, inla_f = FALSE, ...)

## Default S3 method:
ibm_amatrix(mapper, input, inla_f = FALSE, ...)

## Default S3 method:
ibm_valid_input(mapper, input, ...)

## S3 method for class 'bru_mapper_inla_mesh_2d'
ibm_n(mapper, ...)
```

```
## S3 method for class 'bru_mapper_inla_mesh_2d'
ibm_values(mapper, ...)

## S3 method for class 'bru_mapper_inla_mesh_2d'
ibm_amatrix(mapper, input, ...)

## S3 method for class 'bru_mapper_inla_mesh_1d'
ibm_n(mapper, ...)

## S3 method for class 'bru_mapper_inla_mesh_1d'
ibm_values(mapper, ...)

## S3 method for class 'bru_mapper_inla_mesh_1d'
ibm_amatrix(mapper, input, ...)

## S3 method for class 'bru_mapper_index'
ibm_valid_input(mapper, input, ...)

## S3 method for class 'bru_mapper_index'
ibm_amatrix(mapper, input, ...)

## S3 method for class 'bru_mapper_linear'
ibm_n(mapper, ...)

## S3 method for class 'bru_mapper_linear'
ibm_values(mapper, ...)

## S3 method for class 'bru_mapper_linear'
ibm_amatrix(mapper, input, ...)

## S3 method for class 'bru_mapper_matrix'
ibm_n(mapper, ...)

## S3 method for class 'bru_mapper_matrix'
ibm_values(mapper, ...)

## S3 method for class 'bru_mapper_matrix'
ibm_amatrix(mapper, input, ...)

## S3 method for class 'bru_mapper_factor'
ibm_n(mapper, ...)

## S3 method for class 'bru_mapper_factor'
ibm_values(mapper, ...)

## S3 method for class 'bru_mapper_factor'
ibm_amatrix(mapper, input, ...)
```

```
## S3 method for class 'bru_mapper_offset'
ibm_n(mapper, ...)

## S3 method for class 'bru_mapper_offset'
ibm_values(mapper, ...)

## S3 method for class 'bru_mapper_offset'
ibm_amatrix(mapper, input, ...)

## S3 method for class 'bru_mapper_multi'
ibm_n(mapper, inla_f = FALSE, multi = 0L, ...)

## S3 method for class 'bru_mapper_multi'
ibm_values(mapper, inla_f = FALSE, multi = 0L, ...)

## S3 method for class 'bru_mapper_multi'
ibm_amatrix(mapper, input, inla_f = FALSE, multi = 0L, ...)

## S3 method for class 'bru_mapper_multi'
ibm_valid_input(mapper, input, inla_f = FALSE, multi = 0L, ...)

## S3 method for class 'bru_mapper_multi'
x[i, drop = TRUE]

## S3 method for class 'bru_mapper_multi'
names(x)

## S3 replacement method for class 'bru_mapper_multi'
names(x) <- value

## S3 method for class 'bru_mapper_collect'
ibm_n(mapper, inla_f = FALSE, multi = 0L, ...)

## S3 method for class 'bru_mapper_collect'
ibm_values(mapper, inla_f = FALSE, multi = 0L, ...)

## S3 method for class 'bru_mapper_collect'
ibm_amatrix(mapper, input, inla_f = FALSE, multi = 0L, ...)

## S3 method for class 'bru_mapper_collect'
ibm_valid_input(mapper, input, inla_f = FALSE, multi = 0L, ...)

## S3 method for class 'bru_mapper_collect'
x[i, drop = TRUE]

## S3 method for class 'bru_mapper_collect'
names(x)
```

```
## S3 replacement method for class 'bru_mapper_collect'
names(x) <- value

## S3 method for class 'bru_mapper_harmonics'
ibm_n(mapper, inla_f = FALSE, ...)

## S3 method for class 'bru_mapper_harmonics'
ibm_amatrix(mapper, input, inla_f = FALSE, ...)
```

Arguments

`mapper`	A mapper S3 object, normally inheriting from `bru_mapper`
`inla_f`	logical; when `TRUE` in `ibm_n` and `ibm_values`, these must result in values compatible with `INLA::f(...)` an specification and corresponding `INLA::inla.stack(...)` constructions. For `ibm_amatrix` methods, it may influence how the input data is interpreted. Implementations do not normally need to do anything different, except for mappers of the type needed for hidden multicomponent models such as "bym2", which can be handled by `bru_mapper_collect`.
`...`	Arguments passed on to other methods
`input`	The values for which to produce a mapping matrix
`multi`	integer or logical; If positive, the number of levels to recurse in a `bru_collect_mapper`. If `TRUE`, equivalent to `1L`. If `FALSE`, equivalent to `0L`.
`x`	object from which to extract element(s)
`i`	indices specifying element(s) to extract
`drop`	logical; For `[.bru_mapper_collect`, whether to extract an individual mapper when `i` identifies a single element. If `FALSE`, a list of sub-mappers is returned (suitable e.g. for creating a new `bru_mapper_collect` object). Default: `TRUE`
`value`	a character vector of up to the same length as x

Details

- The default `ibm_n()` method returns a non-null element 'n' from the mapper object, and gives an error if it doesn't exist. If `inla_f=TRUE`, first checks for a 'n_inla' element.

- The default `ibm_values()` method returns a non-null element 'values' from the mapper object, and `seq_len(ibm_n(mapper))` if it doesn't exist.

- The default `ibm_amatrix()` gives an error message. Mapper classes must implement their own `ibm_amatrix` method.

- The default `ibm_valid_input()` method returns an all-TRUE logical vector.

- `ibm_amatrix` for `bru_mapper_multi` accepts a list with named entries, or a list with unnamed but ordered elements. The names must match the sub-mappers, see `names.bru_mapper_multi()`. Each list element should take a format accepted by the corresponding sub-mapper. In case each element is a vector, the input can be given as a data.frame with named columns, a matrix with named columns, or a matrix with unnamed but ordered columns.

- `ibm_valid_input` for `bru_mapper_multi` accepts a list with named entries, or a list with unnamed but ordered elements. The names must match the sub-mappers, see `names.bru_mapper_multi()`. Each list element should take a format accepted by the corresponding sub-mapper. In case each element is a vector, the input can be given as a data.frame with named columns, a matrix with named columns, or a matrix with unnamed but ordered columns.

- `ibm_amatrix` for `bru_mapper_collect` accepts a list with named entries, or a list with unnamed but ordered elements. The names must match the sub-mappers, see `names.bru_mapper_collect()`. Each list element should take a format accepted by the corresponding sub-mapper. In case each element is a vector, the input can be given as a data.frame with named columns, a matrix with named columns, or a matrix with unnamed but ordered columns. When `inla_f=TRUE` and `hidden=TRUE` in the mapper definition, the input format should instead match that of the first, non-hidden, sub-mapper.

- `ibm_valid_input` for `bru_mapper_collect` accepts a list with named entries, or a list with unnamed but ordered elements. The names must match the sub-mappers, see `names.bru_mapper_collect()`. Each list element should take a format accepted by the corresponding sub-mapper. In case each element is a vector, the input can be given as a data.frame with named columns, a matrix with named columns, or a matrix with unnamed but ordered columns.

Value

- `[`-indexing a `bru_mapper_multi` extracts a subset `bru_mapper_multi` object (for drop `FALSE`) or an individual sub-mapper (for drop `TRUE`, and `i` identifies a single element)

- The `names()` method for `bru_mapper_multi` returns the names from the sub-mappers list

- `[`-indexing a `bru_mapper_collect` extracts a subset `bru_mapper_collect` object (for drop `FALSE`) or an individual sub-mapper (for drop `TRUE`, and `i` identifies a single element)

- The `names()` method for `bru_mapper_collect` returns the names from the sub-mappers list

See Also

`bru_mapper()`

`bru_options` *Create or update an options objects*

Description

Create a new options object, or merge information from several objects.

The `_get`, `_set`, and `_reset` functions operate on a global package options override object. In many cases, setting options in specific calls to `bru()` is recommended instead.

Usage

```
bru_options(...)

as.bru_options(x = NULL)

bru_options_default()

bru_options_check(options, ignore_null = TRUE)

bru_options_get(name = NULL, include_default = TRUE)

bru_options_set(..., .reset = FALSE)

bru_options_reset()
```

Arguments

`...`	A collection of named options, optionally including one or more `bru_options` objects. Options specified later override the previous options.
`x`	An object to be converted to an `bru_options` object.
`options`	An `bru_options` object to be checked
`ignore_null`	Ignore missing or NULL options.
`name`	Either `NULL`, or single option name string, or character vector or list with option names, Default: NULL
`include_default`	logical; If `TRUE`, the default options are included together with the global override options. Default: `TRUE`
`.reset`	For `bru_options_set`, logical indicating if the global override options list should be emptied before setting the new option(s).

Details

`bru_options_check` checks for valid contents of an `bru_options` object

`bru_options_check()` produces warnings for invalid options.

`bru_options_set()` is used to set global package options.

`bru_options_reset()` clears the global option overrides.

Value

`bru_options()` returns an `bru_options` object.

For `as.bru_options()`, `NULL` or no input returns an empty `bru_options` object, a `list` is converted via `bru_options(...)`, and `bru_options` input is passed through. Other types of input generates an error.

`bru_options_default()` returns an `bru_options` object containing default options.

`bru_options_check()` returns a `logical`; `TRUE` if the object contains valid options for use by other functions

`bru_options_get` returns either an `bru_options` object, for `name == NULL`, the contents of single option, if `name` is a options name string, or a named list of option contents, if `name` is a list of option name strings.

`bru_options_set()` returns a copy of the global override options, invisibly (as `bru_options_get(include_default = FALSE)`).

Valid options

For `bru_options` and `bru_options_set`, recognised options are:

bru_verbose logical or numeric; if `TRUE`, log messages of `verbosity` ≤ 1 are printed by `bru_log_message()`. If numeric, log messages of verbosity $\leq$`bru_verbose` are printed. For line search details, set `bru_verbose=2` or `3`. Default: 0, to not print any messages

bru_verbose_store logical or numeric; if `TRUE`, log messages of `verbosity` ≤ 1 are stored by `bru_log_message()`. If numeric, log messages of verbosity $\leq$ are stored. Default: Inf, to store all messages.

bru_run If TRUE, run inference. Otherwise only return configuration needed to run inference.

bru_max_iter maximum number of inla iterations, default 10. Also see the `bru_method$rel_tol` and related options below.

bru_initial An `inla` object returned from previous calls of `INLA::inla`, `bru()` or `lgcp()`, or a list of named vectors of starting values for the latent variables. This will be used as a starting point for further improvement of the approximate posterior.

bru_int_args List of arguments passed all the way to the integration method `ipoints` and `int.polygon` for 'cp' family models;

- **method** "stable" or "direct". For "stable" (default) integration points are aggregated to mesh vertices.
- **nsub1** Number of integration points per knot interval in 1D. Default 30.
- **nsub2** Number of integration points along a triangle edge for 2D. Default 9.
- **nsub** Deprecated parameter that overrides `nsub1` and `nsub2` if set. Default `NULL`.

bru_method List of arguments controlling the iterative inlabru method:

- **taylor** 'pandemic' (default, from version 2.1.15).
- **search** Either 'all' (default), to use all available line search methods, or one or more of
  - **'finite'** (reduce step size until predictor is finite)
  - **'contract'** (decrease step size until trust hypersphere reached)
  - **'expand'** (increase step size until no improvement)
  - **'optimise'** (fast approximate error norm minimisation)

  To disable line search, set to an empty vector. Line search is not available for `taylor="legacy"`.
- **factor** Numeric, >1 determining the line search step scaling multiplier. Default $(1+\sqrt{5})/2$.
- **rel_tol** Stop the iterations when the largest change in linearisation point (the conditional latent state mode) in relation to the estimated posterior standard deviation is less than `rel_tol`. Default 0.01 (one percent).
- **max_step** The largest allowed line search step factor. Factor 1 is the full INLA step. Default is 2.

lin_opt_method Which method to use for the line search optimisation step. Default "onestep", using a quadratic approximation based on the value and gradient at zero, and the value at the current best step length guess. The method "full" does line optimisation on the full nonlinear predictor; this is slow and intended for debugging purposes only.

bru_compress_cp logical; when `TRUE`, compress the $\sum_{i=1}^{n} \eta_i$ part of the Poisson process likelihood (`family="cp"`) into a single term, with $y = n$, and predictor `mean(eta)`. Default: `TRUE`

`inla()` **options** All options not starting with `bru_` are passed on to `inla()`, sometimes after altering according to the needs of the inlabru method. Warning: Due to how inlabru currently constructs the `inla()` call, the `mean`, `prec`, `mean.intercept`, and `prec.intercept` settings in `control.fixed` will have no effect. Until a more elegant alternative has been implemented, use explicit `mean.linear` and `prec.linear` specifications in each `model="linear"` component instead.

See Also

`bru_options()`, `bru_options_default()`, `bru_options_get()`

Examples

```
## Not run:
if (interactive()) {
  # Combine global and user options:
  options1 <- bru_options(bru_options_get(), bru_verbose = TRUE)
  # Create a proto-options object in two equivalent ways:
  options2 <- as.bru_options(bru_verbose = TRUE)
  options2 <- as.bru_options(list(bru_verbose = TRUE))
  # Combine options objects:
  options3 <- bru_options(options1, options2)
}

## End(Not run)
## Not run:
if (interactive()) {
  # EXAMPLE1
}

## End(Not run)
## Not run:
if (interactive()) {
  bru_options_check(bru_options(bru_max_iter = "text"))
}

## End(Not run)
## Not run:
if (interactive()) {
  # EXAMPLE1
}

## End(Not run)
## Not run:
```

```
if (interactive()) {
  bru_options_set(
    bru_verbose = TRUE,
    verbose = TRUE
  )
}

## End(Not run)
```

`bru_safe_inla` *Load INLA safely for examples and tests*

Description

Loads the INLA package with `requireNamespace("INLA", quietly = TRUE)`, and optionally checks and sets the multicore `num.threads` INLA option.

Usage

```
bru_safe_inla(multicore = NULL, quietly = FALSE)
```

Arguments

`multicore`	logical; if `TRUE`, multiple cores are allowed, and the INLA `num.threads` option is not checked or altered. If `FALSE`, forces `num.threads="1:1"`. Default: NULL, checks if running in testthat or non-interactively, in which case sets `multicore=FALSE`, otherwise `TRUE`.
`quietly`	logical; if `TRUE`, prints diagnostic messages. Default: FALSE.

Value

logical; `TRUE` if INLA was loaded safely, otherwise FALSE

Examples

```
## Not run:
if (bru_safe_inla()) {
  # Run inla dependent calculations
}

## End(Not run)
```

`bru_standardise_names` *Standardise inla hyperparameter names*

Description

The inla hyperparameter output uses parameter names that can include whitespace and special characters. This function replaces those characters with underscores.

Usage

```
bru_standardise_names(x)
```

Arguments

`x`	character vector; names to be standardised

Value

A character vector with standardised names

Examples

```
bru_standardise_names("Precision for the Gaussian observations")
```

`bru_summarise` *Summarise and annotate data*

Description

Summarise and annotate data

Usage

```
bru_summarise(
  data,
  probs = c(0.025, 0.5, 0.975),
  x = NULL,
  cbind.only = FALSE,
  max_moment = 2
)
```

Arguments

`data`	A list of samples, each either numeric or a `data.frame`
`probs`	A numeric vector of probabilities with values in `[0, 1]`, passed to `stats::quantile`
`x`	A `data.frame` of data columns that should be added to the summary data frame
`cbind.only`	If TRUE, only `cbind` the samples and return a matrix where each column is a sample
`max_moment`	integer, at least 2. Determines the largest moment order information to include in the output. If `max_moment` > 2, includes "skew" (skewness, `E[(x-m)^3/s^3]`), and if `max_moment` > 3, includes "ekurtosis" (excess kurtosis, `E[(x-m)^4/s^4] - 3`). Default 2. Note that the Monte Carlo variability of the `ekurtois` estimate may be large.

Value

A `data.frame` or `Spatial[Points/Pixels]DataFrame` with summary statistics, "mean", "sd", `paste0("q", probs)`, "mean.mc_std_err", "sd.mc_std_err"

Examples

```
bru_summarise(matrix(rexp(10000), 10, 1000), max_moment = 4, probs = NULL)
```

`component` *Latent model component construction*

Description

Similar to `glm()`, `gam()` and `inla()`, `bru()` models can be constructed via a formula-like syntax, where each latent effect is specified. However, in addition to the parts of the syntax compatible with `INLA::inla`, `bru` components offer additional functionality which facilitates modelling, and the predictor expression can be specified separately, allowing more complex and non-linear predictors to be defined. The formula syntax is just a way to allow all model components to be defined in a single line of code, but the definitions can optionally be split up into separate component definitions. See Details for more information.

The `component` methods all rely on the `component.character()` method, that defines a model component with a given label/name. The user usually doesn't need to call these methods directly, but can instead supply a formula expression that can be interpreted by the `component_list.formula()` method, called inside `bru()`.

Usage

```
component(...)

