Package ‘spikeSlabGAM’

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evalTerm

Get summaries of the posterior (predictive) distribution of the linear predictor of a model term

Description

Get summaries of the posterior (predictive) distribution of the linear predictor of a model term

Usage

evalTerm(label, model, newdata = NULL, aggregate = mean, quantiles = c(0.1, 0.9), returnData = TRUE)

Arguments

label (character) the label of one of the terms in model.
model a spikeSlabGAM object
newdata data.frame on which to evaluate label. Defaults to NULL, in which case the term is evaluated on the original data.
aggregate (function) a summary statistic that is applied over the mcmc-samples of the linear predictor. Defaults to mean.
quantiles (numeric) a vector of quantiles for borders of credible regions of the linear predictor. Defaults to 10 and 90 percent quantiles, i.e. a (point-wise) 80 percent credible region.
returnData should the relevant original variables be included in the returned data.frame? Defaults to TRUE.
Value

A data.frame that contains the relevant variables from newdata (if returnData is TRUE), the aggregate-summary and the requested quantiles.

Author(s)

Fabian Scheipl

Description

Generate design for a factor covariate

Usage

fct(x, contr = "contr.sum")

Arguments

x a covariate that can be treated as a factor
contr (character) name of the contrasts associated with the factor. Defaults to "contr.sum".

Value

design matrix for a factor

Author(s)

Fabian Scheipl

Description

Get the posterior distribution of the linear predictor of a model term

Usage

getPosteriorTerm(label = NULL, model, betaInd = NULL)
### Arguments

- **label** (character) one of the terms in `model`
- **model** a `spikeSlabGAM` object
- **betaInd** (optional) the column indices of the part of the design matrix for which the linear predictor is to be evaluated.

### Value

A matrix containing the samples of the linear predictor associated with `label`; with attribute 'coef' that contains the posterior samples of the associated coefficients.

### Author(s)

Fabian Scheipl

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#### lin

*Generate orthogonal polynomial base for a numeric covariate without intercept*

### Description

Generate orthogonal polynomial base for a numeric covariate without intercept

### Usage

```r
lin(x, order = 1)
```

### Arguments

- **x** covariate
- **order** order of the polynomial, defaults to 1

### Value

An orthogonal basis for a centered polynomial function in `x`

### Author(s)

Fabian Scheipl
Generate design for a 2-D Gaussian Markov Random Field

Description

The returned design is (a low-rank approximation to) the matrix square root of the implied covariance of the centered MRF. The function stops if 'islands', i.e. regions without any neighbors are found. Regions without observations have to be removed from the neighborhood matrix and there is currently no predict-functionality for regions without observations in the original data.

Usage

mrf(x, N, decomposition = c("ortho", "MM"), tol = 1e-10, rankZ = 0.995)

Arguments

- **x**: a factor: which observation belongs to which region
- **N**: the neighborhood (adjacency) matrix: a symmetric matrix with one column/row for every level of x, defining the neighborhood structure (either 0-1 or with positive weights, e.g. based on shared boundary length or centroid distances). Has to have rownames and column names that correspond to the levels of x, the function checks whether the rows/columns are in the same order as the levels of x. Entries on the diagonal are ignored.
- **decomposition**: use a (truncated) spectral decomposition of the implied prior covariance of \( f(x) \) for a low rank representation with orthogonal basis functions and i.i.d. coefficients ("ortho"), or use the mixed model reparameterization for non-orthogonal basis functions and i.i.d. coefficients ("MM"). Defaults to "MM".
- **tol**: count singular/eigenvalues smaller than this as zero
- **rankZ**: how many eigenvectors to retain from the eigen decomposition: either a number > 3 or the proportion of the sum of eigenvalues the retained eigenvectors must represent at least. Defaults to .999.

