Package 'bandle'

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Type Package

Title An R package for the Bayesian analysis of differential subcellular localisation experiments

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Description The Bandle package enables the analysis and visualisation of differential localisation experiments using mass-spectrometry data. Experimental methods supported include dynamic LOPIT-DC, hyperLOPIT, Dynamic Organellar Maps, Dynamic PCP. It provides Bioconductor infrastructure to analyse these data.

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`bandle-package` *An R package for the Bayesian analysis of differential subcellular localisation experiments*

Description

The Bandle package enables the analysis and visualisation of differential localisation experiments using mass-spectrometry data. Experimental methods supported include dynamic LOPIT-DC, hyperLOPIT, Dynamic Organellar Maps, Dynamic PCP. It provides Bioconductor infrastructure to analyse these data.

Details

The DESCRIPTION file: This package was not yet installed at build time.

Index: This package was not yet installed at build time.
~~ An overview of how to use the package, including the most important functions ~~

Author(s)

Oliver M. Crook [aut, cre] (<https://orcid.org/0000-0001-5669-8506>), Lisa Breckels [aut] (<https://orcid.org/0000-0001-8918-7171>)

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References

~~ Literature or other references for background information ~~

`bandle` *Differential localisation experiments using the bandle method*

Description

These function implement the bandle model for dynamic mass spectrometry based spatial proteomics datasets using MCMC for inference

These functions implement the bandle model for dynamic mass spectrometry based spatial proteomics datasets using MCMC for inference, this is an internal sampling function

Usage

```
bandle(
  objectCond1,
  objectCond2,
  fcol = "markers",
  hyperLearn = "LBFGS",
  numIter = 1000,
  burnin = 100L,
  thin = 5L,
  u = 2,
  v = 10,
  lambda = 1,
  gpParams = NULL,
  hyperIter = 20,
  hyperMean = c(0, 0, 0),
  hyperSd = c(1, 1, 1),
  seed = NULL,
  pg = FALSE,
  pgPrior = NULL,
```

```
  tau = 0.2,
  dirPrior = NULL,
  maternCov = TRUE,
  PC = TRUE,
  pcPrior = matrix(c(0.5, 3, 100), nrow = 1),
  nu = 2,
  propSd = c(0.3, 0.1, 0.05),
  numChains = 4L,
  BPPARAM = BiocParallel::bpparam()
)

diffLoc(
  objectCond1,
  objectCond2,
  fcol = "markers",
  hyperLearn = "MH",
  numIter = 1000,
  burnin = 100L,
  thin = 5L,
  u = 2,
  v = 10,
  lambda = 1,
  gpParams = NULL,
  hyperIter = 20,
  hyperMean = c(0, 0, 0),
  hyperSd = c(1, 1, 1),
  seed = NULL,
  pg = TRUE,
  pgPrior = NULL,
  tau = 0.2,
  dirPrior = NULL,
  maternCov = TRUE,
  PC = TRUE,
  nu = 2,
  pcPrior = NULL,
  propSd = c(0.3, 0.1, 0.05)
)
```

Arguments

objectCond1	A list of MSnbase::MSnSets where each is an experimental replicate for the first condition, usually a control
objectCond2	A list of MSnbase::MSnSets where each is an experimental replicate for the second condition, usually a treatment
fcol	The feature meta-data containing marker definitions. Default is markers
hyperLearn	Algorithm to learn posterior hyperparameters of the Gaussian processes. Default is LBFGS and MH for metropolis-hastings is also implemented.