## S3 method for class 'character'
component(
```

```
  object,
  main = NULL,
  weights = NULL,
  ...,
  model = NULL,
  mapper = NULL,
  main_layer = NULL,
  main_selector = NULL,
  n = NULL,
  values = NULL,
  season.length = NULL,
  copy = NULL,
  weights_layer = NULL,
  weights_selector = NULL,
  group = NULL,
  group_mapper = NULL,
  group_layer = NULL,
  group_selector = NULL,
  ngroup = NULL,
  control.group = NULL,
  replicate = NULL,
  replicate_mapper = NULL,
  replicate_layer = NULL,
  replicate_selector = NULL,
  nrep = NULL,
  A.msk = NULL,
  .envir = parent.frame(),
  envir_extra = NULL
)
```

Arguments

`...`	Parameters passed on to other methods
`object`	A character label for the component
`main`	`main` takes an R expression that evaluates to where the latent variables should be evaluated (coordinates, indices, continuous scalar (for rw2 etc)). Arguments starting with weights, group, replicate behave similarly to main, but for the corresponding features of `INLA::f()`.
`weights, weights_layer, weights_selector`	Optional specification of effect scaling weights. Same syntax as for `main`.
`model`	Either one of "offset", "factor_full", "factor_contrast", "linear", "fixed", or a model name or object accepted by INLA's `f` function. If set to NULL, then "linear" is used for vector inputs, and "fixed" for matrix input (converted internally to an iid model with fixed precision)
`mapper`	Information about how to do the mapping from the values evaluated in `main`, and to the latent variables. Auto-detects spde model objects in model and extracts the mesh object to use as the mapper, and auto-generates mappers for indexed models. (Default: NULL, for auto-determination)

`main_layer`, `main_selector`	The `_layer` is a numeric index or character name of which layer/variable to extract from a covariate data object given in `main` (Default: The effect component name, if it exists i the covariate object, otherwise the first column of the covariate data frame) The `_selector` is character name of a variable whose contents determines which layer to extract from a covariate for each data point. Overrides the `layer`. (Default: NULL)
`n`	The number of latent variables in the model. Should be auto-detected for most or all models (Default: NULL, for auto-detection). An error is given if it can't figure it out by itself.
`values`	Specifies for what covariate/index values INLA should build the latent model. Normally generated internally based on the mapping details. (Default: NULL, for auto-determination)
`season.length`	Passed on to `INLA::f()` for model `"seasonal"` (TODO: check if this parameter is still fully handled)
`copy`	character; label of other component that this component should be a copy of. If the `fixed = FALSE`, a scaling constant is estimated, via a hyperparameter. If `fixed = TRUE`, the component scaling is fixed, by default to 1; for fixed scaling, it's more efficient to express the scaling in the predictor expression instead of making a copy component.
`group`, `group_mapper`, `group_layer`, `group_selector`, `ngroup`	Optional specification of kronecker/group model indexing.
`control.group`	`list` of kronecker/group model parameters, currently passed directly on to `INLA::f`
`replicate`, `replicate_mapper`, `replicate_layer`, `replicate_selector`, `nrep`	Optional specification of indices for an independent replication model. Same syntax as for `main`
`A.msk`	TODO: check/fix/deprecate this parameter. Likely doesn't work at the moment, and I've found no examples that use it.
`.envir`	Evaluation environment
`envir_extra`	TODO: check/fix this parameter.

Details

As shorthand, `bru()` will understand basic additive formulae describing fixed effect models. For instance, the components specification `y ~ x` will define the linear combination of an effect named `x` and an intercept to the response `y` with respect to the likelihood family stated when calling `bru()`. Mathematically, the linear predictor η would be written down as

$$\eta = \beta * x + c,$$

where:

- c is the *intercept*
- $x$is a *covariate*

- β is a *random variable* associated with x and
- $\psi = \beta * x$ is called the *random effect* of x

A problem that arises when using this kind of R formula is that it does not clearly reflect the mathematical formula. For instance, when providing the formula to inla, the resulting object will refer to the random effect $\psi = \beta * x$ as `x`. Hence, it is not clear if `x` refers to the covariate or the effect of the covariate.

The `component.character` method is inlabru's equivalent to INLA's `f` function but adds functionality that is unique to inlabru.

Deprecated parameters:

- map: Use `main` instead.
- mesh: Use `mapper` instead.

Naming random effects

In INLA, the `f()` notation is used to define more complex models, but a simple linear effect model can also be expressed as

- `formula = y ~ f(x, model = "linear")`,

where `f()` is the inla specific function to set up random effects of all kinds. The underlying predictor would again be $\eta = \beta * x + c$ but the result of fitting the model would state `x` as the random effect's name. bru allows rewriting this formula in order to explicitly state the name of the random effect and the name of the associated covariate. This is achieved by replacing `f` with an arbitrary name that we wish to assign to the effect, e.g.

- `components = y ~ psi(x, model = "linear")`.

Being able to discriminate between x and ψ is relevant because of two functionalities bru offers. The formula parameters of both `bru()` and the prediction method predict.bru are interpreted in the mathematical sense. For instance, `predict` may be used to analyze the analytical combination of the covariate x and the intercept using

- `predict(fit, data.frame(x=2)), ~ exp(psi + Intercept)`.

which corresponds to the mathematical expression $e^{x\beta+c}$.

On the other hand, predict may be used to only look at a transformation of the latent variable β_ψ

- `predict(fit, NULL, ~ exp(psi_latent))`.

which corresponds to the mathematical expression e^{β}.

Author(s)

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See Also

Other component constructors: `component_list()`

Examples

```
# As an example, let us create a linear component. Here, the component is
# called "myLinearEffectOfX" while the covariate the component acts on is
# called "x". Note that a list of components is returned because the
# formula may define multiple components

cmp <- component_list(~ myLinearEffectOfX(main = x, model = "linear"))
summary(cmp)
# Equivalent shortcuts:
cmp <- component_list(~ myLinearEffectOfX(x, model = "linear"))
cmp <- component_list(~ myLinearEffectOfX(x))
# Individual component
cmp <- component("myLinearEffectOfX", main = x, model = "linear")
summary(cmp)

if (bru_safe_inla(quietly = TRUE)) {

  # As an example, let us create a linear component. Here, the component is
  # called "myEffectOfX" while the covariate the component acts on is called "x":

  cmp <- component("myEffectOfX", main = x, model = "linear")
  summary(cmp)

  # A more complicated component:
  cmp <- component("myEffectOfX",
    main = x,
    model = INLA::inla.spde2.matern(INLA::inla.mesh.1d(1:10))
  )

  # Compound fixed effect component, where x and z are in the input data.
  # The formula will be passed on to MatrixModels::model.Matrix:
  cmp <- component("eff", ~ -1 + x:z, model = "fixed")
  summary(cmp)
}
```

`component_eval` *Evaluate component values in predictor expressions*

Description

In predictor expressions, `name_eval(...)` can be used to evaluate the effect of a component called "name".

Usage

```
component_eval(main, group = NULL, replicate = NULL, .state = NULL)
```

Arguments

`main, group, replicate`	Specification of where to evaluate a component. The three inputs are passed on to the respective `bru_mapper` methods.
`.state`	The internal component state. Normally supplied automatically by the internal methods for evaluating inlabru predictor expressions.

Value

A vector of values for a component

Examples

```
## Not run:
if (bru_safe_inla()) {
  mesh <- INLA::inla.mesh.2d(
    cbind(0, 0),
    offset = 2, max.edge = 0.25
  )
  spde <- INLA::inla.spde2.pcmatern(mesh,
    prior.range = c(0.1, 0.01),
    prior.sigma = c(2, 0.01)
  )
  data <- sp::SpatialPointsDataFrame(
    matrix(runif(10), 5, 2),
    data = data.frame(z = rnorm(5))
  )
  fit <- bru(z ~ -1 + field(coordinates, model = spde),
    family = "gaussian", data = data
  )
  pred <- predict(
    fit,
    data = data.frame(x = 0.5, y = 0.5),
    formula = ~ field_eval(cbind(x, y))
  )
}

## End(Not run)
```

`component_list` *Methods for inlabru component lists*

Description

Constructor methods for inlabru component lists. Syntax details are given in `component()`.

Usage

```
component_list(object, lhoods = NULL, .envir = parent.frame(), ...)

## S3 method for class 'formula'
component_list(object, lhoods = NULL, .envir = parent.frame(), ...)

## S3 method for class 'list'
component_list(object, lhoods = NULL, .envir = parent.frame(), ...)

## S3 method for class 'component_list'
c(...)

## S3 method for class 'component_list'
x[i]
```

Arguments

`object`	The object to operate on
`lhoods`	A `bru_like_list` object
`.envir`	An evaluation environment for non-formula input
`...`	Parameters passed on to other methods. Also see Details.
`x`	`component_list` object from which to extract element(s)
`i`	indices specifying elements to extract

Details

- `component_list.formula`: Convert a component formula into a `component_list` object

- `component_list.list`: Combine a list of components and/or component formulas into a `component_list` object

- `c.component_list`: The `...` arguments should be `component_list` objects. The environment from the first argument will be applied to the resulting list.

Author(s)

Fabian E. Bachl <`bachlfab@gmail.com`> and Finn Lindgren <`finn.lindgren@gmail.com`>

See Also

Other component constructors: `component()`

Other component constructors: `component()`

Examples

```
# As an example, let us create a linear component. Here, the component is
# called "myLinearEffectOfX" while the covariate the component acts on is
# called "x". Note that a list of components is returned because the
# formula may define multiple components

eff <- component_list(~ myLinearEffectOfX(main = x, model = "linear"))
summary(eff[[1]])
# Equivalent shortcuts:
eff <- component_list(~ myLinearEffectOfX(x, model = "linear"))
eff <- component_list(~ myLinearEffectOfX(x))
# Individual component
eff <- component("myLinearEffectOfX", main = x, model = "linear")
```

`cprod` *Cross product of integration points*

Description

Calculates the cross product of integration points in different dimensions and multiplies their weights accordingly. If the object defining points in a particular dimension has no weights attached to it all weights are assumend to be 1.

Usage

```
cprod(...)
```

Arguments

...	`data.frame` or `SpatialPointsDataFrame` objects, each one usually obtained by a call to the ipoints function.

Value

A `data.frame` or `SpatialPointsDataFrame` of multidimensional integration points and their weights

Author(s)

Fabian E. Bachl <`bachlfab@gmail.com`>

Examples

```
# ipoints needs INLA
if (bru_safe_inla()) {
  # Create integration points in dimension 'myDim' and 'myDiscreteDim'
  ips1 <- ipoints(rbind(c(0, 3), c(3, 8)), 17, name = "myDim")
  ips2 <- ipoints(domain = c(1, 2, 4), name = "myDiscreteDim")
```

```
  # Calculate the cross product
  ips <- cprod(ips1, ips2)

  # Plot the integration points
  plot(ips$myDim, ips$myDiscreteDim, cex = 10 * ips$weight)
}
```

`deltaIC` *Summarise DIC and WAIC from* `lgcp` *objects.*

Description

Calculates DIC and/or WAIC differences and produces an ordered summary.

Usage

```
deltaIC(..., criterion = "DIC")
```

Arguments

`...`	Comma-separated objects inheriting from class `inla` and obtained from a run of `INLA::inla()`, `bru()` or `lgcp()`
`criterion`	character vector. If it includes 'DIC', computes DIC differences; If it contains 'WAIC', computes WAIC differences. Default: 'DIC'

Value

A data frame with each row containing the Model name, DIC and Delta.DIC, and/or WAIC and Delta.WAIC.

Examples

```
if (bru_safe_inla(multicore = FALSE)) {
  # Generate some data
  input.df <- data.frame(idx = 1:10, x = cos(1:10))
  input.df <- within(
    input.df,
    y <- rpois(10, 5 + 2 * cos(1:10) + rnorm(10, mean = 0, sd = 0.1))
  )

  # Fit two models
  fit1 <- bru(y ~ x, family = "poisson", data = input.df)
  fit2 <- bru(y ~ x + rand(idx, model = "iid"), family = "poisson", data = input.df)

  # Compare DIC
```

```
  deltaIC(fit1, fit2)
}
```

`devel.cvmeasure` *Variance and correlations measures for prediction components*

Description

Calculates local and integrated variance and correlation measures as introduced by Yuan et al. (2017).

Usage

```
devel.cvmeasure(joint, prediction1, prediction2, samplers = NULL, mesh = NULL)
```

Arguments

`joint`	A joint `prediction` of two latent model components.
`prediction1`	A `prediction` of the first component.
`prediction2`	A `prediction` of the second component.
`samplers`	A SpatialPolygon object describing the area for which to compute the cumulative variance measure.
`mesh`	The `inla.mesh` for which the prediction was performed (required for cumulative Vmeasure).

Value

Variance and correlations measures.

References

Y. Yuan, F. E. Bachl, F. Lindgren, D. L. Brochers, J. B. Illian, S. T. Buckland, H. Rue, T. Gerrodette. 2017. Point process models for spatio-temporal distance sampling data from a large-scale survey of blue whales. https://arxiv.org/abs/1604.06013

Examples

```
if (bru_safe_inla() && require(ggplot2, quietly = TRUE)) {

  # Load Gorilla data

  data("gorillas", package = "inlabru")

  # Use RColorBrewer

  library(RColorBrewer)
```

```
# Fit a model with two components:
# 1) A spatial smooth SPDE
# 2) A spatial covariate effect (vegetation)

pcmatern <- INLA::inla.spde2.pcmatern(gorillas$mesh,
  prior.sigma = c(0.1, 0.01),
  prior.range = c(0.01, 0.01)
)

cmp <- coordinates ~ vegetation(gorillas$gcov$vegetation, model = "factor_contrast") +
  spde(coordinates, model = pcmatern) -
  Intercept(1)

fit <- lgcp(cmp, gorillas$nests,
  samplers = gorillas$boundary,
  domain = list(coordinates = gorillas$mesh),
  options = list(control.inla = list(int.strategy = "eb"))
)

# Predict SPDE and vegetation at the mesh vertex locations

vrt <- vertices(gorillas$mesh)
pred <- predict(
  fit,
  vrt,
  ~ list(
    joint = spde + vegetation,
    field = spde,
    veg = vegetation
  )
)

# Plot component mean

multiplot(ggplot() +
  gg(gorillas$mesh, color = pred$joint$mean) +
  coord_equal() +
  theme(legend.position = "bottom"),
ggplot() +
  gg(gorillas$mesh, color = pred$field$mean) +
  coord_equal() +
  theme(legend.position = "bottom"),
ggplot() +
  gg(gorillas$mesh, color = pred$veg$mean) +
  coord_equal() +
  theme(legend.position = "bottom"),
cols = 3
)

# Plot component variance

multiplot(ggplot() +
```

```
  gg(gorillas$mesh, color = pred$joint$var) +
  coord_equal() +
  theme(legend.position = "bottom"),
ggplot() +
  gg(gorillas$mesh, color = pred$field$var) +
  coord_equal() +
  theme(legend.position = "bottom"),
ggplot() +
  gg(gorillas$mesh, color = pred$veg$var) +
  coord_equal() +
  theme(legend.position = "bottom"),
cols = 3
)

# Calculate variance and correlation measure

vm <- devel.cvmeasure(pred$joint, pred$field, pred$veg)
lprange <- range(vm$var.joint, vm$var1, vm$var2)

# Variance contribution of the components

csc <- scale_fill_gradientn(colours = brewer.pal(9, "YlOrRd"), limits = lprange)
boundary <- gorillas$boundary

plot.1 <- ggplot() +
  gg(gorillas$mesh, color = vm$var.joint, mask = boundary) +
  csc +
  coord_equal() +
  ggtitle("joint") +
  theme(legend.position = "bottom")
plot.2 <- ggplot() +
  gg(gorillas$mesh, color = vm$var1, mask = boundary) +
  csc +
  coord_equal() +
  ggtitle("SPDE") +
  theme(legend.position = "bottom")
plot.3 <- ggplot() +
  gg(gorillas$mesh, color = vm$var2, mask = boundary) +
  csc +
  coord_equal() +
  ggtitle("vegetation") +
  theme(legend.position = "bottom")

multiplot(plot.1, plot.2, plot.3, cols = 3)

# Covariance of SPDE field and vegetation

ggplot() +
  gg(gorillas$mesh, color = vm$cov)

# Correlation between field and vegetation

ggplot() +
```

```
    gg(gorillas$mesh, color = vm$cor)

  # Variance and correlation integrated over space

  vm.int <- devel.cvmeasure(pred$joint, pred$field, pred$veg,
    samplers = ipoints(gorillas$boundary, gorillas$mesh),
    mesh = gorillas$mesh
  )
  vm.int
}
```

`evaluate_A` *Compute all A-matrices*

Description

Computes the A matrices for included components for each model likelihood

Usage

```
evaluate_A(model, lhoods, inla_f)
```

Arguments

`model`	A `bru_model` object
`lhoods`	A `bru__like_list` object
`inla_f`	logical

`evaluate_index` *Compute all index values*

Description

Computes the index values matrices for included components

Usage

```
evaluate_index(model, lhoods)
```

Arguments

`model`	A `bru_model` object
`lhoods`	A `bru__like_list` object

Value

A named list of `idx_full` and `idx_inla`, named list of indices, and `inla_subset`, and `inla_subset`, a named list of logical subset specifications for extracting the `INLA::f()` compatible index subsets.

`expand_labels` *Expand labels*

Description

Expand labels

Usage

```
expand_labels(labels, expand, suffix)
```

Arguments

`labels`	character vector; original labels
`expand`	character vector; subset of labels to expand
`suffix`	character; the suffix to add to the labels selected by `expand`

Value

a vector of labels with suffix appended to the selected labels

---

`fm_CRS` *Create a coordinate reference system object*

Description

Creates either a CRS object or an inla.CRS object, describing a coordinate reference system

Usage

```
fm_CRS(
  projargs = NULL,
  doCheckCRSArgs = TRUE,
  args = NULL,
  oblique = NULL,
  SRS_string = NULL,
  ...
)

fm_wkt_predef()
```

Arguments

`projargs`	Either 1) a projection argument string suitable as input to `sp::CRS`, or 2) an existing `CRS` object, or 3) a shortcut reference string to a predefined projection; run `names(fm_wkt_predef())` for valid predefined projections.
`doCheckCRSArgs`	default TRUE, must be set to FALSE by package developers including `CRS` in an S4 class definition to avoid uncontrollable loading of the `rgdal` namespace.
`args`	An optional list of name/value pairs to add to and/or override the PROJ4 arguments in `projargs`. `name=value` is converted to `"+name=value"`, and `name=NA` is converted to `"+name"`.
`oblique`	Vector of length at most 4 of rotation angles (in degrees) for an oblique projection, all values defaulting to zero. The values indicate (longitude, latitude, orientation, orbit), as explained in the Details section below.
`SRS_string`	a WKT2 string defining the coordinate system; see `sp::CRS`. This takes precedence over `projargs`.
`...`	Additional parameters. Not currently in use.

Details

The first two elements of the `oblique` vector are the (longitude, latitude) coordinates for the oblique centre point. The third value (orientation) is a counterclockwise rotation angle for an observer looking at the centre point from outside the sphere. The fourth value is the quasi-longitude (orbit angle) for a rotation along the oblique observers equator.

Simple oblique: `oblique=c(0, 45)`

Polar: `oblique=c(0, 90)`

Quasi-transversal: `oblique=c(0, 0, 90)`

Satellite orbit viewpoint: `oblique=c(lon0-time*v1, 0, orbitangle, orbit0+time*v2)`, where `lon0` is the longitude at which a satellite orbit crosses the equator at `time=0`, when the satellite is at an angle `orbit0` further along in its orbit. The orbital angle relative to the equatorial plane is `orbitangle`, and `v1` and `v2` are the angular velocities of the planet and the satellite, respectively. Note that "forward" from the satellite's point of view is "to the right" in the projection.

When `oblique[2]` or `oblique[3]` are non-zero, the resulting projection is only correct for perfect spheres.

Value

Either an `sp::CRS` object or an `inla.CRS` object, depending on if the coordinate reference system described by the parameters can be expressed with a pure `sp::CRS` object or not.

An S3 `inla.CRS` object is a list, usually (but not necessarily) containing at least one element:

`crs`	The basic `sp::CRS` object

`fm_wkt_predef` returns a WKT2 string defining a projection

Author(s)

Finn Lindgren <`finn.lindgren@gmail.com`>

See Also

`sp::CRS()`, `fm_crs_wkt`, `fm_sp_get_crs()`, `fm_identical_CRS()`

Examples

```
if (require(rgdal)) {
  if (fm_has_PROJ6()) {
    crs1 <- fm_CRS("longlat_globe")
    crs2 <- fm_CRS("lambert_globe")
    crs3 <- fm_CRS("mollweide_norm")
    crs4 <- fm_CRS("hammer_globe")
    crs5 <- fm_CRS("sphere")
    crs6 <- fm_CRS("globe")
  } else {
    # Old definitions for pre-PROJ6:
    # Old radius-1 projections have a added "_norm" in the PROJ6 version of
    # the fm_CRS() predefined projections. They are detected and converted
    # to the new versions when RPOJ6 is available.
    crs1 <- fm_CRS("longlat") # PROJ6: longlat_norm
    crs2 <- fm_CRS("lambert") # PROJ6: lambert_norm
    crs3 <- fm_CRS("mollweide") # PROJ6: mollweide_norm
    crs4 <- fm_CRS("hammer") # PROJ6: hammer_norm
    crs5 <- fm_CRS("sphere")
    crs6 <- fm_CRS("globe")
  }
}
## Not run:
names(fm_wkt_predef())

## End(Not run)
```

`fm_has_PROJ6` *PROJ6 detection*

Description

Detect whether PROJ6 is available

Usage

```
fm_has_PROJ6()

fm_not_for_PROJ6(fun = NULL)

fm_not_for_PROJ4(fun = NULL)

fm_fallback_PROJ6(fun = NULL)

fm_requires_PROJ6(fun = NULL)
```

Arguments

`fun`	The name of the function that requires PROJ6. Default: NULL, which uses the name of the calling function.

Details

`fm_not_for_PROJ6` is called to warn about using old PROJ4 features even though PROJ6 is available

`fm_not_for_PROJ4` is called to give an error when calling methods that are only available for PROJ6

`fm_fallback_PROJ6` is called to warn about falling back to using old PROJ4 methods when a PROJ6 method hasn't been implemented

`fm_requires_PROJ6` is called to give an error when PROJ6 is required but not available

Value

For `fm_has_PROJ6`, logical; `TRUE` if PROJ6 is available, `FALSE` otherwise

Examples

```
fm_has_PROJ6()
```

`fm_spTransform` *Handle transformation of various inla objects according to coordinate reference systems of sp::CRS or INLA::inla.CRS class.*

Description

Handle transformation of various inla objects according to coordinate reference systems of sp::CRS or INLA::inla.CRS class.

Usage

```
fm_spTransform(x, ...)