Value

a transformed design matrix for the Markov Random Field

Author(s)

Fabian Scheipl

References

plot.spikeSlabGAM Generates graphical summaries of a fitted model

Description

This function plots the estimated linear predictors of the terms in a model on a grid of values. By default displays all 3-way, 2-way interactions and main effects present in the model. Starting with ggplot-0.9.2 these are no longer aligned by their axes due to internal changes in grid and ggplot2. Uses gridExtra's marrangeGrob to arrange the plots for the terms, also over multiple pages if necessary. This means the graphics device type is temporarily set to the value of interactive.dev in interactive use in RStudio if necessary since the RStudio graphical device does not support opening multiple pages.

Usage

```r
## S3 method for class 'spikeSlabGAM'
plot(x, labels = NULL, cumulative = TRUE,
     commonEtaScale = FALSE, aggregate = mean, quantiles = c(0.1, 0.9),
     gridlength = 20, base_size = 12, ggElems = list(),
     nrow = min(ceiling(sqrt(length(plotList))), 3),
     ncol = min(ceiling(length(plotList)/nrow), 3), interactive.dev = c("x11",
     "quartz", "windows"), ...)
```

Arguments

- `x`: a fitted spikeSlabGAM model
- `labels`: a character vector of names of model terms to be plotted
- `cumulative`: Defaults to TRUE, in which case all lower order terms that are involved in an interaction are cumulated and then plotted (e.g., if a model contains 2 smooth effects and their interaction, ONLY the sum of the marginal smooth and linear terms and all their interactions are plotted.) If FALSE, a separate plot for every term in the model is produced.
- `commonEtaScale`: use the same limits for all vertical axes of the different panels? Defaults to FALSE. Can be useful to compare effect sizes more easily between panels, but tends to mess up the scales.
- `aggregate`: (function) which summary statistic to use for the posterior of the model terms. Defaults to the mean.
- `quantiles`: which quantiles to use for the borders of credible regions. Defaults to 10% and 90% percentiles. Set to NULL to omit plotting credible regions.
- `gridlength`: length of the (univariate) grids for the covariates on which to evaluate the posterior. Defaults to 20.
- `base_size`: default base font size for plot (see e.g. theme_gray)
**plotTerm**

- `ggElems`: a list of plot elements to give to `ggplot`. Use this to supply custom themes or colors, fortify the plot(s) with partial residuals etc. Defaults to an empty list. Unless specified differently here, the default ggplot-theme (`theme_gray`) is changed to a white background with major gridlines in gray (`'grey95'`), no minor grid lines, and smaller text for the legends.

- `nrow`: number of rows per page, defaults to min(sqrt(no. of plots), 3). See `marrangeGrob`.

- `ncol`: number of columns per page, defaults to min((no. of plots)/nrow, 3). See `marrangeGrob`.

- `interactive.dev`: alternative device to use in interactive mode in RStudio if output needs to be spread on multiple pages, since the RStudio graphical device does not support opening multiple displays.

- `...`: arguments passed to `marrangeGrob`.

**Value**

a list of `ggplot`-objects (invisible)

**Note**

Note that `cumulative = TRUE` will only find all relevant terms to accumulate if, for all numeric covariates that have a smooth term, the smooth term is specified after the linear term in the formula.

**Author(s)**

Fabian Scheipl

**See Also**

`plotTerm` for more details on the specific plots

**Examples**

```r
#see ?spikeSlabGAM
```

---

**Description**

Plots the estimated linear predictor for a model term, i.e a main effect or a (2- or 3-way) interaction. Plots for the joint effect of two numerical covariates show an overlay if quantiles were specified: Regions where the pointwise credible intervals do not contain zero are plotted in muted red (> 0) and blue (< 0), overlaid by coloured contour lines that show the aggregate values. Contour lines are shown only inside the convex hull of the original observations. Plots for `srf:lin` terms show the spatially varying coefficient, i.e. the contour lines represent the change in the linear predictor when the lin-covariate increases by 1 standard deviation. For this reason, a cumulative plot makes no sense and the routine will set `cumulative = FALSE` with a warning.
Usage

plotTerm(label, m, cumulative = TRUE, aggregate = mean, quantiles = c(0.1, 0.9), gridlength = 40, contours = 30, ggElems = list())