numIter	The number of iterations of the MCMC algorithm. Default is 1000. Though usually much larger numbers are used
burnin	The number of samples to be discarded from the begining of the chain. Default is 100.
thin	The thinning frequency to be applied to the MCMC chain. Default is 5.
u	The prior shape parameter for Beta(u, v). Default is 2
v	The prior shape parameter for Beta(u, v). Default is 10.
lambda	Controls the variance of the outlier component. Default is 1.
gpParams	Object of class gpParams. parameters from prior fitting of GPs to each niche to accelerate inference. Default is NULL.
hyperIter	The frequency of MCMC interation to update the hyper-parameters default is 20
hyperMean	The prior mean of the log normal prior of the GP parameters. Default is 0 for each. Order is length-scale, amplitude and noise variance
hyperSd	The prior standard deviation of the log normal prior fo the GP parameters. Default is 1 for each. Order is length-scale, ampliture and noise variance.
seed	The random number seed.
pg	logical indicating whether to use polya-gamma prior. Default is FALSE.
pgPrior	A matrix generated by pgPrior function. If param pg is TRUE but pgPrior is NULL then a pgPrior is generated on the fly.
tau	The tau parameter for the polya-Gamma prior (is used). Defaults to 0.2
dirPrior	A matrix generated by dirPrior function. Default is NULL and dirPrior is generated on the fly.
maternCov	logical indicated whether to use a matern or gaussian covariance. Default is True and matern covariance is used
PC	logical indicating whether to use a penalised complexity prior. Default is TRUE.
pcPrior	matrix with 3 columns indicating the lambda paramters for the penalised complexity prior. Default is null which internally sets the penalised complexity prior to c(0.5, 3, 100) for each organelle and the order is length-scale, amplitude and variance. See vignette for more details.
nu	integer indicating the smoothness of the matern prior. Default is 2.
propSd	If MH is used to learn posterior hyperparameters then the proposal standard deviations. A Gaussian random-walk proposal is used.
numChains	integer indicating the number of parallel chains to run. Defaults to 4.
BPPARAM	BiocParallel parameter. Defaults to machine default backend using bpparam()

Details

The bandle function generate the sample from the posterior distributions (object or class bandleParams) based on an annotated quantitative spatial proteomics datasets (object of class MSnbase::MSnSet). Both are then passed to the bandlePredict function to predict the sub-cellular localisation and compute the differential localisation probability of proteins. See the vignette for examples

The diffloc function generate the sample from the posterior distributions (object or class bandleParam) based on an annotated quantitative spatial proteomics datasets (object of class MSnbase::MSnSet). Both are then passed to the bandlePredict function to predict the sub-cellular localisation and compute the differential localisation probability of proteins. See the vignette for examples

Value

bandle returns an instance of class bandleParams

bandle returns an instance of class bandleParams

Examples

```
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                      numDyn = 100L)
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mcmc1 <- bandle(objectCond1 = control1,
 objectCond2 = treatment1, gpParams = gpParams,
 fcol = "markers", numIter = 5L, burnin = 1L, thin = 2L,
 numChains = 1, BPPARAM = SerialParam(RNGseed = 1))

library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                    numRep = 6L,
                   numDyn = 100L)
gpParams <- lapply(tansim$lopitrep,
function(x) fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mcmc1 <- diffLoc(objectCond1 = control1, objectCond2 = treatment1, gpParams = gpParams,
                                  fcol = "markers", numIter = 5L, burnin = 1L, thin = 2L)
```

---

bandleChains-class *Infrastructure to to store and process MCMC results*

Description

The bandleParams infrastructure is used to store and process MCMC results for bandle model from Crook et al 2021