## Default S3 method:
fm_spTransform(x, crs0, crs1, passthrough = FALSE, ...)

## S3 method for class 'SpatialPoints'
fm_spTransform(x, CRSobj, passthrough = FALSE, ...)

## S3 method for class 'SpatialPointsDataFrame'
fm_spTransform(x, CRSobj, passthrough = FALSE, ...)

## S3 method for class 'inla.mesh.lattice'
fm_spTransform(x, CRSobj, passthrough = FALSE, ...)
```

```
## S3 method for class 'inla.mesh.segment'
fm_spTransform(x, CRSobj, passthrough = FALSE, ...)

## S3 method for class 'inla.mesh'
fm_spTransform(x, CRSobj, passthrough = FALSE, ...)
```

Arguments

`x`	The object that should be transformed from it's current CRS to a new CRS
`...`	Potential additional arguments
`crs0`	The source sp::CRS or inla.CRS object
`crs1`	The target sp::CRS or inla.CRS object
`passthrough`	Default is FALSE. Setting to TRUE allows objects with no CRS information to be passed through without transformation.
`CRSobj`	The target sp::CRS or inla.CRS object

Details

The default method handles low level transformation of raw coordinates.

See Also

`fm_CRS()`

`fm_sp_get_crs` *Extract CRS information*

Description

Wrapper for CRS(projargs) (PROJ4) and CRS(wkt) for `sp::Spatial` objects.

Usage

```
fm_sp_get_crs(x)
```

Arguments

`x`	A `sp::Spatial` object

Details

This function is a convenience method to workaround PROJ4/PROJ6 differences, and the lack of a crs extraction method for Spatial objects.

Value

A `CRS` object, or NULL if no valid CRS identified

Author(s)

Finn Lindgren <`finn.lindgren@gmail.com`>

Examples

```
## Not run:
if (interactive()) {
  s <- sp::SpatialPoints(matrix(1:6, 3, 2), proj4string = fm_CRS("sphere"))
  fm_sp_get_crs(s)
}

## End(Not run)
```

`fm_wkt_as_wkt_tree` *Internal WKT handling*

Description

Conversion between WKT and a tree representation

Usage

```
fm_wkt_as_wkt_tree(x, ...)

fm_wkt_tree_as_wkt(x, pretty = FALSE, ...)

fm_wkt_tree_get_item(x, item, duplicate = 1)

fm_wkt_tree_set_item(x, item_tree, duplicate = 1)
```

Arguments

`x`	A WKT2 string, or a `wkt_tree` list structure
`...`	Unused
`pretty`	logical; If TRUE, use pretty formatting. Default: FALSE
`item`	character vector with item labels identifying a parameter item entry.
`duplicate`	For items that have more than one match, `duplicate` indicates the index number of the desired version. Default: 1
`item_tree`	An item tree identifying a parameter item entry

`fm_wkt_is_geocent` *Handling CRS/WKT*

Description

Get and set CRS object or WKT string properties.

Usage

```
fm_wkt_is_geocent(wkt)

fm_crs_is_geocent(crs)

fm_wkt_get_ellipsoid_radius(wkt)

fm_crs_get_ellipsoid_radius(crs)

fm_wkt_set_ellipsoid_radius(wkt, radius)

fm_crs_set_ellipsoid_radius(crs, radius)

fm_wkt_unit_params()

fm_wkt_get_lengthunit(wkt)

fm_wkt_set_lengthunit(wkt, unit, params = NULL)

fm_crs_get_wkt(crs)

fm_crs_get_lengthunit(crs)

fm_crs_set_lengthunit(crs, unit, params = NULL)
```

Arguments

`wkt`	A WKT2 character string
`crs`	A `sp::CRS` or `inla.CRS` object
`radius`	numeric; The new radius value
`unit`	character, name of a unit. Supported names are "metre", "kilometre", and the aliases "meter", "m", International metre", "kilometer", and "km", as defined by `fm_wkt_unit_params` or the `params` argument. (For legacy PROJ4 use, only "m" and "km" are supported)
`params`	Length unit definitions, in the list format produced by `fm_wkt_unit_params()`, Default: NULL, which invokes `fm_wkt_unit_params()`

Value

For `fm_wkt_unit_params`, a list of named unit definitions

For `fm_wkt_get_lengthunit`, a list of length units used in the wkt string, excluding the ellipsoid radius unit.

For `fm_wkt_set_lengthunit`, a WKT2 string with altered length units. Note that the length unit for the ellipsoid radius is unchanged.

For `fm_crs_get_wkt`, WKT2 string.

For `fm_crs_get_lengthunit`, a list of length units used in the wkt string, excluding the ellipsoid radius unit. (For legacy PROJ4 code, the raw units from the proj4string are returned, if present.)

For `fm_crs_set_lengthunit`, a `sp::CRS` object with altered length units. Note that the length unit for the ellipsoid radius is unchanged.

Author(s)

Finn Lindgren <`finn.lindgren@gmail.com`>

See Also

`fm_sp_get_crs()`

Examples

```
## Not run:
if (fm_has_PROJ6()) {
  c1 <- fm_CRS("globe")
  fm_crs_get_lengthunit(c1)
  c2 <- fm_crs_set_lengthunit(c1, "km")
  fm_crs_get_lengthunit(c2)
}

## End(Not run)
```

`generate` *Generate samples from fitted bru models*

Description

Generic function for sampling for fitted models. The function invokes particular methods which depend on the class of the first argument.

Takes a fitted `bru` object produced by the function `bru()` and produces samples given a new set of values for the model covariates or the original values used for the model fit. The samples can be based on any R expression that is valid given these values/covariates and the joint posterior of the estimated random effects.

Usage

```
generate(object, ...)

## S3 method for class 'bru'
generate(
  object,
  data = NULL,
  formula = NULL,
  n.samples = 100,
  seed = 0L,
  num.threads = NULL,
  include = NULL,
  exclude = NULL,
  ...
)
```

Arguments

`object`	A `bru` object obtained by calling `bru()`.
`...`	additional, unused arguments.
`data`	A data.frame or SpatialPointsDataFrame of covariates needed for sampling.
`formula`	A formula where the right hand side defines an R expression to evaluate for each generated sample. If `NULL`, the latent and hyperparameter states are returned as named list elements. See Details for more information.
`n.samples`	Integer setting the number of samples to draw in order to calculate the posterior statistics. The default, 100, is rather low but provides a quick approximate result.
`seed`	Random number generator seed passed on to `INLA::inla.posterior.sample`
`num.threads`	Specification of desired number of threads for parallel computations. Default NULL, leaves it up to INLA. When seed != 0, overridden to "1:1"
`include`	Character vector of component labels that are needed by the predictor expression; Default: NULL (include all components that are not explicitly excluded)
`exclude`	Character vector of component labels that are not used by the predictor expression. The exclusion list is applied to the list as determined by the `include` parameter; Default: NULL (do not remove any components from the inclusion list)

Details

In addition to the component names (that give the effect of each component evaluated for the input data), the suffix `_latent` variable name can be used to directly access the latent state for a component, and the suffix function `_eval` can be used to evaluate a component at other input values than the expressions defined in the component definition itself, e.g. `field_eval(cbind(x, y))` for a component that was defined with `field(coordinates, ...)` (see also `component_eval()`).

For "iid" models with `mapper = bru_mapper_index(n)`, `rnorm()` is used to generate new realisations for indices greater than `n`.

Value

The form of the value returned by gg depends on the class of its argument. See the documentation of the particular methods for details of what is produced by that method.

List of generated samples

See Also

predict.bru

Examples

```
if (bru_safe_inla(multicore = FALSE)) {

  # Generate data for a simple linear model

  input.df <- data.frame(x = cos(1:10))
  input.df <- within(input.df, y <- 5 + 2 * cos(1:10) + rnorm(10, mean = 0, sd = 0.1))

  # Fit the model

  fit <- bru(y ~ xeff(main = x, model = "linear"),
    family = "gaussian", data = input.df
  )
  summary(fit)

  # Generate samples for some predefined x

  df <- data.frame(x = seq(-4, 4, by = 0.1))
  smp <- generate(fit, df, ~ xeff + Intercept, n.samples = 10)

  # Plot the resulting realizations

  plot(df$x, smp[, 1], type = "l")
  for (k in 2:ncol(smp)) points(df$x, smp[, k], type = "l")

  # We can also draw samples form the joint posterior

  df <- data.frame(x = 1)
  smp <- generate(fit, df, ~ data.frame(xeff, Intercept), n.samples = 10)
  smp[[1]]

  # ... and plot them
  if (require(ggplot2, quietly = TRUE)) {
    plot(do.call(rbind, smp))
  }
}


if (bru_safe_inla(multicore = FALSE)) {
```

```
  # Generate data for a simple linear model

  input.df <- data.frame(x = cos(1:10))
  input.df <- within(input.df, y <- 5 + 2 * cos(1:10) + rnorm(10, mean = 0, sd = 0.1))

  # Fit the model

  fit <- bru(y ~ xeff(main = x, model = "linear"),
    family = "gaussian", data = input.df
  )
  summary(fit)

  # Generate samples for some predefined x

  df <- data.frame(x = seq(-4, 4, by = 0.1))
  smp <- generate(fit, df, ~ xeff + Intercept, n.samples = 10)

  # Plot the resulting realizations

  plot(df$x, smp[, 1], type = "l")
  for (k in 2:ncol(smp)) points(df$x, smp[, k], type = "l")

  # We can also draw samples form the joint posterior

  df <- data.frame(x = 1)
  smp <- generate(fit, df, ~ data.frame(xeff, Intercept), n.samples = 10)
  smp[[1]]

  # ... and plot them
  if (require(ggplot2, quietly = TRUE)) {
    plot(do.call(rbind, smp))
  }
}
```

---

gg *ggplot2 geomes for inlabru related objects*

Description

gg is a generic function for generating geomes from various kinds of spatial objects, e.g. Spatial* data, meshes, Raster objects and inla/inlabru predictions. The function invokes particular methods which depend on the class of the first argument.

Usage

```
gg(data, ...)
```

Arguments

`data`	an object for which to generate a geom.
`...`	Arguments passed on to the geom method.

Value

The form of the value returned by gg depends on the class of its argument. See the documentation of the particular methods for details of what is produced by that method.

See Also

Other geomes for inla and inlabru predictions: `gg.data.frame()`, `gg.matrix()`, `gg.prediction()`, `gm()`

Other geomes for spatial data: `gg.SpatialGridDataFrame()`, `gg.SpatialLines()`, `gg.SpatialPixelsDataFrame()`, `gg.SpatialPixels()`, `gg.SpatialPoints()`, `gg.SpatialPolygons()`, `gm()`

Other geomes for meshes: `gg.inla.mesh.1d()`, `gg.inla.mesh()`, `gm()`

Other geomes for Raster data: `gg.RasterLayer()`, `gm()`

Examples

```
if (require("ggplot2", quietly = TRUE) &&
  require(ggpolypath, quietly = TRUE)) {
  # Load Gorilla data

  data(gorillas, package = "inlabru")

  # Invoke ggplot and add geomes for the Gorilla nests and the survey boundary

  ggplot() +
    gg(gorillas$boundary) +
    gg(gorillas$nests)
}
```

`gg.data.frame` *Geom for data.frame*

Description

This geom constructor will simply call gg.prediction for the data provided.

Usage

```
## S3 method for class 'data.frame'
gg(...)
```

Arguments

`...`	Arguments passed on to `gg.prediction()`.

Details

Requires the `ggplot2` package.

Value

Concatenation of a `geom_line` value and optionally a `geom_ribbon` value.

See Also

Other geomes for inla and inlabru predictions: `gg.matrix()`, `gg.prediction()`, `gg()`, `gm()`

Examples

```
if (bru_safe_inla() && require(ggplot2, quietly = TRUE)) {
  # Generate some data

  input.df <- data.frame(x = cos(1:10))
  input.df <- within(input.df, y <- 5 + 2 * cos(1:10) + rnorm(10, mean = 0, sd = 0.1))

  # Fit a model with fixed effect 'x' and intercept 'Intercept'

  fit <- bru(y ~ x, family = "gaussian", data = input.df)

  # Predict posterior statistics of 'x'

  xpost <- predict(fit, data = NULL, formula = ~x_latent)

  # The statistics include mean, standard deviation, the 2.5% quantile, the median,
  # the 97.5% quantile, minimum and maximum sample drawn from the posterior as well as
  # the coefficient of variation and the variance.

  xpost

  # For a single variable like 'x' the default plotting method invoked by gg() will
  # show these statisics in a fashion similar to a box plot:
  ggplot() +
    gg(xpost)


  # The predict function can also be used to simulataneously estimate posteriors
  # of multiple variables:

  xipost <- predict(fit,
    data = NULL,
    formula = ~ c(
      Intercept = Intercept_latent,
      x = x_latent
    )
  )
  xipost
```

```
  # If we still want a plot in the previous style we have to set the bar parameter to TRUE

  p1 <- ggplot() +
    gg(xipost, bar = TRUE)
  p1

  # Note that gg also understands the posterior estimates generated while running INLA

  p2 <- ggplot() +
    gg(fit$summary.fixed, bar = TRUE)
  multiplot(p1, p2)

 # By default, if the prediction has more than one row, gg will plot the column 'mean' against
  # the row index. This is for instance usefuul for predicting and plotting function
  # but not very meaningful given the above example:

  ggplot() +
    gg(xipost)

  # For ease of use we can also type

  plot(xipost)

 # This type of plot will show a ribbon around the mean, which viszualizes the upper and lower
 # quantiles mentioned above (2.5 and 97.5%). Plotting the ribbon can be turned of using the
  # \code{ribbon} parameter

  ggplot() +
    gg(xipost, ribbon = FALSE)

  # Much like the other geomes produced by gg we can adjust the plot using ggplot2 style
  # commands, for instance

  ggplot() +
    gg(xipost) +
    gg(xipost, mapping = aes(y = median), ribbon = FALSE, color = "red")
}
```

`gg.inla.mesh` *Geom for inla.mesh objects*

Description

This function extracts the graph of an inla.mesh object and uses `geom_line` to visualize the graph's edges. Alternatively, if the `color` argument is provided, interpolates the colors across for a set of SpatialPixels covering the mesh area and calls `gg.SpatialPixelsDataFrame()` to plot the interpolation. Requires the `ggplot2` package.

Usage

```
## S3 method for class 'inla.mesh'
gg(
  data,
  color = NULL,
  alpha = NULL,
  edge.color = "grey",
  interior = TRUE,
  int.color = "blue",
  exterior = TRUE,
  ext.color = "black",
  crs = NULL,
  mask = NULL,
  nx = 500,
  ny = 500,
  ...
)
```

Arguments

`data`	An `INLA::inla.mesh` object.
`color`	A vector of scalar values to fill the mesh with colors. The length of the vector mus correspond to the number of mesh vertices. The alternative name `colour` is also recognised.
`alpha`	A vector of scalar values setting the alpha value of the colors provided.
`edge.color`	Color of the mesh edges.
`interior`	If TRUE, plot the interior boundaries of the mesh.
`int.color`	Color used to plot the interior boundaries.
`exterior`	If TRUE, plot the exterior boundaries of the mesh.
`ext.color`	Color used to plot the interior boundaries.
`crs`	A CRS object defining the coordinate system to project the mesh to before plotting.
`mask`	A SpatialPolygon defining the region that is plotted.
`nx`	Number of pixels in x direction (when plotting using the color parameter).
`ny`	Number of pixels in y direction (when plotting using the color parameter).
`...`	ignored arguments (S3 generic compatibility).

Value

`geom_line` return values or, if the color argument is used, the values of `gg.SpatialPixelsDataFrame()`.

See Also

Other geomes for meshes: `gg.inla.mesh.1d()`, `gg()`, `gm()`

Examples

```
if (bru_safe_inla() &&
    require(ggplot2, quietly = TRUE) &&
    require(ggpolypath, quietly = TRUE)) {

  # Load Gorilla data
  data("gorillas", package = "inlabru")

  # Plot mesh using default edge colors

  ggplot() +
    gg(gorillas$mesh)

  # Don't show interior and exterior boundaries

  ggplot() +
    gg(gorillas$mesh, interior = FALSE, exterior = FALSE)

  # Change the edge colors

  ggplot() +
    gg(gorillas$mesh,
      edge.color = "green",
      int.color = "black",
      ext.color = "blue"
    )

  # Use the x-coordinate of the vertices to colorize the triangles and
  # mask the plotted area by the survey boundary, i.e. only plot the inside

  xcoord <- gorillas$mesh$loc[, 1]
  ggplot() +
    gg(gorillas$mesh, color = (xcoord - 580), mask = gorillas$boundary) +
    gg(gorillas$boundary)
}
```

`gg.inla.mesh.1d` *Geom for inla.mesh.1d objects*

Description

This function generates a `geom_point` object showing the knots (vertices) of a 1D mesh. Requires the `ggplot2` package.

Usage

```
## S3 method for class 'inla.mesh.1d'
```

```
gg(
  data,
  mapping = ggplot2::aes(.data[["x"]], .data[["y"]]),
  y = 0,
  shape = 4,
  ...
)
```

Arguments

`data`	An inla.mesh.1d object.
`mapping`	aesthetic mappings created by `aes`. These are passed on to `geom_point`.
`y`	Single or vector numeric defining the y-coordinates of the mesh knots to plot.
`shape`	Shape of the knot markers.
`...`	parameters passed on to `geom_point`.

Value

An object generated by `geom_point`.

See Also

Other geomes for meshes: `gg.inla.mesh()`, `gg()`, `gm()`

Examples

```
# Some features use the INLA package.
if (require("INLA", quietly = TRUE) &&
  require("ggplot2", quietly = TRUE)) {

  # Create a 1D mesh

  mesh <- inla.mesh.1d(seq(0, 10, by = 0.5))

  # Plot it

  ggplot() +
    gg(mesh)

  # Plot it using a different shape and size for the mesh nodes

  ggplot() +
    gg(mesh, shape = "|", size = 5)
}
```

`gg.matrix` *Geom for matrix*

Description

Creates a tile geom for plotting a matrix

Usage

```
## S3 method for class 'matrix'
gg(data, mapping = NULL, ...)
```

Arguments

`data`	A `matrix` object.
`mapping`	a set of aesthetic mappings created by `aes`. These are passed on to `geom_tile`.
`...`	Arguments passed on to `geom_tile`.

Details

Requires the `ggplot2` package.

Value

A `geom_tile` with reversed y scale.

See Also

Other geomes for inla and inlabru predictions: `gg.data.frame()`, `gg.prediction()`, `gg()`, `gm()`

Examples