Arguments

label (character) the label of the effect to be plotted.
m a fitted spikeslabGAM model
cumulative Defaults to TRUE, in which case the lower order terms that are associated with the covariates involved in label are cumulated and then plotted. (e.g. if label denotes a smooth term, the sum of the linear and smooth effect is displayed if TRUE, if label is a factor-factor interaction, the sum of both main effects and their interaction is displayed etc.) If FALSE, only the marginal effect of label is displayed.
aggregate (function) which summary statistic to use for the posterior of the effect. Defaults to the mean.
quantiles which quantiles to use for the borders of credible regions. Defaults to 10 regions. Cannot deal with more than two quantiles.
gridlength length of the (univariate) grids on which to evaluate the posterior.
contours use how many contour lines for the joint effect of two numerical covariates. Defaults to 30.

ggElems a list of plot elements to give to ggplot. Use this to supply custom themes, colour schemes etc. Defaults to an empty list, which yields the standard settings.

Details

Limitations: Plots for 4-way (or higher) interactions are not implemented. Requesting such a plot will return the NULL object with a warning. Plots for mrf just treat the grouping variable as a conventional factor i.e. will not incorporate any neighborhood or map information.

Value

an object of class ggplot. Use print or wrap the call to plotTerm in parentheses to directly render on a graphic device.

Author(s)

Fabian Scheipl

Examples

#see help for spikeslabGAM
predict.spikeSlabGAM  Obtain posterior predictive/credible intervals from a spike-and-slab model

Description
Obtain posterior predictive/credible intervals from a spike-and-slab model

Usage

```r
## S3 method for class 'spikeSlabGAM'
predict(object, newdata = NULL, type = c("response", "link", "terms"), terms = NULL, aggregate = mean, quantiles = NULL, addIntercept = is.null(terms), ...)
```

Arguments

- `object`  
a spikeSlabGAM model
- `newdata`  
an optional data.frame on which to evaluate predictions. Defaults to NULL, in which case the fitted values for the original data are returned
- `type`  
the type of prediction required. The default is on the scale of response, the alternative 'link' is on the scale of the linear predictor. Specifying 'terms' returns a list giving the linear predictors of the terms specified in terms.
- `terms`  
an optional character vector of term labels or variable names for which to return fits/predictions/credible regions. If variable names instead of term labels are supplied, the function returns predictions/estimates for all terms associated with these variables, i.e. their main effects (usually both linear and smooth for numeric covariates) and all interaction terms they are involved in.
- `aggregate`  
(function) the summary statistic of the posterior predictive of the linear predictor. Defaults to mean.
- `quantiles`  
(numeric) an optional vector of quantiles for borders of credible regions of the returned values. Defaults to NULL.
- `addIntercept`  
include global intercept term in prediction/estimate? Defaults to TRUE if `terms = NULL`.
- `...`  
arguments passed from or to other methods (not used)

Value

If `type` ="terms", a list of data.frames containing the requested pointwise summary statistics for the supplied terms (use e.g. `Reduce("+", ...)` to get row-wise sums of the list-entries). Otherwise, a data.frame containing the requested pointwise summary statistics of the posterior predictive of the linear predictor (type ="link") or the conditional expectation of the response (type ="response") is returned.

Author(s)

Fabian Scheipl
print.summary.spikeSlabGAM

Print summary for posterior of a spikeSlabGAM fit

Description

The model table shows at least the 10 and at most the 20 most probable models as found by SSVS, or enough models to account for 90% of the probability mass in the model space as found by SSVS by default.

Usage

```r
## S3 method for class 'summary.spikeSlabGAM'
print(x, digits = 3, printPGamma = TRUE,
      printModels = TRUE, showModels = NULL, ...)
```

Arguments

- `x` an object of class `summary.spikeSlabGAM`
- `digits` see `options`, defaults to 3
- `printPGamma` print marginal inclusion probabilities and norm of the linear predictor for each term? Defaults to TRUE
- `printModels` print most probable models visited by the SSVS? Defaults to TRUE
- `showModels` how many of the most probable models to display. See details for default.
- `...` arguments based from or to other methods (not used)

Value

invisibly returns x

Author(s)