Usage

```
chains(object)

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

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

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

## S4 method for signature 'bandleChains'
length(x)

## S4 method for signature 'bandleParams'
length(x)

## S4 method for signature 'bandleSummaries'
length(x)

## S4 method for signature 'nicheParams'
length(x)

## S4 method for signature 'nicheParams'
length(x)

posteriorEstimates(object)

## S4 method for signature 'bandleSummary'
posteriorEstimates(object)

summaries(object)

params(object)

bandleJoint(object)

## S4 method for signature 'bandleSummary'
bandleJoint(object)

## S4 method for signature 'bandleChains,ANY,ANY'
x[[i, j = "missing", drop = "missing"]]

## S4 method for signature 'bandleParams,ANY,ANY'
x[[i, j = "missing", drop = "missing"]]

## S4 method for signature 'bandleChains,ANY,ANY,ANY'
```

```
x[i, j = "missing", drop = "missing"]

## S4 method for signature 'bandleParams,ANY,ANY,ANY'
x[i, j = "missing", drop = "missing"]

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

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

## S4 method for signature 'bandleSummaries,ANY,ANY'
x[[i, j = "missing", drop = "missing"]]

## S4 method for signature 'bandleSummaries,ANY,ANY'
x[[i, j = "missing", drop = "missing"]]

## S4 method for signature 'bandleSummaries,ANY,ANY,ANY'
x[i, j = "missing", drop = "missing"]

## S4 method for signature 'nicheParams,ANY,ANY'
x[[i, j = "missing", drop = "missing"]]

## S4 method for signature 'nicheParams,ANY,ANY'
x[[i, j = "missing", drop = "missing"]]

## S4 method for signature 'nicheParams,ANY,ANY,ANY'
x[i, j = "missing", drop = "missing"]

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

Arguments

object	object of class nicheParams.
x	Object to be subset.
i	An integer(). Should be of length 1 for [[.
j	Missing.
drop	Missing.

Details

Objects of the bandleParams class are created with the bandle() function These objects store the *priors* for the model and the results of the MCMC chains, which themselves are stored as an instance of class bandleChains and can be accessed with the chains() function. A summary of the bandleChains (or class bandleSummary) can be further computed with the bandleProcess function.

see the *bandle* vignette for examples

Value

An object of class bandleParams which stores the main results for the analysis when using bandle

Slots

chains list() containing the individual full MCMC chain results in an bandleChains instance. Each element must be a valid bandleChain instance.

posteriorEstimates A DataFrame documenting the posteriors in an bandleSummary instance

diagnostics A matrix of dimensions 1 by 2 containing the bandleSummary diagnostics.

bandle.joint A matrix of dimensions N by K storing the joint probability in an bandleSummary instance for each of the first condition

chains list() containing the individual bandle Summaries for different conditions results in an bandleSummaries instance. Each element must be a valid bandleSummary instance.

method A character() storing the bandle method name

priors A list() with the priors for the parameters

seed An integer() with the random number generation seed.

summary Object of class bandleSummary the summarised MCMC results available in the bandleParams instance.

chains Object of class bandleChains containing the full MCMC results in the bandleParams instance

datset character indicating which dataset i.e control or treatment

replicate integer an integer indicating which replicate

K integer(1) indicating the number of components.

D integer(1) indicating the number of samples.

method character(1) defining the method used. Currently bandle

mk matrix(K, D)

lambdak numeric(K)

nuk numeric(K)

sk array(K, D, D)

params list() containing the individual nicheParam objects results in an bandleParams instance. Each element must be a valid bandleParam instance.

dataset character indicating the dataset usaully control or treatment

replicate integer indicating the number of dataset replicate

n integer(1) indicating the number of MCMC interactions. Stored in an bandleChain instance.

K integer(1) indicating the number of components. Stored in an bandleChain instance.

N integer(1) indicating the number of proteins. Stored in an bandleChain instance.

niche matrix(N, n) component allocation results of an bandleChain instance.

nicheProb matrix(N, n, K) component allocation probabilities of an bandleChain instance.

outlier matrix(N, n) outlier allocation results.

outlierProb matrix(N, n, 2) outlier allocation probabilities of an bandleChain instance.

`bandlePredict` *Make predictions from a bandle analysis*

Description

Make predictions from a bandle analysis

Usage

```
bandlePredict(objectCond1, objectCond2, params, fcol = "markers")
```

Arguments

`objectCond1`	A list of instances of class `MSnbase::MSnSet`s where each is an experimental replicate for the first condition, usually a control
`objectCond2`	A list of instance of class `MSnbase::MSnSet`s where each is an experimental replicate for the second condition, usually a treatment
`params`	An instance of class `bandleParams`, as generated by `bandle()`.
`fcol`	A feature column indicating the markers. Defaults to "markers"

Value

`bandlePredict` returns an instance of class `MSnbase::MSnSet` containing the localisation predictions as a new `bandle.allocation` feature variable. The allocation probability is encoded as `bandle.probability` (corresponding to the mean of the distribution probability). In addition the upper and lower quantiles of the allocation probability distribution are available as `bandle.probability.lowerquantile` and `bandle.probability.upperquantile` feature variables. The Shannon entropy is available in the `bandle.mean.shannon` feature variable, measuring the uncertainty in the allocations (a high value representing high uncertainty; the highest value is the natural logarithm of the number of classes). An additional variable indicating the differential localization probability is also added as `bandle.differential.localisation`

Examples

```
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mcmc1 <- bandle(objectCond1 = control1, objectCond2 = treatment1, gpParams = gpParams,
                                    fcol = "markers", numIter = 5L, burnin = 1L, thin = 2L,
```

```
                                        numChains = 1, BPPARAM = SerialParam(RNGseed = 1))
mcmc1 <- bandleProcess(mcmc1)
out <- bandlePredict(objectCond1 = control1, objectCond2 = treatment1, params = mcmc1)
```

---

bandleProcess *process bandle results*

Description

process bandle results

Usage

```
bandleProcess(params)
```

Arguments

params	An object of class bandleParams

Value

bandleProcess returns an instance of class bandleParams with its summary slot populated.

Examples