```
if (require("ggplot2", quietly = TRUE)) {
  A <- matrix(runif(100), nrow = 10)
  ggplot() +
    gg(A)
}
```

`gg.prediction` *Geom for predictions*

Description

This geom serves to visualize `prediction` objects which usually results from a call to `predict.bru()`. Predictions objects provide summary statistics (mean, median, sd, ...) for one or more random variables. For single variables (or if requested so by setting `bar = TRUE`), a boxplot-style geom is constructed to show the statistics. For multivariate predictions the mean of each variable (y-axis) is plotted agains the row number of the varriable in the prediction data frame (x-axis) using `geom_line`. In addition, a `geom_ribbon` is used to show the confidence interval.

Note: `gg.prediction` also understands the format of INLA-style posterior summaries, e.g. `fit$summary.fixed` for an inla object `fit`

Requires the `ggplot2` package.

Usage

```
## S3 method for class 'prediction'
gg(data, mapping = NULL, ribbon = TRUE, alpha = 0.3, bar = FALSE, ...)
```

Arguments

`data`	A prediction object, usually the result of a `predict.bru()` call.
`mapping`	a set of aesthetic mappings created by `aes`. These are passed on to `geom_line`.
`ribbon`	If TRUE, plot a ribbon around the line based on the smalles and largest quantiles present in the data, found by matching names starting with `q` and followed by a numerical value. `inla()`-style `numeric+"quant"` names are converted to inlabru style before matching.
`alpha`	The ribbons numeric alpha (transparency) level in `[0,1]`.
`bar`	If TRUE plot boxplot-style summary for each variable.
`...`	Arguments passed on to `geom_line`.

Value

Concatenation of a `geom_line` value and optionally a `geom_ribbon` value.

See Also

Other geomes for inla and inlabru predictions: `gg.data.frame()`, `gg.matrix()`, `gg()`, `gm()`

Examples

```
if (bru_safe_inla() && require(ggplot2, quietly = TRUE)) {
  # Generate some data

  input.df <- data.frame(x = cos(1:10))
  input.df <- within(input.df, y <- 5 + 2 * cos(1:10) + rnorm(10, mean = 0, sd = 0.1))

  # Fit a model with fixed effect 'x' and intercept 'Intercept'

  fit <- bru(y ~ x, family = "gaussian", data = input.df)

  # Predict posterior statistics of 'x'

  xpost <- predict(fit, data = NULL, formula = ~x_latent)

  # The statistics include mean, standard deviation, the 2.5% quantile, the median,
  # the 97.5% quantile, minimum and maximum sample drawn from the posterior as well as
  # the coefficient of variation and the variance.

  xpost

  # For a single variable like 'x' the default plotting method invoked by gg() will
  # show these statisics in a fashion similar to a box plot:
  ggplot() +
    gg(xpost)


  # The predict function can also be used to simulataneously estimate posteriors
  # of multiple variables:

  xipost <- predict(fit,
    data = NULL,
    formula = ~ c(
      Intercept = Intercept_latent,
      x = x_latent
    )
  )
  xipost

 # If we still want a plot in the previous style we have to set the bar parameter to TRUE

  p1 <- ggplot() +
    gg(xipost, bar = TRUE)
  p1

  # Note that gg also understands the posterior estimates generated while running INLA

  p2 <- ggplot() +
    gg(fit$summary.fixed, bar = TRUE)
  multiplot(p1, p2)
```

```
# By default, if the prediction has more than one row, gg will plot the column 'mean' against
 # the row index. This is for instance usefuul for predicting and plotting function
 # but not very meaningful given the above example:

 ggplot() +
   gg(xipost)

 # For ease of use we can also type

 plot(xipost)

# This type of plot will show a ribbon around the mean, which viszualizes the upper and lower
# quantiles mentioned above (2.5 and 97.5%). Plotting the ribbon can be turned of using the
 # \code{ribbon} parameter

 ggplot() +
   gg(xipost, ribbon = FALSE)

 # Much like the other geomes produced by gg we can adjust the plot using ggplot2 style
 # commands, for instance

 ggplot() +
   gg(xipost) +
   gg(xipost, mapping = aes(y = median), ribbon = FALSE, color = "red")
}
```

`gg.RasterLayer` *Geom for RasterLayer objects*

Description

This function takes a RasterLayer object, converts it into a `SpatialPixelsDataFrame` and uses `geom_tile` to plot the data.

Usage

```
## S3 method for class 'RasterLayer'
gg(
  data,
 mapping = ggplot2::aes(x = .data[["x"]], y = .data[["y"]], fill = .data[["layer"]]),
  ...
)
```

Arguments

`data`	A RasterLayer object.
`mapping`	aesthetic mappings created by `aes`. These are passed on to `geom_tile`.
`...`	Arguments passed on to `geom_tile`.

Details

This function requires the `raster` and `ggplot2` packages.

Value

An object returned by `geom_tile`

See Also

Other geomes for Raster data: `gg()`, `gm()`

Examples

```
## Not run:
# Some features require the raster and spatstat.data packages.
if (require("spatstat.data", quietly = TRUE) &&
  require("raster", quietly = TRUE) &&
  require("ggplot2", quietly = TRUE)) {

  # Load Gorilla data
  data("gorillas", package = "spatstat.data")

  # Convert elevation covariate to RasterLayer

  elev <- as(gorillas.extra$elevation, "RasterLayer")

  # Plot the elevation

  ggplot() +
    gg(elev)
}

## End(Not run)
```

`gg.SpatialGridDataFrame`

Geom for SpatialGridDataFrame objects

Description

Coerces input `SpatialGridDataFrame` to `SpatialPixelsDataFrame` and calls `gg.SpatialPixelsDataFrame()` to plot it. Requires the `ggplot2` package.

Usage

```
## S3 method for class 'SpatialGridDataFrame'
gg(data, ...)
```

Arguments

`data`	A SpatialGridDataFrame object.
`...`	Arguments passed on to `gg.SpatialPixelsDataFrame()`.

Value

A `geom_tile` value.

See Also

Other geomes for spatial data: `gg.SpatialLines()`, `gg.SpatialPixelsDataFrame()`, `gg.SpatialPixels()`, `gg.SpatialPoints()`, `gg.SpatialPolygons()`, `gg()`, `gm()`

Examples

```
if (require(ggplot2, quietly = TRUE) &&
    require(ggpolypath, quietly = TRUE)) {
  # Load Gorilla data

  data("gorillas", package = "inlabru")

  # Plot Gorilla elevation covariate provided as SpatialPixelsDataFrame.
  # The same syntax applies to SpatialGridDataFrame objects.

  ggplot() +
    gg(gorillas$gcov$elevation)

  # Add Gorilla survey boundary and nest sightings

  ggplot() +
    gg(gorillas$gcov$elevation) +
    gg(gorillas$boundary) +
    gg(gorillas$nests)

  # Load pantropical dolphin data

  data("mexdolphin")

  # Plot the pantropiical survey boundary, ship transects and dolphin sightings

  ggplot() +
    gg(mexdolphin$ppoly) + # survey boundary as SpatialPolygon
    gg(mexdolphin$samplers) + # ship transects as SpatialLines
    gg(mexdolphin$points) # dolphin sightings as SpatialPoints

  # Change color

  ggplot() +
    gg(mexdolphin$ppoly, color = "green") + # survey boundary as SpatialPolygon
    gg(mexdolphin$samplers, color = "red") + # ship transects as SpatialLines
```

```
    gg(mexdolphin$points, color = "blue") # dolphin sightings as SpatialPoints


  # Visualize data annotations: line width by segment number

  names(mexdolphin$samplers) # 'seg' holds the segment number
  ggplot() +
    gg(mexdolphin$samplers, aes(color = seg))

  # Visualize data annotations: point size by dolphin group size

  names(mexdolphin$points) # 'size' holds the group size
  ggplot() +
    gg(mexdolphin$points, aes(size = size))
}
```

`gg.SpatialLines` *Geom for SpatialLines objects*

Description

Extracts start and end points of the lines and calls `geom_segment` to plot lines between them. Requires the `ggplot2` package.

Usage

```
## S3 method for class 'SpatialLines'
gg(data, mapping = NULL, crs = NULL, ...)
```

Arguments

`data`	A `SpatialLines` or `SpatialLinesDataFrame` object.
`mapping`	Aesthetic mappings created by `ggplot2::aes` or `ggplot2::aes_` used to update the default mapping. The default mapping is `ggplot2::aes(x = .data[[coordnames(data)[1]]], y = .data[[coordnames(data)[2]]], xend = .data[[paste0("end.", coordnames(data)[1])]], yend = .data[[paste0("end.", coordnames(data)[2])]])`.
`crs`	A `CRS` object defining the coordinate system to project the data to before plotting.
`...`	Arguments passed on to `ggplot2::geom_segment`.

Value

A ‘geom_segment“ return value.

See Also

Other geomes for spatial data: `gg.SpatialGridDataFrame()`, `gg.SpatialPixelsDataFrame()`, `gg.SpatialPixels()`, `gg.SpatialPoints()`, `gg.SpatialPolygons()`, `gg()`, `gm()`

Examples

```
if (require(ggplot2, quietly = TRUE) &&
    require(ggpolypath, quietly = TRUE)) {
  # Load Gorilla data

  data("gorillas", package = "inlabru")

  # Plot Gorilla elevation covariate provided as SpatialPixelsDataFrame.
  # The same syntax applies to SpatialGridDataFrame objects.

  ggplot() +
    gg(gorillas$gcov$elevation)

  # Add Gorilla survey boundary and nest sightings

  ggplot() +
    gg(gorillas$gcov$elevation) +
    gg(gorillas$boundary) +
    gg(gorillas$nests)

  # Load pantropical dolphin data

  data("mexdolphin")

  # Plot the pantropiical survey boundary, ship transects and dolphin sightings

  ggplot() +
    gg(mexdolphin$ppoly) + # survey boundary as SpatialPolygon
    gg(mexdolphin$samplers) + # ship transects as SpatialLines
    gg(mexdolphin$points) # dolphin sightings as SpatialPoints

  # Change color

  ggplot() +
    gg(mexdolphin$ppoly, color = "green") + # survey boundary as SpatialPolygon
    gg(mexdolphin$samplers, color = "red") + # ship transects as SpatialLines
    gg(mexdolphin$points, color = "blue") # dolphin sightings as SpatialPoints


  # Visualize data annotations: line width by segment number

  names(mexdolphin$samplers) # 'seg' holds the segment number
  ggplot() +
    gg(mexdolphin$samplers, aes(color = seg))

  # Visualize data annotations: point size by dolphin group size

  names(mexdolphin$points) # 'size' holds the group size
  ggplot() +
    gg(mexdolphin$points, aes(size = size))
}
```

`gg.SpatialPixels` *Geom for SpatialPixels objects*

Description

Uses `geom_point` to plot the pixel centers. Requires the `ggplot2` package.

Usage

```
## S3 method for class 'SpatialPixels'
gg(data, ...)
```

Arguments

`data`	A SpatialPixels object.
`...`	Arguments passed on to `geom_tile`.

Value

A `geom_tile` return value.

See Also

Other geomes for spatial data: `gg.SpatialGridDataFrame()`, `gg.SpatialLines()`, `gg.SpatialPixelsDataFrame()`, `gg.SpatialPoints()`, `gg.SpatialPolygons()`, `gg()`, `gm()`

Examples

```
if (require("ggplot2", quietly = TRUE)) {
  # Load Gorilla data

  data(gorillas, package = "inlabru")

  # Turn elevation covariate into SpatialPixels
  pxl <- SpatialPixels(SpatialPoints(gorillas$gcov$elevation))

  # Plot the pixel centers
  ggplot() +
    gg(pxl, size = 0.1)
}
```

`gg.SpatialPixelsDataFrame` *Geom for SpatialPixelsDataFrame objects*

Description

Coerces input SpatialPixelsDataFrame to data.frame and uses `geom_tile` to plot it. Requires the `ggplot2` package.

Usage

```
## S3 method for class 'SpatialPixelsDataFrame'
gg(data, mapping = NULL, crs = NULL, mask = NULL, ...)
```

Arguments

`data`	A SpatialPixelsDataFrame object.
`mapping`	Aesthetic mappings created by `aes` used to update the default mapping. The default mapping is `ggplot2::aes(x = .data[[coordnames(data)[1]]], y = .data[[coordnames(data)[2]]], fill = .data[[names(data)[[1]]]])`.
`crs`	A CRS object defining the coordinate system to project the data to before plotting.
`mask`	A SpatialPolygon defining the region that is plotted.
`...`	Arguments passed on to `geom_tile`.

Value

A `geom_tile` return value.

See Also

Other geomes for spatial data: `gg.SpatialGridDataFrame()`, `gg.SpatialLines()`, `gg.SpatialPixels()`, `gg.SpatialPoints()`, `gg.SpatialPolygons()`, `gg()`, `gm()`

Examples

```
if (require(ggplot2, quietly = TRUE) &&
    require(ggpolypath, quietly = TRUE)) {
  # Load Gorilla data

  data("gorillas", package = "inlabru")

  # Plot Gorilla elevation covariate provided as SpatialPixelsDataFrame.
  # The same syntax applies to SpatialGridDataFrame objects.

  ggplot() +
```

```
    gg(gorillas$gcov$elevation)

  # Add Gorilla survey boundary and nest sightings

  ggplot() +
    gg(gorillas$gcov$elevation) +
    gg(gorillas$boundary) +
    gg(gorillas$nests)

  # Load pantropical dolphin data

  data("mexdolphin")

  # Plot the pantropiical survey boundary, ship transects and dolphin sightings

  ggplot() +
    gg(mexdolphin$ppoly) + # survey boundary as SpatialPolygon
    gg(mexdolphin$samplers) + # ship transects as SpatialLines
    gg(mexdolphin$points) # dolphin sightings as SpatialPoints

  # Change color

  ggplot() +
    gg(mexdolphin$ppoly, color = "green") + # survey boundary as SpatialPolygon
    gg(mexdolphin$samplers, color = "red") + # ship transects as SpatialLines
    gg(mexdolphin$points, color = "blue") # dolphin sightings as SpatialPoints


  # Visualize data annotations: line width by segment number

  names(mexdolphin$samplers) # 'seg' holds the segment number
  ggplot() +
    gg(mexdolphin$samplers, aes(color = seg))

  # Visualize data annotations: point size by dolphin group size

  names(mexdolphin$points) # 'size' holds the group size
  ggplot() +
    gg(mexdolphin$points, aes(size = size))
}
```

`gg.SpatialPoints` *Geom for SpatialPoints objects*

Description

This function coerces the `SpatialPoints` into a `data.frame` and uses `geom_point` to plot the points. Requires the `ggplot2` package.

Usage

```
## S3 method for class 'SpatialPoints'
gg(data, mapping = NULL, crs = NULL, ...)
```

Arguments

`data`	A SpatialPoints object.
`mapping`	Aesthetic mappings created by `aes` used to update the default mapping. The default mapping is `ggplot2::aes(x = .data[[coordnames(data)[1]]], y = .data[[coordnames(data)[2]]])`.
`crs`	A CRS object defining the coordinate system to project the data to before plotting.
`...`	Arguments passed on to `geom_point`.

Value

A `geom_point` return value

See Also

Other geomes for spatial data: `gg.SpatialGridDataFrame()`, `gg.SpatialLines()`, `gg.SpatialPixelsDataFrame()`, `gg.SpatialPixels()`, `gg.SpatialPolygons()`, `gg()`, `gm()`

Examples

```
if (require(ggplot2, quietly = TRUE) &&
    require(ggpolypath, quietly = TRUE)) {
  # Load Gorilla data

  data("gorillas", package = "inlabru")

  # Plot Gorilla elevation covariate provided as SpatialPixelsDataFrame.
  # The same syntax applies to SpatialGridDataFrame objects.

  ggplot() +
    gg(gorillas$gcov$elevation)

  # Add Gorilla survey boundary and nest sightings

  ggplot() +
    gg(gorillas$gcov$elevation) +
    gg(gorillas$boundary) +
    gg(gorillas$nests)

  # Load pantropical dolphin data

  data("mexdolphin")

  # Plot the pantropiical survey boundary, ship transects and dolphin sightings
```

```
    ggplot() +
      gg(mexdolphin$ppoly) + # survey boundary as SpatialPolygon
      gg(mexdolphin$samplers) + # ship transects as SpatialLines
      gg(mexdolphin$points) # dolphin sightings as SpatialPoints

    # Change color

    ggplot() +
      gg(mexdolphin$ppoly, color = "green") + # survey boundary as SpatialPolygon
      gg(mexdolphin$samplers, color = "red") + # ship transects as SpatialLines
      gg(mexdolphin$points, color = "blue") # dolphin sightings as SpatialPoints


    # Visualize data annotations: line width by segment number

    names(mexdolphin$samplers) # 'seg' holds the segment number
    ggplot() +
      gg(mexdolphin$samplers, aes(color = seg))

    # Visualize data annotations: point size by dolphin group size

    names(mexdolphin$points) # 'size' holds the group size
    ggplot() +
      gg(mexdolphin$points, aes(size = size))
  }
```

`gg.SpatialPolygons` *Geom for SpatialPolygons objects*

Description

Uses the `ggplot2::fortify()` function to turn the `SpatialPolygons` objects into a `data.frame`. Then calls `geom_polygon` to plot the polygons. Requires the `ggplot2` package.

Usage

```
## S3 method for class 'SpatialPolygons'
gg(data, mapping = NULL, crs = NULL, ...)
```

Arguments

`data`	A `SpatialPolygons` or `SpatialPolygonsDataFrame` object.
`mapping`	Aesthetic mappings created by `aes` used to update the default mapping. The default mapping is `ggplot2::aes(x = long, y = lat, group = group)`.
`crs`	A `CRS` object defining the coordinate system to project the data to before plotting.
`...`	Arguments passed on to `geom_polypath`. Unless specified by the user, the arguments `colour = "black"` (polygon colour) and `alpha = 0.2` (Alpha level for polygon filling).

Details

Requires the `ggpolypath` package to ensure proper plotting, since the `ggplot::geom_polygon` function doesn't always handle geometries with holes properly.

Value

A `ggpolypath::geom_polypath` object.

See Also

Other geomes for spatial data: `gg.SpatialGridDataFrame()`, `gg.SpatialLines()`, `gg.SpatialPixelsDataFrame()`, `gg.SpatialPixels()`, `gg.SpatialPoints()`, `gg()`, `gm()`

Examples

```
if (require(ggplot2, quietly = TRUE) &&
    require(ggpolypath, quietly = TRUE)) {
  # Load Gorilla data

  data("gorillas", package = "inlabru")

  # Plot Gorilla elevation covariate provided as SpatialPixelsDataFrame.
  # The same syntax applies to SpatialGridDataFrame objects.

  ggplot() +
    gg(gorillas$gcov$elevation)

  # Add Gorilla survey boundary and nest sightings

  ggplot() +
    gg(gorillas$gcov$elevation) +
    gg(gorillas$boundary) +
    gg(gorillas$nests)

  # Load pantropical dolphin data

  data("mexdolphin")

  # Plot the pantropiical survey boundary, ship transects and dolphin sightings

  ggplot() +
    gg(mexdolphin$ppoly) + # survey boundary as SpatialPolygon
    gg(mexdolphin$samplers) + # ship transects as SpatialLines
    gg(mexdolphin$points) # dolphin sightings as SpatialPoints

  # Change color

  ggplot() +
    gg(mexdolphin$ppoly, color = "green") + # survey boundary as SpatialPolygon
    gg(mexdolphin$samplers, color = "red") + # ship transects as SpatialLines
    gg(mexdolphin$points, color = "blue") # dolphin sightings as SpatialPoints
```