Fabian Scheipl

See Also

`summary.spikeSlabGAM`
**rnd**

Generate design for a random intercept

**Description**

Generate design for a random intercept

**Usage**

```r
rnd(x, C = NULL)
```

**Arguments**

- `x`: a covariate that can be treated as a factor
- `C`: an optional known correlation structure of the random effects associated with `x`

**Value**

design matrix for a random intercept for `x`

**Author(s)**

Fabian Scheipl

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**sm**

Generate a reparameterized P-spline base

**Description**

The returned matrix is a low-rank approximation of the original P-spline basis (unless `decomposition = "asIs"`), that is projected into the complement of the nullspace of the associated penalty (unless `centerBase = FALSE`), i.e. for the default second order difference penalty, the resulting basis cannot reproduce linear or constant functions and parameterizes the "wiggly" part of the influence of `x` only. This means that it very rarely makes sense to run a model with `sm(x)` without also using `lin(x)` or `u(x)`. The projection improves the separability between the linear and smooth parts of the influence of `x` and centers the resulting function estimates s.t. \( \sum_i f(x_i) = 0 \).

**Usage**

```r
sm(x, K = min(length(unique(x)), 20), spline.degree = 3, diff.ord = 2,
    rankZ = 0.999, centerBase = T, centerx = x, decomposition = c("ortho",
    "MM", "asIs"), tol = 1e-10)
```
spikeAndSlab

Arguments

- **x**: covariate
- **K**: number of basis functions in the original basis (defaults to 20)
- **spline.degree**: defaults to 3 for cubic B-plines
- **diff.ord**: order of the difference penalty, defaults to 2 for penalizing deviations from linearity
- **rankZ**: how many eigenvectors to retain from the eigen decomposition: either a number > 3 or the proportion of the sum of eigenvalues the retained eigenvectors must represent at least. Defaults to .999.
- **centerBase**: project the basis of the penalized part into the complement of the column space of the basis of the unpenalized part? defaults to TRUE
- **centerx**: vector of x-values used for centering (defaults to \(x\))
- **decomposition**: use a truncated spectral decomposition of the implied prior covariance of \(f(x)\) for a low rank representation with orthogonal basis functions and i.i.d. coefficients ("ortho"), or use the mixed model reparameterization for non-orthogonal basis functions and i.i.d. coefficients ("MM") or use basis functions as they are with i.i.d. coefficients ("asis"). Defaults to "ortho".
- **tol**: count eigenvalues smaller than this as zero

Value

- a basis for a smooth function in \(x\)

Author(s)

- Fabian Scheipl

References


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spikeAndSlab Set up and sample a spike-and-slab prior model.

Description

This function sets up a spike-and-slab model for variable selection and model choice in generalized additive models and samples its posterior. It uses a blockwise Metropolis-within-Gibbs sampler and the redundant multiplicative parameter expansion described in the reference. This routine is not meant to be called directly by the user – spikeSlabGAM provides a formula-based interface for specifying models and takes care of (most of) the housekeeping. Sampling of the chains is done in parallel using package parallel. A "SOCK" cluster is set up under Windows to do so (and closed after computations are done, I try to clean up after myself), see makeCluster etc. Use options(mc.cores = <foo>) to set the (maximal) number of processes forked by the parallelization. If options()$mc.cores is unspecified, it is set to 2.
spikeAndSlab

Usage

spikeAndSlab(y, X, family = c("gaussian", "binomial", "poisson"),
    hyperparameters = list(), model = list(), mcmc = list(),
    start = list())

Arguments

y            response
X            design matrix
family       (character) the family of the response, defaults to normal/Gaussian response
hyperparameters
    a list of hyperparameters controlling the priors (see details)
model        a list with information about the grouping structure of the model (see details)
mcmc         (optional) list setting arguments for the sampler (see details)
start        (optional) list containing the starting values for $\beta, \gamma, \tau^2, \sigma^2, w$ and, optionally, the random seed

Details

Details for model specification:

hyperparameters A list:
    w     hyperparameters for the Beta-prior for $w$; defaults to c(alphaW = 1, betaW = 1), i.e. a uniform distribution.
    tau2  hyperparameters for the $\Gamma^{-1}$-prior of the hypervariances $\tau^2$; defaults to c(a1 = 5, a2 = 25)
    gamma sets $v_0$, the ratio between the spike and slab variances, defaults to c(v0 = 0.00025)
    sigma2 hyperparameters for $\Gamma^{-1}$-prior for error variance; defaults to c(b1 = 1e-4, b2 = 1e-4).
    Only relevant for Gaussian response.
    varKsi variance for prior of $\xi$, defaults to 1
    ksiDF defaults to 0 for a gaussian prior for $\xi$, else induces a t-prior for $\xi$ with ksiDF degrees of freedom.
model A list:
    groupIndicators a factor that maps the columns of X to the different model terms
    H a matrix containing the hierarchy of the penalized model terms
    n  number of observations
    q  length of $\beta$
    scale  scale/weights of the response, defaults to rep(1, n), use this to specify number of trials for binomial data
    offset defaults to rep(0, n)
mcmc A list:
    nChains how many parallel chains to run: defaults to 3
    chainLength how many samples should be generated per chain, defaults to 500
    burnin how many initial iterations should be discarded, defaults to 100
    thin save only every thin-th iteration, defaults to 5
verbose: verbose output and report progress? defaults to TRUE
returnSamples: defaults to TRUE
sampleY: generate samples of y and its conditional expectation from posterior predictive? defaults to FALSE
useRandomStart: use random draw or ridge estimate for beta as starting value? defaults to TRUE, i.e. random starting values.
blocksize: approx. block sizes of the updates for $\alpha, \xi$. Defaults to 50 for gaussian responses and 5/15 for non-gaussian responses.
scalemode: how to do term-wise rescaling of subvectors of $\xi$ in each iteration: 0 means no rescaling, 1 means rescaling s.t. each mean($|G_{ij}|$) = 1, 2 means rescaling s.t. each max($|G_{ij}|$) = 1
modeSwitching: probability to do P-IWLS with the mode of the proposal set to the current value, which is useful if the chain gets stuck. Defaults to 0.05. Increase if acceptance rates are too low.
reduceRet: don’t return data and samples for $\alpha, \xi, \tau^2$? defaults to FALSE

start: A list:
- beta: starting values for $\beta$. Defaults to a modified approximate ridge-penalized ML estimate. See vignette for details on default specification.
- gamma: starting values for $\gamma$. Defaults to a vector of 1’s if mcmc$useRandomStart$ is FALSE, otherwise drawn from the prior.
- tau2: starting values for $\tau^2$. Defaults to the mode of the prior if mcmc$useRandomStart$ is FALSE, otherwise drawn from the prior.
- sigma2: starting values for $\sigma^2$. Only relevant for Gaussian response. Defaults to the variance of the response divided by the number of covariates if mcmc$useRandomStart$ is FALSE, otherwise drawn from the prior.
- w: starting value for $w$. Defaults to the mean of the prior if mcmc$useRandomStart$ is FALSE, otherwise drawn from the prior.
- seed: Sets RNG seed for reproducible results. Parallel chains are seeded with this seed incremented by the number of the chain.

Value: a list with components:
- formula: see arguments
- data: see arguments
- family: see arguments
- y: see arguments
- X: see arguments
- hyperparameters: see arguments
- model: see arguments
- mcmc: see arguments
- start: see arguments
spikeSlabGAM

**posteriorPred** a list with entries \( \mu \) and \( y \) containing samples of the expected values and realizations of the response from the posterior predictive

**postMeans** a list containing the posterior means of the parameters:
- beta the regression coefficients
- alpha
- ksi
- tau hypervariances of the penalized model terms
- gamma inclusion indicator variables of the model terms
- pV1 \( P(\gamma = 1) \)
- w hyperparameter for gamma
- sigma2 error variance (for Gaussian data)
- logLik log likelihood
- logPost log of (unnormalized) posterior

**samples** a list containing the posterior samples of the parameters, see above for explanation of the entries

**DIC** a vector with \( DIC, pD, \bar{D}, \hat{D} \). Usually doesn’t make much sense for this kind of model because of the posterior’s multimodality.