```
    # Visualize data annotations: line width by segment number

    names(mexdolphin$samplers) # 'seg' holds the segment number
    ggplot() +
      gg(mexdolphin$samplers, aes(color = seg))

    # Visualize data annotations: point size by dolphin group size

    names(mexdolphin$points) # 'size' holds the group size
    ggplot() +
      gg(mexdolphin$points, aes(size = size))
  }
```

---

globe *Plot a globe using rgl*

Description

Creates a textured sphere and lon/lat coordinate annotations.

Usage

```
globe(
  R = 1,
  R.grid = 1.05,
  specular = "black",
  axes = FALSE,
  box = FALSE,
  xlab = "",
  ylab = "",
  zlab = ""
)
```

Arguments

`R`	Radius of the globe
`R.grid`	Radius of the annotation sphere.
`specular`	Light color of specular effect.
`axes`	If TRUE, plot x, y and z axes.
`box`	If TRUE, plot a box around the globe.
`xlab, ylab, zlab`	Axes labels

Details

This funciton requires the `rgl` and `sphereplot` packages.

Value

No value, used for plotting side effect.

See Also

Other inlabru RGL tools: `glplot.SpatialLines()`, `glplot.SpatialPoints()`, `glplot.inla.mesh()`, `glplot()`

Examples

```
## Not run:
if (bru_safe_inla() &&
  require("rgl", quietly = TRUE) &&
  require("sphereplot", quietly = TRUE)) {

  # Load pantropoical dolphin data

  data("mexdolphin", package = "inlabru")

  # Show the globe

  globe()

  # Add mesh, ship transects and dolphin sightings stored
  # as inla.mesh, SpatialLines and SpatialPoints objects, respectively

  glplot(mexdolphin$mesh)
  glplot(mexdolphin$samplers)
  glplot(mexdolphin$points)
}

## End(Not run)
```

`glplot` *Render Spatial* and inla.mesh objects using RGL*

Description

glplot is a generic function for renders various kinds of spatial objects, i.e. Spatial* data and inla.mesh objects. The function invokes particular methods which depend on the class of the first argument.

Usage

```
glplot(object, ...)
```

Arguments

`object`	an object used to select a method.
`...`	further arguments passed to or from other methods.

See Also

Other inlabru RGL tools: `globe()`, `glplot.SpatialLines()`, `glplot.SpatialPoints()`, `glplot.inla.mesh()`

Examples

```
## Not run:
if (bru_safe_inla() &&
  require("rgl", quietly = TRUE) &&
  require("sphereplot", quietly = TRUE)) {

  # Load pantropoical dolphin data

  data("mexdolphin", package = "inlabru")

  # Show the globe

  globe()

  # Add mesh, ship transects and dolphin sightings stored
  # as inla.mesh, SpatialLines and SpatialPoints objects, respectively

  glplot(mexdolphin$mesh)
  glplot(mexdolphin$samplers)
  glplot(mexdolphin$points)
}

## End(Not run)
```

`glplot.inla.mesh` *Visualize SpatialPoints using RGL*

Description

This function transforms the mesh to 3D cartesian coordinates and uses inla.plot.mesh() with `rgl=TRUE` to plot the result.

Usage

```
## S3 method for class 'inla.mesh'
glplot(object, add = TRUE, col = NULL, ...)
```

Arguments

`object`	an inla.mesh object.
`add`	If TRUE, add the lines to an existing plot. If FALSE, create new plot.
`col`	Color specification. A single named color, a vector of scalar values, or a matrix of RGB values.
`...`	Parameters passed on to plot.inla.mesh()

See Also

Other inlabru RGL tools: `globe()`, `glplot.SpatialLines()`, `glplot.SpatialPoints()`, `glplot()`

Examples

```
## Not run:
if (bru_safe_inla() &&
  require("rgl", quietly = TRUE) &&
  require("sphereplot", quietly = TRUE)) {

  # Load pantropoical dolphin data

  data("mexdolphin", package = "inlabru")

  # Show the globe

  globe()

  # Add mesh, ship transects and dolphin sightings stored
  # as inla.mesh, SpatialLines and SpatialPoints objects, respectively

  glplot(mexdolphin$mesh)
  glplot(mexdolphin$samplers)
  glplot(mexdolphin$points)
}

## End(Not run)
```

`glplot.SpatialLines` *Visualize SpatialLines using RGL*

Description

This function will calculate a cartesian representation of the lines provided and use rgl.linestrip() in order to render them.

Usage

```
## S3 method for class 'SpatialLines'
glplot(object, add = TRUE, ...)
```

Arguments

`object`	a SpatialLines or SpatialLinesDataFrame object.
`add`	If TRUE, add the lines to an existing plot. If FALSE, create new plot.
`...`	Parameters passed on to rgl.linestrips().

See Also

Other inlabru RGL tools: `globe()`, `glplot.SpatialPoints()`, `glplot.inla.mesh()`, `glplot()`

Examples

```
## Not run:
if (bru_safe_inla() &&
  require("rgl", quietly = TRUE) &&
  require("sphereplot", quietly = TRUE)) {

  # Load pantropoical dolphin data

  data("mexdolphin", package = "inlabru")

  # Show the globe

  globe()

  # Add mesh, ship transects and dolphin sightings stored
  # as inla.mesh, SpatialLines and SpatialPoints objects, respectively

  glplot(mexdolphin$mesh)
  glplot(mexdolphin$samplers)
  glplot(mexdolphin$points)
}

## End(Not run)
```

`glplot.SpatialPoints` *Visualize SpatialPoints using RGL*

Description

This function will calculate the cartesian coordinates of the points provided and use rgl.points() in order to render them.

Usage

```
## S3 method for class 'SpatialPoints'
glplot(object, add = TRUE, color = "red", ...)
```

Arguments

`object`	a SpatialPoints or SpatialPointsDataFrame object.
`add`	If TRUE, add the points to an existing plot. If FALSE, create new plot.
`color`	vector of R color characters. See rgl.material() for details.
`...`	Parameters passed on to rgl.points()

See Also

Other inlabru RGL tools: `globe()`, `glplot.SpatialLines()`, `glplot.inla.mesh()`, `glplot()`

Examples

```
## Not run:
if (bru_safe_inla() &&
  require("rgl", quietly = TRUE) &&
  require("sphereplot", quietly = TRUE)) {

  # Load pantropoical dolphin data

  data("mexdolphin", package = "inlabru")

  # Show the globe

  globe()

  # Add mesh, ship transects and dolphin sightings stored
  # as inla.mesh, SpatialLines and SpatialPoints objects, respectively

  glplot(mexdolphin$mesh)
  glplot(mexdolphin$samplers)
  glplot(mexdolphin$points)
}

## End(Not run)
```

`gm` *ggplot geom for spatial data*

Description

gm is a wrapper for the gg method. It will take the first argument and transform its coordinate system to latitude and longitude. Thereafter, gg is called using the transformed data and the arguments provided via `...`. gm is intended to replace gg whenever the data is supposed to be plotted over a spatial map generated by gmap, which only works if the coordinate system is latitude/longitude.

Usage

```
gm(data, ...)
```

Arguments

`data`	an object for which to generate a geom.
`...`	Arguments passed on to `gg()`.

Value

The form of the value returned by gm depends on the class of its argument. See the documentation of the particular methods for details of what is produced by that method.

See Also

Other geomes for inla and inlabru predictions: `gg.data.frame()`, `gg.matrix()`, `gg.prediction()`, `gg()`

Other geomes for spatial data: `gg.SpatialGridDataFrame()`, `gg.SpatialLines()`, `gg.SpatialPixelsDataFrame()`, `gg.SpatialPixels()`, `gg.SpatialPoints()`, `gg.SpatialPolygons()`, `gg()`

Other geomes for meshes: `gg.inla.mesh.1d()`, `gg.inla.mesh()`, `gg()`

Other geomes for Raster data: `gg.RasterLayer()`, `gg()`

Examples

```
## Not run:
if (require("ggplot2", quietly = TRUE) &&
  require(ggpolypath, quietly = TRUE)) {
  # Load the Gorilla data
  data(gorillas, package = "inlabru")

  # Create a base map centered around the nests and plot the boundary as well as the nests
  gmap(gorillas$nests, maptype = "satellite") +
    gm(gorillas$boundary) +
    gm(gorillas$nests, color = "white", size = 0.5)
}

## End(Not run)
```

---

gmap *Plot a map using extend of a spatial object*

Description

Uses get_map() to query map services like Google Maps for a region centered around the spatial object provided. Then calls ggmap() to plot the map.

Usage

```
gmap(data, ...)
```

Arguments

`data`	A Spatial* object.
`...`	Arguments passed on to get_map().

Details

This function requires the `ggmap` package.

Value

a ggplot object

Examples

```
## Not run:
if (require("ggplot2", quietly = TRUE) &&
  require(ggpolypath, quietly = TRUE)) {
  # Load the Gorilla data
  data(gorillas, package = "inlabru")

  # Create a base map centered around the nests and plot the boundary as well
  # as the nests
  ggplot() +
    gg(gorillas$boundary) +
    gg(gorillas$nests, color = "white", size = 0.5)
  if (requireNamespace("ggmap", quietly = TRUE)) {
    gmap(gorillas$nests, maptype = "satellite") +
      gm(gorillas$boundary) +
      gm(gorillas$nests, color = "white", size = 0.5)
  }
}

## End(Not run)
```

`gorillas` *Gorilla nesting sites*

Description

This is the `gorillas` dataset from the package `spatstat.data`, reformatted as point process data for use with `inlabru`.

Usage

```
data(gorillas)
```

Format

The data are a list that contains these elements:

- `nests`**:** A `SpatialPointsDataFrame` object containing the locations of the gorilla nests.
- `boundary`**:** An `SpatialPolygonsDataFrame` object defining the boundary of the region that was searched for the nests.
- `mesh`**:** An `inla.mesh` object containing a mesh that can be used with function `lgcp` to fit a LGCP to the nest data.
- `gcov`**:** A list of SpatialGridDataFrame objects, one for each of these spatial covariates:
    - `aspect` Compass direction of the terrain slope. Categorical, with levels N, NE, E, SE, S, SW, W and NW, which are coded as integers 1 to 8.
    - `elevation` Digital elevation of terrain, in metres.
    - `heat` Heat Load Index at each point on the surface (Beer's aspect), discretised. Categorical with values Warmest (Beer's aspect between 0 and 0.999), Moderate (Beer's aspect between 1 and 1.999), Coolest (Beer's aspect equals 2). These are coded as integers 1, 2 and 3, in that order.
    - `slopangle` Terrain slope, in degrees.
    - `slopetype` Type of slope. Categorical, with values Valley, Toe (toe slope), Flat, Midslope, Upper and Ridge. These are coded as integers 1 to 6.
    - `vegetation` Vegetation type: a categorical variable with 6 levels coded as integers 1 to 6 (in order of increasing expected habitat suitability)
    - `waterdist` Euclidean distance from nearest water body, in metres.
- `plotsample` Plot sample of gorilla nests, sampling 9x9 over the region, with 60\
    - `counts` A SpatialPointsDataFrame frame with elements `x`, `y`, `count`, `exposure`, being the x- and y-coordinates of the centre of each plot, the count in each plot and the area of each plot.
    - `plots` A `SpatialPolygonsDataFrame` defining the individual plot boundaries.
    - `nests` A `SpatialPointsDataFrame` giving the locations of each detected nest.

Source

Library `spatstat.data`.

References

Funwi-Gabga, N. (2008) A pastoralist survey and fire impact assessment in the Kagwene Gorilla Sanctuary, Cameroon. M.Sc. thesis, Geology and Environmental Science, University of Buea, Cameroon.

Funwi-Gabga, N. and Mateu, J. (2012) Understanding the nesting spatial behaviour of gorillas in the Kagwene Sanctuary, Cameroon. Stochastic Environmental Research and Risk Assessment 26 (6), 793-811.

Examples

```
if (bru_safe_inla() &&
  require(ggplot2, quietly = TRUE) &&
  require(ggpolypath, quietly = TRUE)) {
  data(gorillas, package = "inlabru") # get the data

  # plot all the nests, mesh and boundary
  ggplot() +
    gg(gorillas$mesh) +
    gg(gorillas$boundary) +
    gg(gorillas$nests)

  # Plot the elevation covariate
  plot(gorillas$gcov$elevation)

  # Plot the plot sample
  ggplot() +
    gg(gorillas$plotsample$plots) +
    gg(gorillas$plotsample$nests)
}
```

`inla.stack.mjoin` *Join stacks intended to be run with different likelihoods*

Description

Join stacks intended to be run with different likelihoods

Usage

```
inla.stack.mjoin(
  ...,
  compress = TRUE,
  remove.unused = TRUE,
  old.names = "BRU.response",
  new.name = "BRU.response"
)
```

Arguments

`...`	List of stacks that contain vector observations (existing multi-likelihood observation matrices are also permitted)
`compress`	If `TRUE`, compress the model by removing duplicated rows of effects, replacing the corresponding A-matrix columns with a single column containing the sum.
`remove.unused`	If `TRUE`, compress the model by removing rows of effects corresponding to all-zero columns in the A matrix (and removing those columns).
`old.names`	A vector of strings with the names of the observation vector/matrix for each stack. If a single string, this is assumed for all the stacks. (default "BRU.response")

`new.name`	The name to be used for the expanded observation matrix, possibly the same as an old name. (default "BRU.response")

`inlabru` *inlabru*

Description

Convenient model fitting using (iterated) INLA.

Details

`inlabru` facilitates Bayesian spatial modelling using integrated nested Laplace approximations. It is heavily based on R-inla (`https://www.r-inla.org`) but adds additional modelling abilities and simplified syntax for (in particular) spatial models. Tutorials and more information can be found at `https://inlabru-org.github.io/inlabru/` and `http://www.inlabru.org/`. The iterative method used for non-linear predictors is documented in the `method` vignette.

The main function for inference using inlabru is `bru()`. For point process inference `lgcp()` is a good starting point. The general model specification details is documented in `component()` and `like()`. Posterior quantities beyond the basic summaries can be calculated with a `predict()` method, documented in `predict.bru()`.

The package comes with multiple real world data sets, namely gorillas, mexdolphin, seals. Plotting these data sets is straight forward using inlabru's extensions to `ggplot2`, e.g. the `gg()` function. For educational purposes some simulated data sets are available as well, e.g. Poisson1_1D, Poisson2_1D, Poisson2_1D and toygroups.

Author(s)

Fabian E. Bachl `<bachlfab@gmail.com>` and Finn Lindgren `<finn.lindgren@gmail.com>`

`int` *Weighted summation (integration) of data frame subsets*

Description

A typical task in statistical inference to integrate a (multivariate) function along one or more dimensions of its domain. For this purpose, the function is evaluated at some points in the domain and the values are summed up using weights that depend on the area being integrated over. This function performs the weighting and summation conditional for each level of the dimensions that are not integrated over. The parameter `dims` states the the dimensions to integrate over. The set of dimensions that are held fixed is the set difference of all column names in `data` and the dimensions stated by `dims`.

Usage

```
int(data, values, dims = NULL)
```

Arguments

`data`	A `data.frame` or `Spatial` object. Has to have a `weight` column with numeric values.
`values`	Numerical values to be summed up, usually the result of function evaluations.
`dims`	Column names (dimension names) of the `data` object to integrate over.

Value

A `data.frame` of integrals, one for each level of the cross product of all dimensions not being integrated over.

Examples

```
# ipoints needs INLA
if (bru_safe_inla(quietly = TRUE)) {
  # Create integration points in two dimensions, x and y

  ips <- cprod(
    ipoints(c(0, 10), 10, name = "x"),
    ipoints(c(1, 5), 10, name = "y")
  )

  # The sizes of the domains are 10 and 4 for x and y, respectively.
  # Integrating f(x,y) = 1 along x and y should result in the total
  # domain size 40

  int(ips, rep(1, nrow(ips)), c("x", "y"))
}
```

`ipoints` *Generate integration points*

Description

This function generates points in one or two dimensions with a weight attached to each point. The weighted sum of a function evaluated at these points is the integral of that function approximated by linear basis functions. The parameter `samplers` describes the area(s) integrated over.

In case of a single dimension `samplers` is supposed to be a two-column `matrix` where each row describes the start and end point of the interval to integrate over. In the two-dimensional case `samplers` can be either a `SpatialPolygon`, an `inla.mesh` or a `SpatialLinesDataFrame` describing the area to integrate over. If a `SpatialLineDataFrame` is provided it has to have a column called 'weight' in order to indicate the width of the line.

The domain parameter is an `inla.mesh.1d` or `inla.mesh` object that can be employed to project the integration points to the vertices of the mesh. This reduces the final number of integration points and reduces the computational cost of the integration. The projection can also prevent numerical issues in spatial LGCP models where each observed point is ideally surrounded by three integration point sitting at the corresponding mesh vertices. This is controlled by `int.args$method="stable"` (default) or `"direct"`, where the latter uses the integration points directly, without aggregating to the mesh vertices.

For convenience, the `domain` parameter can also be a single integer setting the number of equally spaced integration points in the one-dimensional case.

Usage

```
ipoints(
  samplers = NULL,
  domain = NULL,
  name = NULL,
  group = NULL,
  int.args = NULL,
  project = NULL
)
```

Arguments

`samplers`	Description of the integration region boundary. In 1D, a length 2 vector or two-column matrix where each row describes an interval, or `NULL` In 2D either a `SpatialPolygon` or a `SpatialLinesDataFrame` with a `weight` column defining the width of the a transect line, and optionally further columns used by the `group` argument, or `NULL`. When `domain` is `NULL`, `samplers` may also be an `inla.mesh.1d` or `inla.mesh` object, that is then treated as a `domain` argument instead.
`domain`	Either • when `samplers` is a 1D interval(s) definition only, `domain` can be a single integer for the number of integration points to place in each 1D interval, overriding `int.args[["nsub1"]]`, and otherwise • when `samplers` is `NULL`, `domain` can be a numeric vector of points, each given integration weight 1 (and no additional points are added in between), • an `inla.mesh.1d` object for continuous 1D integration, or • an `inla.mesh.2d` object for continuous 2D integration.
`name`	Character array stating the name of the domains dimension(s). If `NULL`, the names are taken from coordinate names from `samplers` for `Spatial*` objects, otherwise "x", "y", "coordinateZ" for 2D regions and `"x"` for 1D regions
`group`	Column names of the `samplers` object (if applicable) for which the integration points are calculated independently and not merged when aggregating to mesh nodes.
`int.args`	List of arguments passed to `bru_int_polygon`. • `method`: "stable" (to aggregate integration weights onto mesh nodes) or "direct" (to construct a within triangle/segment integration scheme without aggregating onto mesh nodes)

	• `nsub1`, `nsub2`: integers controlling the number of internal integration points before aggregation. Points per triangle: `(nsub2+1)^2`. Points per knot segment: `nsub1` • `poly_method`: if set to "legacy", selects an old polygon integration method that doesn't handle holes. Currently only used for debugging purposes.
`project`	Deprecated in favour of `int.args(method=...)`. If TRUE, aggregate the integration points to mesh vertices. Default: `project = (identical(int.args$method, "stable"))`

Value

A `data.frame` or `SpatialPointsDataFrame` of 1D and 2D integration points, respectively.

Author(s)

Fabian E. Bachl <`bachlfab@gmail.com`> and <`finn.lindgren@gmail.com`>

Examples

```
if (require("INLA", quietly = TRUE) &&
  require("ggplot2", quietly = TRUE)) {

  # Create 50 integration points covering the dimension 'myDim' between 0 and 10.

  ips <- ipoints(c(0, 10), 50, name = "myDim")
  plot(ips)