**fitted** a matrix with the posterior mean of the linear predictor in the first column and the posterior mean of the expected response in the second.

**runTime** of the sampler, in seconds

**Author(s)**
Fabian Scheipl, Daniel Sabanes Bove

**References**

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**spikeSlabGAM**

*Generate posterior samples for a GAMM with spike-and-slab priors*

**Description**
This function fits structured additive regression models with spike-and-slab priors via MCMC. The spike-and-slab prior results in an SSVS-like term selection that can be used to aid model choice, e.g. to decide between linear and smooth modelling of numeric covariates or which interaction effects are relevant. Model terms can be factors (fct), linear/polynomial terms (lin), uni- or bivariate splines (sm, srf), random intercepts (rnd) or Markov random fields (mrf) and their interactions, i.e. an interaction between two smooth terms yields an effect surface, an interaction between a linear term and a random intercept yields random slopes, an interaction between a linear term and a smooth term yields a varying coefficient term etc.
Usage

spikeSlabGAM(formula, data, ..., family = "gaussian",
hyperparameters = list(), model = list(), mcmc = list(),
start = list())

Arguments

formula the model formula (see details below and ssGAMDesign).
data the data containing the variables in the function
... additional arguments for ssGAMDesign
family (character) the family of the response, defaults to normal/Gaussian response,
"poisson" and "binomial" are implemented as well.
hyperparameters A list of arguments specifying the prior settings. See spikeAndSlab.
model A list of arguments describing the model structure. See spikeAndSlab. Usersupplied groupIndicators and H entries will be overwritten by ssGAMDesign.
mcmc A list of arguments specifying MCMC sampler options. See spikeAndSlab.
start A list of starting values for the MCMC sampler. See spikeAndSlab. Use
start = list(seed =<your_seed^I to set the RNG seed for reproducible results.

Details

Implemented types of terms:

u unpenalized model terms associated with a flat prior (no selection)
lin linear/polynomial terms
fct factors
sm univariate smooth functions
rnd random intercepts
mrf Markov random fields
srf surface estimation

Terms in the formula that are not in the list of specials (i.e. the list of term types above) are automatically assigned an appropriate special wrapper, i.e. numerical covariates x are treated as lin(x) + sm(x), factors f (and numerical covariates with very few distinct values, see ssGAMDesign) are treated as fct(f). Valid model formulas have to satisfy the following conditions:

1. All variables that are involved in interactions have to be present as main effects as well, i.e. y ~ x1 + x1:x2 will produce an error because the main effect of x2 is missing.
2. Interactions between unpenalized terms not under selection (i.e. terms of type u) and penalized terms are not allowed, i.e. y ~ u(x1)* x2 will produce an error.
3. If main effects are specified as special terms, the interactions involving them have to be given as special terms as well, i.e. y ~ lin(x1) + lin(x2) + x1:x2 will produce an error.
The default prior settings for Gaussian data work best for a response with unit variance. If your data is scaled very differently, either rescale the response (recommended) or adjust the hyperparameters accordingly.

Sampling of the chains is done in parallel using package multicore if available. If not, a socket cluster set up with snow is used where available. Use options(mc.cores = foo) to set the (maximal) number of processes spawned by the parallelization. If options()$mc.cores is unspecified, snow uses 8.

Value

an object of class spikeSlabGAM with methods summary.spikeSlabGAM, predict.spikeSlabGAM, and plot.spikeSlabGAM.

Author(s)

Fabian Scheipl

References


See Also

ssGAMDesign for details on model specification, spikeAndSlab for more details on the MCMC sampler and prior specification, and ssGAM2Bugs for MCMC diagnostics. Check out the vignette for theoretical background and code examples.