  # Create integration points for the two intervals [0,3] and [5,10]

  ips <- ipoints(matrix(c(0, 3, 5, 10), nrow = 2, byrow = TRUE), 50)
  plot(ips)


  # Convert a 1D mesh into integration points
  mesh <- inla.mesh.1d(seq(0, 10, by = 1))
  ips <- ipoints(mesh, name = "time")
  plot(ips)


  # Obtain 2D integration points from a SpatialPolygon

  data(gorillas, package = "inlabru")
  ips <- ipoints(gorillas$boundary)
  ggplot() +
    gg(gorillas$boundary) +
    gg(ips, aes(size = weight))


  #' Project integration points to mesh vertices
```

```
  ips <- ipoints(gorillas$boundary, domain = gorillas$mesh)
  ggplot() +
    gg(gorillas$mesh) +
    gg(gorillas$boundary) +
    gg(ips, aes(size = weight))


  # Turn a 2D mesh into integration points

  ips <- ipoints(gorillas$mesh)
  ggplot() +
    gg(gorillas$boundary) +
    gg(ips, aes(size = weight))
}
```

`lgcp` *Log Gaussian Cox process (LGCP) inference using INLA*

Description

This function performs inference on a LGCP observed via points residing possibly multiple dimensions. These dimensions are defined via the left hand side of the formula provided via the model parameter. The left hand side determines the intensity function that is assumed to drive the LGCP. This may include effects that lead to a thinning (filtering) of the point process. By default, the log intensity is assumed to be a linear combination of the effects defined by the formula's RHS. More sofisticated models, e.g. non-linear thinning, can be achieved by using the predictor argument. The latter requires multiple runs of INLA for improving the required approximation of the predictor. In many applications the LGCP is only observed through subsets of the dimensions the process is living in. For example, spatial point realizations may only be known in sub-areas of the modelled space. These observed subsets of the LGCP domain are called samplers and can be provided via the respective parameter. If samplers is NULL it is assumed that all of the LGCP's dimensions have been observed completely.

Usage

```
lgcp(
  components,
  data,
  samplers = NULL,
  domain = NULL,
  ips = NULL,
  formula = . ~ .,
  E = NULL,
  ...,
  options = list()
)
```

Arguments

`components`	A formula describing the latent components
`data`	A data frame or `SpatialPoints(DataFrame)` object
`samplers`	A data frame or `Spatial[Points/Lines/Polygons]DataFrame` objects
`domain`	Named list of domain definitions
`ips`	Integration points (overrides `samplers`)
`formula`	If NULL, the linear combination implied by the `components` is used as a predictor for the point location intensity. If a (possibly non-linear) expression is provided the respective Taylor approximation is used as a predictor. Multiple runs if INLA are then required for a better approximation of the posterior.
`E`	Single numeric used rescale all integration weights by a fixed factor
`...`	Further arguments passed on to `like()`
`options`	See `bru_options_set()`

Value

An `bru()` object

Examples

```
if (bru_safe_inla() &&
  require(ggplot2, quietly = TRUE)) {

  # Load the Gorilla data
  data(gorillas, package = "inlabru")

  # Plot the Gorilla nests, the mesh and the survey boundary
  ggplot() +
    gg(gorillas$mesh) +
    gg(gorillas$nests) +
    gg(gorillas$boundary) +
    coord_fixed()

  # Define SPDE prior
  matern <- INLA::inla.spde2.pcmatern(gorillas$mesh,
    prior.sigma = c(0.1, 0.01),
    prior.range = c(0.01, 0.01)
  )

  # Define domain of the LGCP as well as the model components (spatial SPDE
  # effect and Intercept)
  cmp <- coordinates ~ mySmooth(coordinates, model = matern) + Intercept(1)

  # Fit the model (with int.strategy="eb" to make the example take less time)
  fit <- lgcp(cmp, gorillas$nests,
    samplers = gorillas$boundary,
    domain = list(coordinates = gorillas$mesh),
```

```
    options = list(control.inla = list(int.strategy = "eb"))
  )

  # Predict the spatial intensity surface
  lambda <- predict(fit, pixels(gorillas$mesh), ~ exp(mySmooth + Intercept))

  # Plot the intensity
  ggplot() +
    gg(lambda) +
    gg(gorillas$mesh) +
    gg(gorillas$nests) +
    gg(gorillas$boundary) +
    coord_fixed()
}
```

`like` *Likelihood construction for usage with* `bru()`

Description

Likelihood construction for usage with `bru()`

Usage

```
like(
  formula = . ~ .,
  family = "gaussian",
  data = NULL,
  response_data = NULL,
  mesh = NULL,
  E = NULL,
  Ntrials = NULL,
  samplers = NULL,
  ips = NULL,
  domain = NULL,
  include = NULL,
  exclude = NULL,
  allow_latent = FALSE,
  allow_combine = NULL,
  control.family = NULL,
  options = list(),
  .envir = parent.frame()
)

like_list(...)
```

```
## S3 method for class 'list'
like_list(object, envir = NULL, ...)

## S3 method for class 'bru_like'
like_list(..., envir = NULL)

## S3 method for class 'bru_like_list'
x[i]
```

Arguments

`formula`	a `formula` where the right hand side is a general R expression defines the predictor used in the model.
`family`	A string identifying a valid `INLA::inla` likelihood family. The default is `gaussian` with identity link. In addition to the likelihoods provided by inla (see `names(INLA::inla.models()$lik` inlabru supports fitting latent Gaussian Cox processes via `family = "cp"`. As an alternative to `bru()`, the `lgcp()` function provides a convenient interface to fitting Cox processes.
`data`	Likelihood-specific data, as a `data.frame` or `SpatialPoints[DataFrame]` object.
`response_data`	Likelihood-specific data for models that need different size/format for inputs and response variables, as a `data.frame` or `SpatialPoints[DataFrame]` object.
`mesh`	An inla.mesh object. Obsolete.
`E`	Exposure parameter for family = 'poisson' passed on to `INLA::inla`. Special case if family is 'cp': rescale all integration weights by E. Default taken from `options$E`.
`Ntrials`	A vector containing the number of trials for the 'binomial' likelihood. Default value is rep(1, n.data). Default taken from `options$Ntrials`.
`samplers`	Integration domain for 'cp' family.
`ips`	Integration points for 'cp' family. Overrides `samplers`.
`domain`	Named list of domain definitions.
`include`	Character vector of component labels that are needed by the predictor expression; Default: NULL (include all components that are not explicitly excluded)
`exclude`	Character vector of component labels that are not used by the predictor expression. The exclusion list is applied to the list as determined by the `include` parameter; Default: NULL (do not remove any components from the inclusion list)
`allow_latent`	logical. If `TRUE`, the latent state of each component is directly available to the predictor expression, with a `_latent` suffix. This also makes evaluator functions with suffix `_eval` available, taking parameters `main`, `group`, and `replicate`, taking values for where to evaluate the component effect that are different than those defined in the component definition itself (see `component_eval()`). Default `FALSE`
`allow_combine`	logical; If `TRUE`, the predictor expression may involve several rows of the input data to influence the same row. Default `FALSE`, but forced to `TRUE` if `response_data` is `NULL` or `data` is a `list`

`control.family`	A optional `list` of `INLA::control.family` options
`options`	A bru_options options object or a list of options passed on to `bru_options()`
`.envir`	The evaluation environment to use for special arguments (`E` and `Ntrials`) if not found in `response_data` or `data`. Defaults to the calling environment.
`...`	For `like_list.bru_like`, one or more `bru_like` objects
`object`	A list of `bru_like` objects
`envir`	An optional environment for the new `bru_like_list` object
`x`	`bru_like_list` object from which to extract element(s)
`i`	indices specifying elements to extract

Details

- `like_list`: Combine a `bru_like` likelihoods into a `bru_like_list` object
- `like_list.list`: Combine a list of `bru_like` likelihoods into a `bru_like_list` object
- `like_list.bru_like`: Combine several `bru_like` likelihoods into a `bru_like_list` object

Value

A likelihood configuration which can be used to parameterize `bru()`.

Author(s)

Fabian E. Bachl <`bachlfab@gmail.com`>

Examples

```
if (bru_safe_inla() &&
    require(ggplot2, quietly = TRUE)) {

  # The like function's main purpose is to set up models with multiple likelihoods.
  # The following example generates some random covariates which are observed through
  # two different random effect models with different likelihoods

  # Generate the data

  set.seed(123)

  n1 <- 200
  n2 <- 10

  x1 <- runif(n1)
  x2 <- runif(n2)
  z2 <- runif(n2)

  y1 <- rnorm(n1, mean = 2 * x1 + 3)
  y2 <- rpois(n2, lambda = exp(2 * x2 + z2 + 3))
```

```
  df1 <- data.frame(y = y1, x = x1)
  df2 <- data.frame(y = y2, x = x2, z = z2)

  # Single likelihood models and inference using bru are done via

  cmp1 <- y ~ -1 + Intercept(1) + x
  fit1 <- bru(cmp1, family = "gaussian", data = df1)
  summary(fit1)

  cmp2 <- y ~ -1 + Intercept(1) + x + z
  fit2 <- bru(cmp2, family = "poisson", data = df2)
  summary(fit2)

  # A joint model has two likelihoods, which are set up using the like function

  lik1 <- like("gaussian", formula = y ~ x + Intercept, data = df1)
  lik2 <- like("poisson", formula = y ~ x + z + Intercept, data = df2)

  # The union of effects of both models gives the components needed to run bru

  jcmp <- ~ x + z + Intercept(1)
  jfit <- bru(jcmp, lik1, lik2)

  # Compare the estimates

  p1 <- ggplot() +
    gg(fit1$summary.fixed, bar = TRUE) +
    ylim(0, 4) +
    ggtitle("Model 1")
  p2 <- ggplot() +
    gg(fit2$summary.fixed, bar = TRUE) +
    ylim(0, 4) +
    ggtitle("Model 2")
  pj <- ggplot() +
    gg(jfit$summary.fixed, bar = TRUE) +
    ylim(0, 4) +
    ggtitle("Joint model")

  multiplot(p1, p2, pj)
}
```

`mexdolphin` *Pan-tropical spotted dolphins in the Gulf of Mexico*

Description

This a version of the `mexdolphins` dataset from the package `dsm`, reformatted as point process data for use with `inlabru`. The data are from a combination of several NOAA shipboard surveys conducted on pan-tropical spotted dolphins in the Gulf of Mexico. 47 observations of groups of dolphins wre detected. The group size was recorded, as well as the Beaufort sea state at the time of the observation. Transect width is 16 km, i.e. maximal detection distance 8 km (transect half-width 8 km).

Usage

```
data(mexdolphin)
```

Format

A list of objects:

- **`points`:** A `SpatialPointsDataFrame` object containing the locations of detected dolphin groups, with their size as an attribute.
- **`samplers`:** A `SpatialLinesDataFrame` object containing the transect lines that were surveyed.
- **`mesh`:** An `inla.mesh` object containing a Delaunay triangulation mesh (a type of discretization of continuous space) covering the survey region.
- **`ppoly`:** An `SpatialPolygonsDataFrame` object defining the boundary of the survey region.
- **`simulated`:** A `SpatialPointsDataFrame` object containing the locations of a *simulated* population of dolphin groups. The population was simulated from a 'codeinlabru model fitted to the actual survey data. Note that the simulated data do not have any associated size information.

Source

Library `dsm`.

References

Halpin, P.N., A.J. Read, E. Fujioka, B.D. Best, B. Donnelly, L.J. Hazen, C. Kot, K. Urian, E. LaBrecque, A. Dimatteo, J. Cleary, C. Good, L.B. Crowder, and K.D. Hyrenbach. 2009. OBIS-SEAMAP: The world data center for marine mammal, sea bird, and sea turtle distributions. Oceanography 22(2):104-115

NOAA Southeast Fisheries Science Center. 1996. Report of a Cetacean Survey of Oceanic and Selected Continental Shelf Waters of the Northern Gulf of Mexico aboard NOAA Ship Oregon II (Cruise 220)

Examples

```
if (bru_safe_inla(quietly = TRUE) &&
  require("ggplot2", quietly = TRUE) &&
  require("ggpolypath", quietly = TRUE)) {
  data(mexdolphin, package = "inlabru")
  ggplot() +
    gg(mexdolphin$mesh) +
    gg(mexdolphin$ppoly, color = "blue") +
    gg(mexdolphin$samplers) +
    gg(mexdolphin$points, aes(size = size), color = "red") +
```

```
    coord_equal()

  ggplot() +
    gg(mexdolphin$mesh, col = mexdolphin$lambda, mask = mexdolphin$ppoly) +
    coord_equal()
}

## Not run:
if (requireNamespace("ggmap", quietly = TRUE) &&
  require("ggplot2", quietly = TRUE) &&
  require("ggpolypath", quietly = TRUE)) {
  gmap(mexdolphin$depth) +
    gm(mexdolphin$ppoly, color = "blue") +
    gm(mexdolphin$samplers) +
    gm(mexdolphin$points, aes(size = size), color = "red")

  gmap(mexdolphin$depth) +
    gm(mexdolphin$depth, aes(col = depth)) +
    gm(mexdolphin$ppoly)
}

## End(Not run)
```

`mrsea` *Marine renewables strategic environmental assessment*

Description

Data imported from package MRSea, see http://creem2.st-andrews.ac.uk/software/

Usage

`data(mrsea)`

Format

A list of objects:

`points`: A `SpatialPointsDataFrame` object containing the locations of XXXXX.

`samplers`: A `SpatialLinesDataFrame` object containing the transect lines that were surveyed.

`mesh`: An `inla.mesh` object containing a Delaunay triangulation mesh (a type of discretization of continuous space) covering the survey region.

`boundary`: An `SpatialPolygonsDataFrame` object defining the boundary of the survey region.

`covar`: An `SpatialPointsDataFrame` containing sea depth estimates.

Source

Library `MRSea`.

References

NONE YET

Examples

```
if (bru_safe_inla() &&
  require(ggplot2, quietly = TRUE) &&
  require(ggpolypath, quietly = TRUE)) {
  data(mrsea)
  ggplot() +
    gg(mrsea$mesh) +
    gg(mrsea$samplers) +
    gg(mrsea$points) +
    gg(mrsea$boundary)
}
```

`multiplot` *Multiple ggplots on a page.*

Description

Renders multiple ggplots on a single page.

Usage

```
multiplot(..., plotlist = NULL, cols = 1, layout = NULL)
```

Arguments

`...`	Comma-separated `ggplot` objects.
`plotlist`	A list of `ggplot` objects - an alternative to the comma-separated argument above.
`cols`	Number of columns of plots on the page.
`layout`	A matrix specifying the layout. If present, 'cols' is ignored. If the layout is something like matrix(c(1,2,3,3), nrow=2, byrow=TRUE), then plot 1 will go in the upper left, 2 will go in the upper right, and 3 will go all the way across the bottom.

Author(s)

David L. Borchers `<dlb@st-andrews.ac.uk>`

Source

`http://www.cookbook-r.com/Graphs/Multiple_graphs_on_one_page_(ggplot2)/`

Examples

```
if (require("ggplot2", quietly = TRUE)) {
  df <- data.frame(x = 1:10, y = 1:10, z = 11:20)
  pl1 <- ggplot(data = df) +
    geom_line(mapping = aes(x, y), color = "red")
  pl2 <- ggplot(data = df) +
    geom_line(mapping = aes(x, z), color = "blue")
  multiplot(pl1, pl2, cols = 2)
}
```

`pixels` *Generate* `SpatialPixels` *covering an* `inla.mesh`

Description

Generate `SpatialPixels` covering an `inla.mesh`

Usage

```
pixels(mesh, nx = 150, ny = 150, mask = TRUE)
```

Arguments

`mesh`	An `inla.mesh` object
`nx`	Number of pixels in x direction
`ny`	Number of pixels in y direction
`mask`	If logical and TRUE, remove pixels that are outside the mesh. If `mask` is a `Spatial` object, only return pixels covered by this object.

Value

`SpatialPixelsDataFrame` covering the mesh

Author(s)

Fabian E. Bachl <`bachlfab@gmail.com`>

Examples

```
if (require(ggplot2, quietly = TRUE)) {
  data("mrsea", package = "inlabru")
  pxl <- pixels(mrsea$mesh, nx = 50, ny = 50, mask = mrsea$boundary)
  ggplot() +
    gg(pxl, fill = "grey", alpha = 0.5) +
    gg(mrsea$mesh)
}
```

`plot.bru` *Plot method for posterior marginals estimated by bru*

Description

`bru()` uses `INLA::inla()` to fit models. The latter estimates the posterior densities of all random effects in the model. This function serves to access and plot the posterior densities in a convenient way.

Requires the `ggplot2` package.

Usage

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

Arguments

`x`	a fitted `bru()` model.
`...`	A character naming the effect to plot, e.g. "Intercept". For random effects, adding `index = ...` plots the density for a single component of the latent model.

Value

an object of class gg

Examples

```
## Not run:
if (require("ggplot2", quietly = TRUE)) {
  # Generate some data and fit a simple model
  input.df <- data.frame(x = cos(1:10))
  input.df <- within(input.df, y <- 5 + 2 * cos(1:10) + rnorm(10, mean = 0, sd = 0.1))
  fit <- bru(y ~ x, family = "gaussian", data = input.df)
  summary(fit)

  # Plot the posterior of the model's x-effect
  plot(fit, "x")
}

## End(Not run)
```

`plot.prediction` *Plot prediction using ggplot2*

Description

Generates a base ggplot2 using `ggplot()` and adds a geom for input `x` using gg.

Usage

```
## S3 method for class 'prediction'
plot(x, y = NULL, ...)
```

Arguments

`x`	a prediction object.
`y`	Ignored argument but required for S3 compatibility.
`...`	Arguments passed on to gg.prediction.

Details

Requires the `ggplot2` package.

Value

an object of class gg

Examples

```
if (bru_safe_inla() && require(ggplot2, quietly = TRUE)) {
  # Generate some data

  input.df <- data.frame(x = cos(1:10))
  input.df <- within(input.df, y <- 5 + 2 * cos(1:10) + rnorm(10, mean = 0, sd = 0.1))

  # Fit a model with fixed effect 'x' and intercept 'Intercept'

  fit <- bru(y ~ x, family = "gaussian", data = input.df)

  # Predict posterior statistics of 'x'

  xpost <- predict(fit, data = NULL, formula = ~x_latent)

  # The statistics include mean, standard deviation, the 2.5% quantile, the median,
  # the 97.5% quantile, minimum and maximum sample drawn from the posterior as well as
  # the coefficient of variation and the variance.

  xpost
```

```
# For a single variable like 'x' the default plotting method invoked by gg() will
# show these statisics in a fashion similar to a box plot:
ggplot() +
  gg(xpost)


# The predict function can also be used to simulataneously estimate posteriors
# of multiple variables:

xipost <- predict(fit,
  data = NULL,
  formula = ~ c(
    Intercept = Intercept_latent,
    x = x_latent
  )
)
xipost

# If we still want a plot in the previous style we have to set the bar parameter to TRUE

p1 <- ggplot() +
  gg(xipost, bar = TRUE)
p1

# Note that gg also understands the posterior estimates generated while running INLA

p2 <- ggplot() +
  gg(fit$summary.fixed, bar = TRUE)
multiplot(p1, p2)

# By default, if the prediction has more than one row, gg will plot the column 'mean' against
# the row index. This is for instance usefuul for predicting and plotting function
# but not very meaningful given the above example:

ggplot() +
  gg(xipost)

# For ease of use we can also type

plot(xipost)

# This type of plot will show a ribbon around the mean, which viszualizes the upper and lower
# quantiles mentioned above (2.5 and 97.5%). Plotting the ribbon can be turned of using the
# \code{ribbon} parameter

ggplot() +
  gg(xipost, ribbon = FALSE)

# Much like the other geomes produced by gg we can adjust the plot using ggplot2 style
# commands, for instance

ggplot() +
  gg(xipost) +
```

```
    gg(xipost, mapping = aes(y = median), ribbon = FALSE, color = "red")
}
```

`plotsample` *Create a plot sample.*

Description

Creates a plot sample on a regular grid with a random start location.

Usage

```
plotsample(spdf, boundary, x.ppn = 0.25, y.ppn = 0.25, nx = 5, ny = 5)
```

Arguments

`spdf`	A `SpatialPointsDataFrame` defining the points that are to be sampled by the plot sample.
`boundary`	A `SpatialPolygonsDataFrame` defining the survey boundary within which the points occur.
`x.ppn`	The proportion of the x=axis that is to be included in the plots.
`y.ppn`	The proportion of the y=axis that is to be included in the plots.
`nx`	The number of plots in the x-dimension.
`ny`	The number of plots in the y-dimension.

Value

A list with three components:

- **`plots`:** A `SpatialPolygonsDataFrame` object containing the plots that were sampled.
- **`dets`:** A `SpatialPointsDataFrame` object containing the locations of the points within the plots.
- **`counts`:** A `dataframe` containing the following columns
  - **`x`:** The x-coordinates of the centres of the plots within the boundary.
  - **`y`:** The y-coordinates of the centres of the plots within the boundary.
  - **`n`:** The numbers of points in each plot.
  - **`area`:** The areas of the plots within the boundary

.

Examples

```
# Some features require the raster package
if (require("raster", quietly = TRUE) &&
  require("ggplot2", quietly = TRUE)) {
  data(gorillas, package = "inlabru")
  plotpts <- plotsample(gorillas$nests, gorillas$boundary,
    x.ppn = 0.4, y.ppn = 0.4, nx = 5, ny = 5
  )
  ggplot() +
    gg(plotpts$plots) +
    gg(plotpts$dets, pch = "+", cex = 2) +
    gg(gorillas$boundary)
}
```

`point2count` *Convert a plot sample of points into one of counts.*

Description

Converts a plot sample with locations of each point within each plot, into a plot sample with only the count within each plot.

Usage

```
point2count(plots, dets)
```

Arguments

`plots`	A `SpatialPolygonsDataFrame` object containing the plots that were sampled.
`dets`	A `SpatialPointsDataFrame` object containing the locations of the points within the plots.

Value

A `SpatialPolygonsDataFrame` with counts in each plot contained in slot `@data$n`.

Examples

```
# Some features require the raster package
if (require("raster", quietly = TRUE) &&
  require("ggplot2", quietly = TRUE)) {
  data(gorillas, package = "inlabru")
  plotpts <- plotsample(gorillas$nests, gorillas$boundary,
    x.ppn = 0.4, y.ppn = 0.4, nx = 5, ny = 5
  )
```

```
  p1 <- ggplot() +
    gg(plotpts$plots) +
    gg(plotpts$dets) +
    gg(gorillas$boundary)
  countdata <- point2count(plotpts$plots, plotpts$dets)
  x <- coordinates(countdata)[, 1]
  y <- coordinates(countdata)[, 2]
  count <- countdata@data$n
  p2 <- ggplot() +
    gg(gorillas$boundary) +
    gg(plotpts$plots) +
    geom_text(aes(label = count, x = x, y = y))
  multiplot(p1, p2, cols = 2)
}
```

`Poisson1_1D` *1-Dimensional Homogeneous Poisson example.*

Description

Point data and count data, together with intensity function and expected counts for a homogeneous 1-dimensional Poisson process example.

Usage

```
data(Poisson1_1D)
```

Format

The data contain the following `R` objects:

- `lambda1_1D`**:** A function defining the intensity function of a nonhomogeneous Poisson process. Note that this function is only defined on the interval (0,55).
- `E_nc1` The expected counts of the gridded data.
- `pts1` The locations of the observed points (a data frame with one column, named `x`).
- `countdata1` A data frame with three columns, containing the count data:
  - `x` The grid cell midpoint.
  - `count` The number of detections in the cell.
  - `exposure` The width of the cell.

Examples

```
if (require("ggplot2", quietly = TRUE)) {
  data(Poisson1_1D)
  ggplot(countdata1) +
    geom_point(data = countdata1, aes(x = x, y = count), col = "blue") +
    ylim(0, max(countdata1$count)) +
    geom_point(data = pts1, aes(x = x), y = 0.2, shape = "|", cex = 4) +
    geom_point(
      data = countdata1, aes(x = x), y = 0, shape = "+",
      col = "blue", cex = 4
    ) +
    xlab(expression(bold(s))) +
    ylab("count")
}
```

`Poisson2_1D` *1-Dimensional NonHomogeneous Poisson example.*

Description

Point data and count data, together with intensity function and expected counts for a unimodal nonhomogeneous 1-dimensional Poisson process example.

Usage

```
data(Poisson2_1D)
```

Format

The data contain the following `R` objects:

`lambda2_1D`**:** A function defining the intensity function of a nonhomogeneous Poisson process. Note that this function is only defined on the interval (0,55).

`cov2_1D`**:** A function that gives what we will call a 'habitat suitability' covariate in 1D space.

`E_nc2` The expected counts of the gridded data.

`pts2` The locations of the observed points (a data frame with one column, named `x`).

`countdata2` A data frame with three columns, containing the count data:

- `x` The grid cell midpoint.
- `count` The number of detections in the cell.
- `exposure` The width of the cell.

Examples

```
if (require("ggplot2", quietly = TRUE)) {
  data(Poisson2_1D)
  p1 <- ggplot(countdata2) +
    geom_point(data = countdata2, aes(x = x, y = count), col = "blue") +
    ylim(0, max(countdata2$count, E_nc2)) +
    geom_point(
      data = countdata2, aes(x = x), y = 0, shape = "+",
      col = "blue", cex = 4
    ) +
    geom_point(
      data = data.frame(x = countdata2$x, y = E_nc2), aes(x = x),
      y = E_nc2, shape = "_", cex = 5
    ) +
    xlab(expression(bold(s))) +
    ylab("count")
  ss <- seq(0, 55, length = 200)
  lambda <- lambda2_1D(ss)
  p2 <- ggplot() +
    geom_line(
      data = data.frame(x = ss, y = lambda),
      aes(x = x, y = y), col = "blue"
    ) +
    ylim(0, max(lambda)) +
    geom_point(data = pts2, aes(x = x), y = 0.2, shape = "|", cex = 4) +
    xlab(expression(bold(s))) +
    ylab(expression(lambda(bold(s))))
  multiplot(p1, p2, cols = 1)
}
```

`Poisson3_1D` *1-Dimensional NonHomogeneous Poisson example.*

Description

Point data and count data, together with intensity function and expected counts for a multimodal nonhomogeneous 1-dimensional Poisson process example. Counts are given for two different gridded data interval widths.

Usage

```
data(Poisson3_1D)
```

Format

The data contain the following `R` objects:

`lambda3_1D`**:** A function defining the intensity function of a nonhomogeneous Poisson process. Note that this function is only defined on the interval (0,55).

`E_nc3a` The expected counts of gridded data for the wider bins (10 bins).

`E_nc3b` The expected counts of gridded data for the wider bins (20 bins).

`pts3` The locations of the observed points (a data frame with one column, named `x`).

`countdata3a` A data frame with three columns, containing the count data for the 10-interval case:

`countdata3b` A data frame with three columns, containing the count data for the 20-interval case:

- `x` The grid cell midpoint.
- `count` The number of detections in the cell.
- `exposure` The width of the cell.

Examples

```
if (require("ggplot2", quietly = TRUE)) {
  data(Poisson3_1D)
  # first the plots for the 10-bin case:
  p1a <- ggplot(countdata3a) +
    geom_point(data = countdata3a, aes(x = x, y = count), col = "blue") +
    ylim(0, max(countdata3a$count, E_nc3a)) +
    geom_point(
      data = countdata3a, aes(x = x), y = 0, shape = "+",
      col = "blue", cex = 4
    ) +
    geom_point(
      data = data.frame(x = countdata3a$x, y = E_nc3a),
      aes(x = x), y = E_nc3a, shape = "_", cex = 5
    ) +
    xlab(expression(bold(s))) +
    ylab("count")
  ss <- seq(0, 55, length = 200)
  lambda <- lambda3_1D(ss)
  p2a <- ggplot() +
    geom_line(
      data = data.frame(x = ss, y = lambda), aes(x = x, y = y),
      col = "blue"
    ) +
    ylim(0, max(lambda)) +
    geom_point(data = pts3, aes(x = x), y = 0.2, shape = "|", cex = 4) +
    xlab(expression(bold(s))) +
    ylab(expression(lambda(bold(s))))
  multiplot(p1a, p2a, cols = 1)

  # Then the plots for the 20-bin case:
  p1a <- ggplot(countdata3b) +
    geom_point(data = countdata3b, aes(x = x, y = count), col = "blue") +
    ylim(0, max(countdata3b$count, E_nc3b)) +
    geom_point(
      data = countdata3b, aes(x = x), y = 0, shape = "+",
      col = "blue", cex = 4
```

```
    ) +
    geom_point(
      data = data.frame(x = countdata3b$x, y = E_nc3b),
      aes(x = x), y = E_nc3b, shape = "_", cex = 5
    ) +
    xlab(expression(bold(s))) +
    ylab("count")
  ss <- seq(0, 55, length = 200)
  lambda <- lambda3_1D(ss)
  p2a <- ggplot() +
    geom_line(
      data = data.frame(x = ss, y = lambda), aes(x = x, y = y),
      col = "blue"
    ) +
    ylim(0, max(lambda)) +
    geom_point(data = pts3, aes(x = x), y = 0.2, shape = "|", cex = 4) +
    xlab(expression(bold(s))) +
    ylab(expression(lambda(bold(s))))
  multiplot(p1a, p2a, cols = 1)
}
```

`predict.bru` *Prediction from fitted bru model*

Description

Takes a fitted bru object produced by the function `bru()` and produces predictions given a new set of values for the model covariates or the original values used for the model fit. The predictions can be based on any R expression that is valid given these values/covariates and the joint posterior of the estimated random effects.

Usage

```
## S3 method for class 'bru'
predict(
  object,
  data = NULL,
  formula = NULL,
  n.samples = 100,
  seed = 0L,
  probs = c(0.025, 0.5, 0.975),
  num.threads = NULL,
  include = NULL,
  exclude = NULL,
  drop = FALSE,
  ...
)
```

Arguments

`object`	An object obtained by calling `bru()` or `lgcp()`.
`data`	A data.frame or SpatialPointsDataFrame of covariates needed for the prediction.
`formula`	A formula where the right hand side defines an R expression to evaluate for each generated sample. If `NULL`, the latent and hyperparameter states are returned as named list elements. See Details for more information.
`n.samples`	Integer setting the number of samples to draw in order to calculate the posterior statistics. The default is rather low but provides a quick approximate result.
`seed`	Random number generator seed passed on to `inla.posterior.sample`
`probs`	A numeric vector of probabilities with values in `[0, 1]`, passed to `stats::quantile`
`num.threads`	Specification of desired number of threads for parallel computations. Default NULL, leaves it up to INLA. When seed != 0, overridden to "1:1"
`include`	Character vector of component labels that are needed by the predictor expression; Default: NULL (include all components that are not explicitly excluded)
`exclude`	Character vector of component labels that are not used by the predictor expression. The exclusion list is applied to the list as determined by the `include` parameter; Default: NULL (do not remove any components from the inclusion list)
`drop`	logical; If `keep=FALSE`, `data` is a `Spatial*DataFrame`, and the prediciton summary has the same number of rows as `data`, then the output is a `Spatial*DataFrame` object. Default `FALSE`.
`...`	Additional arguments passed on to `inla.posterior.sample`

Details

Mean value predictions are accompanied by the standard errors, upper and lower 2.5% quantiles, the median, variance, coefficient of variation as well as the variance and minimum and maximum sample value drawn in course of estimating the statistics.

Internally, this method calls `generate.bru()` in order to draw samples from the model.

In addition to the component names (that give the effect of each component evaluated for the input data), the suffix `_latent` variable name can be used to directly access the latent state for a component, and the suffix function `_eval` can be used to evaluate a component at other input values than the expressions defined in the component definition itself, e.g. `field_eval(cbind(x, y))` for a component that was defined with `field(coordinates, ...)` (see also `component_eval()`).

For "iid" models with `mapper = bru_mapper_index(n)`, `rnorm()` is used to generate new realisations for indices greater than `n`.

Value

a data.frame or Spatial* object with predicted mean values and other summary statistics attached.

Examples

```
if (bru_safe_inla(multicore = FALSE) &&
    require("ggplot2", quietly = TRUE)) {

  # Load the Gorilla data

  data(gorillas, package = "inlabru")

  # Plot the Gorilla nests, the mesh and the survey boundary

  ggplot() +
    gg(gorillas$mesh) +
    gg(gorillas$nests) +
    gg(gorillas$boundary) +
    coord_fixed()

  # Define SPDE prior

  matern <- INLA::inla.spde2.pcmatern(gorillas$mesh,
    prior.sigma = c(0.1, 0.01),
    prior.range = c(0.01, 0.01)
  )

 # Define domain of the LGCP as well as the model components (spatial SPDE effect and Intercept)

  cmp <- coordinates ~ mySmooth(main = coordinates, model = matern) + Intercept(1)

  # Fit the model, with "eb" instead of full Bayes
  fit <- lgcp(cmp, gorillas$nests,
    samplers = gorillas$boundary,
    domain = list(coordinates = gorillas$mesh),
    options = list(control.inla = list(int.strategy = "eb"))
  )

  # Once we obtain a fitted model the predict function can serve various purposes.
  # The most basic one is to determine posterior statistics of a univariate
  # random variable in the model, e.g. the intercept

  icpt <- predict(fit, NULL, ~ c(Intercept = Intercept_latent))
  plot(icpt)

  # The formula argument can take any expression that is valid within the model, for
  # instance a non-linear transformation of a random variable

  exp.icpt <- predict(fit, NULL, ~ c(
    "Intercept" = Intercept_latent,
    "exp(Intercept)" = exp(Intercept_latent)
  ))
  plot(exp.icpt, bar = TRUE)

  # The intercept is special in the sense that it does not depend on other variables
```

```
  # or covariates. However, this is not true for the smooth spatial effects 'mySmooth'.
  # In order to predict 'mySmooth' we have to define where (in space) to predict. For
  # this purpose, the second argument of the predict function can take \code{data.frame}
  # objects as well as Spatial objects. For instance, we might want to predict
  # 'mySmooth' at the locations of the mesh vertices. Using

  vrt <- vertices(gorillas$mesh)

  # we obtain these vertices as a SpatialPointsDataFrame

  ggplot() +
    gg(gorillas$mesh) +
    gg(vrt, color = "red")

  # Predicting 'mySmooth' at these locations works as follows

  mySmooth <- predict(fit, vrt, ~mySmooth)

  # Note that just like the input also the output will be a SpatialPointsDataFrame
  # and that the predicted statistics are simply added as columns

  class(mySmooth)
  head(vrt)
  head(mySmooth)

  # Plotting the mean, for instance, at the mesh node is straight forward

  ggplot() +
    gg(gorillas$mesh) +
    gg(mySmooth, aes(color = mean), size = 3)

  # However, we are often interested in a spatial field and thus a linear interpolation,
  # which can be achieved by using the gg mechanism for meshes

  ggplot() +
    gg(gorillas$mesh, color = mySmooth$mean)

  # Alternatively, we can predict the spatial field at a grid of locations, e.g. a
  # SpatialPixels object covering the mesh

  pxl <- pixels(gorillas$mesh)
  mySmooth2 <- predict(fit, pxl, ~mySmooth)

  # This will give us a SpatialPixelDataFrame with the columns we are looking for

  head(mySmooth2)
  ggplot() +
    gg(mySmooth2)
}
```

`robins_subset` *robins_subset*

Description

This is the `robins_subset` dataset, which is a subset of the full robins data set used to demonstrate a spatially varying trend coefficient model in Meehan et al. 2019. The dataset includes American Robin counts, along with time, location, and effort information, from Audubon Christmas Bird Counts (CBC) conducted in six US states between 1987 and 2016.

Usage

```
data(robins_subset)
```

Format

The data are a data.frame with variables

`circle`**:** Four-letter code of the CBC circle.

`bcr`**:** Numeric code for the bird conservation region encompassing the count circle.

`state`**:** US state encompassing the count circle.

`year`**:** calendar year the count was conducted.

`std_yr`**:** transformed year, with 2016 = 0.

`count`**:** number of robins recorded.

`log_hrs`**:** the natural log of party hours.

`lon`**:** longitude of the count circle centroid.

`lat`**:** latitude of the count circle centroid.

`obs`**:** unique record identifier.

Source

https://github.com/tmeeha/inlaSVCBC

References

Meehan, T.D., Michel, N.L., and Rue, H. 2019. Spatial modeling of Audubon Christmas Bird Counts reveals fine-scale patterns and drivers of relative abundance trends. Ecosphere, 10(4), p.e02707.

Examples

```
if (require(ggplot2, quietly = TRUE)) {
  data(robins_subset, package = "inlabru") # get the data

  # plot the counts for one year of data
  ggplot(robins_subset[robins_subset$std_yr == 0, ]) +
    geom_point(aes(lon, lat, colour = count + 1)) +
    scale_colour_gradient(low = "blue", high = "red", trans = "log")
}
```

`row_kron` *Row-wise Kronecker products*

Description

Takes two Matrices and computes the row-wise Kronecker product. Optionally applies row-wise weights and/or applies an additional 0/1 row-wise Kronecker matrix product.

Usage

```
row_kron(M1, M2, repl = NULL, n.repl = NULL, weights = NULL)
```

Arguments

`M1`	A matrix that can be transformed into a sparse Matrix.
`M2`	A matrix that can be transformed into a sparse Matrix.
`repl`	An optional index vector. For each entry, specifies which replicate the row belongs to, in the sense used in `INLA::inla.spde.make.A`
`n.repl`	The maximum replicate index, in the sense used in `INLA::inla.spde.make.A()`.
`weights`	Optional scaling weights to be applied row-wise to the resulting matrix.

Value

A `Matrix::sparseMatrix` object.

Author(s)

Finn Lindgren <`finn.lindgren@gmail.com`>

`sample.lgcp` *Sample from an inhomogeneous Poisson process*

Description

This function provides point samples from one- and two-dimensional inhomogeneous Poisson processes. The log intensity has to be provided via its values at the nodes of an `inla.mesh.1d` or `inla.mesh` object. In between mesh nodes the log intensity is assumed to be linear.

Usage