Examples

```r
## Not run:
## examples not run due to time constraints on CRAN checks.
## Full examples below should take about 2-4 minutes.

set.seed(91179)
n <- 400
d <- data.frame(f1 = sample(gl(3, n/3)), f2 = sample(gl(4, n/4)), x1 = runif(n), x2 = runif(n), x3 = runif(n))
# true model:
# - interaction between f1 and x1
# - smooth interaction between x1 and x2,
# - x3 and f2 are noise variables without influence on y
nf1 <- as.numeric(d$f1)
d$f <- with(d, 5 * (nf1 + 2 * sin(4 * pi * (x1 - 0.2) * (x2 - 0.7)) - nf1 * x1))
d$y <- with(d, scale(f + rnorm(n)))
d$yp <- with(d, rpois(n, exp(f/10)))
```
Generate design for penalized surface estimation.

Description

This function generates the design for a 2-D penalized spline using (almost) radial basis functions. Use this type of term to account for spatial variation. Smooth interactions between covariates are often better fitted via the interactions of lin and sm terms, because they allow a decomposition into (linear and smooth) marginal trends and (linear-linear, linear-smooth/"varying coefficients", and smooth-smooth) interactions. This decomposition usually makes no sense for spatial data.

Usage

srf(coords, K = min(50, sum(nd)/4), rankZ = 0.999, centerBase = TRUE,
    baseType = c("B", "thinPlate"), decomposition = c("ortho", "MM", "asIs"),
    tol = 1e-10)
Arguments

- `coords`: a data.frame with two columns containing the coordinates.
- `K`: (approximate) number of basis functions in the original basis (defaults to 50). If `baseType = "B"` you can specify a vector giving the number of marginal basis functions in each direction.
- `rankZ`: how many eigenvectors to retain from the eigen decomposition: either a number > 3 or the proportion of the sum of eigenvalues the retained eigenvectors must represent at least. Defaults to .999.
- `centerBase`: project the basis of the penalized part into the complement of the column space of the basis of the unpenalized part? defaults to TRUE.
- `baseType`: Defaults to "B", i.e. a tensor product basis based on marginal cubic B-splines with ridge penalty (i.e. penalizing deviations from the constant). Set to "thinPlate" if cubic thin plate splines are desired, see note below.
- `decomposition`: use a (truncated) spectral decomposition of the implied prior covariance of \( f(x, y) \) for a low rank representation with orthogonal basis functions and i.i.d. coefficients ("ortho"), or use the mixed model reparameterization for non-orthogonal basis functions and i.i.d. coefficients ("mm") or use basis functions as they are with i.i.d. coefficients ("asIs"). Defaults to "ortho".
- `tol`: count eigenvalues smaller than this as zero.

Details

Note that `srf()` expects `coords` to be a data.frame within the larger data.frame supplied to `spikeSlabGAM` in its data argument, i.e. coords is considered a two-dimensional covariate.

If `baseType` is 'thinPlate', knot locations for the thin plate spline basis are chosen via a space-filling algorithm (i.e. medoids returned by `clara`) as suggested in Ruppert/Wand/Carroll, ch. 13.5. Since the thin plate penalty term penalizes deviations from a linear trend, it is recommended to add marginal linear trends and their interaction to the model if `baseType = "thinPlate"` to improve the fit.

Value

a design matrix for the 2-D spline.

Note

TODO: prediction seems very unstable when extrapolating outside the convex hull, sometimes even nonsensical values inside conv.hull close to border - problem in akima::interp?

Author(s)

Fabian Scheipl

References

ssGAM2Bugs  Convert samples from a model fitted with spikeSlabGAM into a bugs-object

Description
Use `plot` and `print` on the returned `bugs` object for convergence diagnostics. Lack of convergence for \( \alpha \) or \( \xi \) does not necessarily mean that the sampler has not converged for \( \beta \).

Usage
```r
ssGAM2Bugs(m, rm = c("alpha", "ksi", "gamma"))
```

Arguments
- `m`: a model fitted with `spikeSlabGAM`
- `rm`: which parameter blocks to omit from the conversion. Defaults to omission of \( \alpha, \xi, \) and \( \gamma \). Set to `NULL` to keep all MCMC samples.

Value
- A `bugs` object which has convenience functions for assessing convergence based on parallel MCMC runs.

Author(s)
Fabian Scheipl

Examples
```r
# see help for spikeSlabGAM
```

ssGAMDesign  Generate design and model information for spikeSlabGAM

Description
This function generates the design matrix for a generalized additive (mixed) model, based on smoothing spline ANOVA-like orthogonal decomposition of the model terms and their interactions. It parses the formula given to `spikeSlabGAM` to provide all the arguments necessary for the MCMC sampler.

Usage
```r
ssGAMDesign(formula, data, specials = c("u", "lin", "fct", "sm", "rnd", "mrf", "srf"), minUniqueValues = 6, lowRankInteractions = TRUE, orthogonalizeInteractions = TRUE, decomposition = NULL)
```
ssGAMDesign

Arguments

formula
  the model formula. Follows the usual R syntax described in formula. Terms
  in the formula that are not in the list of specials are automatically assigned an
  appropriate special, i.e. numerical covariates x are treated as \( \text{lin}(x) + \text{sm}(x) \),
  factors f are treated as \( \text{fct}(f) \) (see specials argument). See spikeslabgam
  for more details.

data
  data.frame containing all the variables in the function

specials
  a vector of the types of possible model terms. These must be implemented as
  functions generating a design matrix with a label attribute. See also sm() for an
  example. The documentation for spikeslabgam contains a list of implemented
  model term types and usage examples.

minUniqueValues
  the minimal number of unique values a covariate has to have in order to not be
  treated as a factor. Defaults to 6.

lowRankInteractions
  should a low-rank approximation of the design matrix for interaction terms
  based on a (truncated) spectral decomposition of the implied covariance matrix
  be used? defaults to TRUE.

orthogonalizeInteractions
  should the design matrices for interaction terms be projected into the comple-
  ment of the column space of the respective main effects? Can help separate
  marginal and interaction effects. Defaults to TRUE.

decomposition
  which decomposition to use, see sm. Defaults to the default of sm.

Details

Setting lowRankInteractions to FALSE can result in very large models, especially if higher-order
interactions or interactions between terms with lots of parameters are involved. Note that numeric
covariates with fewer unique values than minUniqueValues are treated as factors unless wrapped
in a special argument.

This function is not meant to be called directly by the user, spikeslabgam is the user interface.

Value

a list with components:

response
  the left hand side of the model formula

Design
  the design matrix of the model specified in formula

groupIndicators
  a factor that maps the columns of Design to the different model terms

H
  a matrix containing the hierarchy of the penalization groups (not used, included
  for backwards compatibility)

Author(s)

Fabian Scheipl
Description

Returns basic information about prior and model structure, posterior means of inclusion probabilities, term importance and the most probable models found by the SSVS.

Usage

```r
## S3 method for class 'spikeSlabGAM'
summary(object, threshold = 0.5, ...)
```

Arguments

- `object`: an object of class `spikeSlabGAM`
- `threshold`: threshold for inclusion of a model term. Defaults to 0.5.
- `...`: arguments passed from or to other methods (not used)

Details

Two scalar summaries of term importance are included:

- `P(gamma = 1)` The posterior mean of \( P(\gamma = 1) \), i.e. the marginal posterior inclusion probability of the term.
- `pi` The scaled dot products of the posterior mean of the linear predictor \( \eta_i \) associated with the \( i \)-th term and the total linear predictor \( \eta \): \( \pi_i = \eta_i^T \eta / \eta^T \eta \). They sum to one (but can be negative as well), and (for mutually orthogonal \( \eta_i \)) provide a percentage decomposition of the sum of squares of \( \eta \). See references for details.

The summary also shows the dimensionality of the basis associated with a term.

The top row in the model table shows the relative frequency of the respective model, the bottom row shows cumulative relative frequencies for the models visited most often.

Value

An object of class `summary.spikeslabGAM`

Author(s)

Fabian Scheipl

References

Gu, Chong (2002). Smoothing Spline ANOVA models. Springer. (see chapter 3.6)
Generate design for an always included covariate

**Description**

Basically a wrapper for `model.matrix(~ x, ...)`.  

**Usage**

```
u(x, ...)
```

**Arguments**

- `x` covariate
- `...` arguments passed to `model.matrix`

**Value**

A design matrix for `x`

**Author(s)**

Fabian Scheipl
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