```
sample.lgcp(
  mesh,
  loglambda,
  strategy = NULL,
  R = NULL,
  samplers = NULL,
  ignore.CRS = FALSE
)
```

Arguments

`mesh`	An `INLA::inla.mesh` object
`loglambda`	vector or matrix; A vector of log intensities at the mesh vertices (for higher order basis functions, e.g. for `inla.mesh.1d` meshes, `loglambda` should be given as `mesh$m` basis function weights rather than the values at the `mesh$n` vertices) A single scalar is expanded to a vector of the appropriate length. If a matrix is supplied, one process sample for each column is produced.
`strategy`	Only relevant for 2D meshes. One of `'triangulated'`, `'rectangle'`, `'sliced-spherical'`, `'spherical'`. The `'rectangle'` method is only valid for CRS-less flat 2D meshes. If `NULL` or `'auto'`, the the likely fastest method is chosen; `'rectangle'` for flat 2D meshes with no CRS, `'sliced-spherical'` for CRS `'longlat'` meshes, and `'triangulated'` for all other meshes.
`R`	Numerical value only applicable to spherical and geographical meshes. It is interpreted as `R` is the equivalent Earth radius, in km, used to scale the lambda intensity. For CRS enabled meshes, the default is 6371. For CRS-less spherical meshes, the default is 1.
`samplers`	A `SpatialPolygonsDataFrame` or `inla.mesh` object. Simulated points that fall outside these polygons are discarded.
`ignore.CRS`	logical; if `TRUE`, ignore any CRS information in the mesh. Default `FALSE`. This affects `R` and the permitted values for `strategy`.

Details

For 2D processes on a sphere the `R` parameter can be used to adjust to sphere's radius implied by the mesh. If the intensity is very high the standard `strategy` "spherical" can cause memory issues. Using the "sliced-spherical" strategy can help in this case.

- For crs-less meshes on R2: Lambda is interpreted in the raw coordinate system. Output has an NA CRS.
- For crs-less meshes on S2: Lambda with raw units, after scaling the mesh to radius `R`, if specified. Output is given on the same domain as the mesh, with an NA CRS.
- For crs meshes on R2: Lambda is interpreted as per km^2, after scaling the globe to the Earth radius 6371 km, or `R`, if specified. Output given in the same CRS as the mesh.
- For crs meshes on S2: Lambda is interpreted as per km^2, after scaling the globe to the Earth radius 6371 km, or `R`, if specified. Output given in the same CRS as the mesh.

Value

A `data.frame` (1D case), SpatialPoints (2D flat and 3D spherical surface cases) SpatialPointsDataFrame (2D/3D surface cases with multiple samples). For multiple samples, the `data.frame` output has a column `'sample'` giving the index for each sample. object of point locations.

Author(s)

Daniel Simpson <`dp.simpson@gmail.com`> (base rectangle and spherical algorithms), Fabian E. Bachl <`bachlfab@gmail.com`> (inclusion in inlabru, sliced spherical sampling), Finn Lindgren <`finn.lindgren@gmail.com`> (extended CRS support, triangulated sampling)

Examples

```
# The INLA package is required
if (bru_safe_inla(quietly = TRUE)) {
  vertices <- seq(0, 3, by = 0.1)
  mesh <- INLA::inla.mesh.1d(vertices)
  loglambda <- 5 - 0.5 * vertices
  pts <- sample.lgcp(mesh, loglambda)
  pts$y <- 0
  plot(vertices, exp(loglambda), type = "l", ylim = c(0, 150))
  points(pts, pch = "|")
}



# The INLA package and PROJ6 are required
if (bru_safe_inla(quietly = TRUE) &&
  fm_has_PROJ6() &&
  require(ggplot2, quietly = TRUE)) {
  data("gorillas", package = "inlabru")
  pts <- sample.lgcp(gorillas$mesh,
    loglambda = 1.5,
    samplers = gorillas$boundary
```

```
  )
  ggplot() +
    gg(gorillas$mesh) +
    gg(pts)
}
```

`seals` *Seal pups*

Description

This is a single transect of an aereal photo seal pup survey in the Greenland Sea

Usage

```
data(seals)
```

Format

The data contain these objects:

`points`: A `SpatialPointsDataFrame` Center locations of the photos

`mesh`: An `inla.mesh` enclosing the plane's transect

`ice.data`: An `SpatialPointsDataFrame` with MODIS ice concentration estimates

`ice.cv`: An `covdata` object with interpolated ice coverage data

Source

Martin Jullum <`Martin.Jullum@nr.no`>

References

Oigard, T. A. (2013) From pup production to quotas: current status of harp seals in the Greenland Sea. ICES Journal of Marine Science, doi.10.1093/icesjms/fst155.

Oigard, T. A. (2014) Current status of hooded seals in the Greenland Sea. Victims of climate change and predation?, Biological Conservation , 2014, 172, 29 - 36.

Examples

```
if (require(ggplot2, quietly = TRUE)) {
  data(seals, package = "inlabru")
  ggplot() +
    gg(seals$mesh) +
    gg(seals$points)
}
```

`shrimp` *Blue and red shrimp in the Western Mediterranean Sea*

Description

Blue and red shrimp in the Western Mediterranean Sea.

Usage

```
data(shrimp)
```

Format

A list of objects:

`haul`: A `SpatialPointsDataFrame` object containing haul locations

`mesh`: An `inla.mesh` object containing a Delaunay triangulation mesh (a type of discretization of continuous space) covering the haul locations.

- `catch` Catch in Kg.
- `landing` Landing in Kg.
- `depth` Mean depth of the fishery haul.

Source

Pennino, Maria Grazia. Personal communication.

References

Pennino, M. G., Paradinas, I., Munoz, F., Illian, J.,Quilez-Lopez, A., Bellido, J.M., Conesa, D. Accounting for preferential sampling in species distribution models. Ecology and Evolution, In Press.

Examples

```
if (require(ggplot2, quietly = TRUE)) {
  data(shrimp, package = "inlabru")
  ggplot() +
    gg(shrimp$mesh) +
    gg(shrimp$hauls) +
    coord_equal()
}
```

`sline` *Convert data frame to SpatialLinesDataFrame*

Description

A line in 2D space is defined by a start and an and point, each associated with 2D coordinates. This function takes a /codedata.frame as input and assumes that each row defines a line in space. In order to do so, the data frame must have at least four columns and the `start.cols` and `end.cols` parameters must be used to point out the names of the columns that define the start and end coordinates of the line. The data is then converted to a `SpatialLinesDataFrame` `DF`. If a coordinate reference system `crs` is provided it is attached to `DF`. If also `to.crs` is provided, the coordinate system of `DF` is transfromed accordingly. Additional columns of the input data, e.g. covariates, are retained and attached to `DF`.

Usage

```
sline(data, start.cols, end.cols, crs = CRS(as.character(NA)), to.crs = NULL)
```

Arguments

`data`	A data.frame
`start.cols`	Character array poitning out the columns of `data` that hold the start points of the lines
`end.cols`	Character array poitning out the columns of `data` that hold the end points of the lines
`crs`	Coordinate reference system of the original `data`
`to.crs`	Coordinate reference system for the SpatialLines ouput.

Value

SpatialLinesDataFrame

Examples

```
# Create a data frame defining three lines
lns <- data.frame(
  xs = c(1, 2, 3), ys = c(1, 1, 1), # start points
  xe = c(2, 3, 4), ye = c(2, 2, 2)
) # end points


# Conversion to SpatialLinesDataFrame without CRS
spl <- sline(lns,
  start.cols = c("xs", "ys"),
  end.cols = c("xe", "ye")
)
```

```
if (require(ggplot2, quietly = TRUE)) {
  # Plot the lines
  ggplot() +
    gg(spl)
}
```

`spatial.to.ppp` *Convert SpatialPoints and boundary polygon to spatstat ppp object*

Description

Spatstat point pattern objects consist of points and an observation windows. This function uses a SpatialPoints object and a SpatialPolygon object to generate the points and the window. Lastly, the ppp() function is called to create the ppp object.

Usage

```
spatial.to.ppp(points, samplers)
```

Arguments

`points`	A `SpatialPoints[DataFrame]` object describing the point pattern.
`samplers`	A `SpatialPolygons[DataFrame]` object describing the observation window.

Value

A spatstat `spatstat` ppp object

Examples

```
if (require("spatstat.geom")) {
  # Load Gorilla data

  data("gorillas", package = "inlabru")

  # Use nest locations and survey boundary to create a spatstat ppp object

  gp <- spatial.to.ppp(gorillas$nests, gorillas$boundary)
  class(gp)

  # Plot it

  plot(gp)
}
```

`spde.posterior` *Posteriors of SPDE hyper parameters and Matern correlation or covariance function.*

Description

Calculate posterior distribution of the range, log(range), variance, or log(variance) parameter of a model's SPDE component. Can also plot Matern correlation or covariance function. `inla.spde.result`.

Usage

```
spde.posterior(result, name, what = "range")
```

Arguments

`result`	An object inheriting from `inla`.
`name`	Character stating the name of the SPDE effect, see `names(result$summary.random)`.
`what`	One of "range", "log.range", "variance", "log.variance", "matern.correlation" or "matern.covariance".

Value

A `prediction` object.

Author(s)

Finn Lindgren <`Finn.Lindgren@ed.ac.uk`>

Examples

```
if (bru_safe_inla() && require(ggplot2, quietly = TRUE)) {

  # Load 1D Poisson process data

  data(Poisson2_1D, package = "inlabru")


  # Take a look at the point (and frequency) data

  ggplot(pts2) +
   geom_histogram(aes(x = x), binwidth = 55 / 20, boundary = 0, fill = NA, color = "black") +
    geom_point(aes(x), y = 0, pch = "|", cex = 4) +
    coord_fixed(ratio = 1)

  # Fit an LGCP model with  and SPDE component

  x <- seq(0, 55, length = 20)
```

```
  mesh1D <- INLA::inla.mesh.1d(x, boundary = "free")
  mdl <- x ~ spde1D(x, model = INLA::inla.spde2.matern(mesh1D)) + Intercept
  fit <- lgcp(mdl, data = pts2, domain = list(x = mesh1D))

  # Calculate and plot the posterior range

  range <- spde.posterior(fit, "spde1D", "range")
  plot(range)

  # Calculate and plot the posterior log range

  lrange <- spde.posterior(fit, "spde1D", "log.range")
  plot(lrange)

  # Calculate and plot the posterior variance

  variance <- spde.posterior(fit, "spde1D", "variance")
  plot(variance)

  # Calculate and plot the posterior log variance

  lvariance <- spde.posterior(fit, "spde1D", "log.variance")
  plot(lvariance)

  # Calculate and plot the posterior Matern correlation

  matcor <- spde.posterior(fit, "spde1D", "matern.correlation")
  plot(matcor)

  # Calculate and plot the posterior Matern covariance

  matcov <- spde.posterior(fit, "spde1D", "matern.covariance")
  plot(matcov)
}
```

`spoly` *Convert a data.frame of boundary points into a SpatialPolgons-DataFrame*

Description

A polygon can be described as a sequence of points defining the polygon's boundary. When given such a sequence (anti clockwise!) this function creates a SpatialPolygonsDataFrame holding the polygon decribed. By default, the first two columns of `data` are assumed to define the x and y coordinates of the points. This behavior can ba changed using the `cols` parameter, which points out the names of the columns holding the coordinates. The coordinate reference system of the resulting spatial polygon can be set via the `crs` paraemter. Posterior conversion to a different CRS is supported using the `to.crs` parameter.

Usage

```
spoly(
  data,
  cols = colnames(data)[1:2],
  crs = CRS(NA_character_),
  to.crs = NULL
)
```

Arguments

`data`	A data.frame of points describing the boundary of the polygon
`cols`	Column names of the x and y coordinates within the data
`crs`	Coordinate reference system of the points
`to.crs`	Coordinate reference system for the SpatialLines ouput.

Value

SpatialPolygonsDataFrame

Examples

```
# Create data frame of boundary points (anti clockwise!)
pts <- data.frame(
  x = c(1, 2, 1.7, 1.3),
  y = c(1, 1, 2, 2)
)

# Convert to SpatialPolygonsDataFrame
pol <- spoly(pts)

if (require(ggplot2, quietly = TRUE) &&
  require(ggpolypath, quietly = TRUE)) {
  # Plot it!
  ggplot() +
    gg(pol)
}
```

`stransform` *Coordinate transformation for spatial objects*

Description

This is a wrapper for the spTransform function provided by the `sp` package. Given a spatial object (or a list thereof) it will transform the coordinate system according to the parameter `crs`. In addition to the usual spatial objects this function is also capables of transforming `INLA::inla.mesh` objects that are equipped with a coordinate system.#'

Usage

```
stransform(splist, crs)
```

Arguments

`splist`	list of Spatial* objects
`crs`	Coordinate reference system to change to

Value

List of Spatial* objects

Examples

```

# Load Gorilla data
data("gorillas", package = "inlabru")

# Take the mesh and transform it to latitude/longitude
tmesh <- stransform(gorillas$mesh, crs = CRS("+proj=longlat"))

# Compare original and transformed mesh

if (require(ggplot2, quietly = TRUE)) {
  multiplot(
    ggplot() +
      gg(gorillas$mesh) +
      ggtitle("Original mesh"),
    ggplot() +
      gg(tmesh) +
      ggtitle("Transformed mesh")
  )
}
```

`summary.bru` *Summary for an inlabru fit*

Description

Takes a fitted bru object produced by `bru()` or `lgcp()` and creates various summaries from it.

Usage

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

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

Arguments

`object`	An object obtained from a `bru()` or `lgcp()` call
`...`	ignored arguments
`x`	An `summary_bru2` object

Examples

```
if (bru_safe_inla(multicore = FALSE)) {

  # Simulate some covariates x and observations y
  input.df <- data.frame(x = cos(1:10))
  input.df <- within(input.df, y <- 5 + 2 * x + rnorm(10, mean = 0, sd = 0.1))

  # Fit a Gaussian likelihood model
  fit <- bru(y ~ x + Intercept, family = "gaussian", data = input.df)

  # Obtain summary
  fit$summary.fixed
}


if (bru_safe_inla(multicore = FALSE)) {

  # Alternatively, we can use the like() function to construct the likelihood:

  lik <- like(family = "gaussian", formula = y ~ x + Intercept, data = input.df)
  fit <- bru(~ x + Intercept(1), lik)
  fit$summary.fixed
}

# An important addition to the INLA methodology is bru's ability to use
# non-linear predictors. Such a predictor can be formulated via like()'s
# \code{formula} parameter. The z(1) notation is needed to ensure that
# the z component should be interpreted as single latent variable and not
# a covariate:

if (bru_safe_inla(multicore = FALSE)) {
  z <- 2
  input.df <- within(input.df, y <- 5 + exp(z) * x + rnorm(10, mean = 0, sd = 0.1))
  lik <- like(
    family = "gaussian", data = input.df,
    formula = y ~ exp(z) * x + Intercept
  )
  fit <- bru(~ z(1) + Intercept(1), lik)

  # Check the result (z posterior should be around 2)
  fit$summary.fixed
}
```

`summary.bru_info` *Methods for bru_info objects*

Description

Methods for bru_info objects

Summary for bru_info objects

Usage

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

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

bru_info(...)

## S3 method for class 'character'
bru_info(method, ..., inlabru_version = NULL, INLA_version = NULL)

## S3 method for class 'bru'
bru_info(object, ...)
```

Arguments

`object`	Object to operate on
`...`	Arguments passed on to other methods
`x`	A `summary_bru_info` object to be printed
`method`	character; The type of estimation method used
`inlabru_version`	character; inlabru package version. Default: NULL, for automatically detecting the version
`INLA_version`	character; INLA package version. Default: NULL, for automatically detecting the version

---

`summary.bru_options` *Print inlabru options*

Description

Print inlabru options

Usage

```
## S3 method for class 'bru_options'
summary(
  object,
  legend = TRUE,
  include_global = TRUE,
  include_default = TRUE,
  ...
)

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

Arguments

`object`	A bru_options object to be summarised
`legend`	logical; If `TRUE`, include explanatory text, Default: `TRUE`
`include_global`	logical; If `TRUE`, include global override options
`include_default`	logical; If `TRUE`, include default options
`...`	Further parameters, currently ignored
`x`	A `summary_bru_options` object to be printed

Examples

```
if (interactive()) {
  options <- bru_options(verbose = TRUE)

  # Don't print options only set in default:
  print(options, include_default = FALSE)

  # Only include options set in the object:
  print(options, include_default = FALSE, include_global = FALSE)
}
```

`summary_bru` *Deprecated functions in inlabru*

Description

These functions still attempt to do their job, but will be removed in a future version.

Usage

```
summary_bru(object, ...)

iinla.getOption(name = NULL)

iinla.setOption(...)

init.tutorial()
```

Arguments

`object`	An object obtained from a `bru()` or `lgcp()` call
`...`	arguments passed on to other methods or ignored
`name`	character; an option name

Functions

- `summary_bru()`: Old summary for an inlabru fit.

  Takes a fitted bru object produced by `bru()` or `lgcp()` and creates various summaries from it.
- `iinla.getOption()`: Use `bru_option_get` instead.
- `iinla.setOption()`: Use `bru_option_set` instead.
- `init.tutorial()`: Global setting for tutorial sessions.

  Use `bru_options_set()` to set specific options instead instead. In versions <= 2.1.15, this function set the INLA integration strategy to "eb" to speed up calculations. This is normally not needed since version 2.2.0, since the only the final iteration will use other than "eb".

Author(s)

Fabian E. Bachl <`bachlfab@gmail.com`>

Examples

```
## Not run:
# Note: Only run this if you want to change the inlabru options for this session

# Determine current bru defaults:
bo <- bru_options_get()

init.tutorial()

# Check if it worked:
bru_options_get("control.inla")

## End(Not run)
```

`toygroups` *Simulated 1D animal group locations and group sizes*

Description

This data set serves to teach the concept of modelling species that gather in groups and where the grouping behaviour depends on space.

Usage

`data(toygroups)`

Format

The data are a list that contains these elements:

`groups`: A `data.frame` of group locations `x` and size `size`

`df.size`: IGNORE THIS

`df.intensity`: A `data.frame` with Poisson process intensity `d.lambda` at locations `x`

`df.rate`: A `data.frame` the locations `x` and associated `rate` which parameterized the exponential distribution from which the group sizes were drawn.

Examples

```
if (require(ggplot2, quietly = TRUE)) {
  # Load the data

  data("toygroups", package = "inlabru")

  # The data set is a simulation of animal groups residing in a 1D space. Their
  # locations in x-space are sampled from a Cox process with intensity

  ggplot(toygroups$df.intensity) +
    geom_line(aes(x = x, y = g.lambda))

  # Adding the simulated group locations to this plot we obtain

  ggplot(toygroups$df.intensity) +
    geom_line(aes(x = x, y = g.lambda)) +
    geom_point(data = toygroups$groups, aes(x, y = 0), pch = "|")

  # Each group has a size mark attached to it.
  # These group sizes are sampled from an exponential distribution
  # for which the rate parameter depends on the x-coordinate

  ggplot(toygroups$groups) +
    geom_point(aes(x = x, y = size))
```

```
  ggplot(toygroups$df.rate) +
    geom_line(aes(x, rate))
}
```

`vertices` *Vertices*

Description

This is a generic function. The outcome depends on the `object` provided

Usage

```
vertices(object)

## S4 method for signature 'inla.mesh'
vertices(object)
```

Arguments

`object`	An object for which to call the particular vertices method.

Value

The form of the value returned by vertices() depends on the class of its argument. See the documentation of the particular methods for details of what is produced by that method.

`vertices.inla.mesh` *Extract vertex locations from an* `inla.mesh`

Description

Converts the vertices of an `inla.mesh` object into a `SpatialPointsDataFrame`.

Usage

```
vertices.inla.mesh(object)
```

Arguments

`object`	An `inla.mesh` object.

Value

A SpatialPointsDataFrame of mesh vertex locations. The `vrt` column indicates the internal vertex id.

Author(s)

Fabian E. Bachl <`bachlfab@gmail.com`>

Examples

```
if (require(ggplot2, quietly = TRUE)) {
  data("mrsea", package = "inlabru")
  vrt <- vertices(mrsea$mesh)
  ggplot() +
    gg(mrsea$mesh) +
    gg(vrt, color = "red")
}
```

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