```
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mcmc1 <- bandle(objectCond1 = control1, objectCond2 = treatment1, gpParams = gpParams,
                                    fcol = "markers", numIter = 5L, burnin = 1L, thin = 2L,
                                       numChains = 1, BPPARAM = SerialParam(RNGseed = 1))
mcmc1 <- bandleProcess(mcmc1)
```

besselK_boost *bessel function of the second kind from boost library*

Description

Leapfrog routine

Leapfrog routine

Usage

```
besselK_boost(x, v)

besselK(x, v)

matern(nu, a, rho, tau, D)

trenchDetcpp(c)

trenchInvcpp(v)

loglikeGPcpp(Y, Z, A, logcovDet, sigmak, nk, D, Y2)

likelihoodGPcpp(Xk, tau, h, nk, D, materncov = 0L, nu = 2)

gradientrhomatern(Y, drvrhomatern, nk, D, Z, A, sigmak)

gradientamatern(Y, amatern, nk, D, Z, A, sigmak)

gradientGPcppmatern(Xk, tau, h, nk, D, nu)

LeapfrogGPcppPC(Xk, lambda, tau, p, x, m, nk, D, L, delta, nu)

sampleGPmeanmaterncpp(Xk, tau, h, nk, D, nu)

makeComponent(X, BX, Y, BY, j)

sampleGPmeancpp(Xk, tau, h, nk, D)

normalisedData(Xknown, BX, Xunknown, BXun, hypers, nk, tau, D, j)

normalisedDatamatern(Xknown, BX, Xunknown, BXun, hypers, nk, tau, D, j, nu)

centeredDatamatern(Xknown, BX, Xunknown, BXun, hypers, nk, tau, D, K, nu)

componentloglike(centereddata, sigmak)
```

```
comploglike(centereddata, sigmak)

comploglikelist(centereddata, sigmak)

sampleDirichlet(numSamples, alpha)

sampleOutliercpp(allocoutlierprob)

sampleAlloccpp(allocprob)

centeredData(Xknown, BX, Xunknown, BXun, hypers, nk, tau, D, K)

mahaInt(X, mu, sigma, isChol = FALSE)

dmvtInt(X, mu, cholDec, log, df)

dmvtCpp(X_, mu_, sigma_, df_, log_, isChol_)

gradientGPcpp(Xk, tau, h, nk, D)

LeapfrogGPcpp(Xk, tau, p, x, m, nk, D, L, delta)

rcpp_pgdraw(b, c)
```

Arguments

x	position
v	argument of trench algorithm
nu	smoothness parameter of matern covariance
a	amplitude
rho	length-scale
tau	indexing term
D	number of samples
c	parameter of PG distribution
Y	pointer to data to be subset. X and Y will be joined
Z	special matrix from trench algorithm (see Crook et al arxiv 2019)
A	special matrix from trench algorithm (see Crook et al arxiv 2019)
logcovDet	log determine of the covariancematrix
sigmak	variance term
nk	number of observations
Y2	vectorised data (see Crook et al arxiv 2019)
Xk	The data
h	vector of hyperparamters

materncov	logical indicating whether to use matern or gaussian covariance. Defaults to Guassian covariance
drvrhomatern	deterivate of matern covariance wrt to rho
amatern	deterivate of matern covariance wrt to amplitude
lambda	parameters of penalised complexity prior
p	momentum
m	mass
L	iterations
delta	stepsize
X	data
BX	indexing set to make component
BY	pointer to subsetting matrix
j	indicator of localisations i.e. niche j
Xknown	data with known localisations
Xunknown	data with unknown localisations
BXun	indexing set for unknown localisations
hypers	vector of hyperparameters
K	number of components
centereddata	pointer to centered data
numSamples	The number of samples desired
alpha	The concentration parameter
allocoutlierprob	The probabilities of being allocated to the outlier component
allocprob	probability of being allocated to particular component
mu	mean
sigma	variance matrix
isChol	boolen indicated whether sigma is cholesky decomposition
cholDec	Cholesky decomposition of variance matrix
log	boolen of log density
df	degrees of freedom for t distribution
X_	the data
mu_	the mean
sigma_	the variance matrix
df_	the degrees of freedom
log_	return log density (boolean).
isChol_	is variance matrix in cholesky decomposition
b	parameter of PG distribution

Value

A numeric indicating the density of the t-distribution

Examples

```
dmvtCpp(diag(1,1,1), 1, diag(1,1,1), 1, TRUE, TRUE)
```

`diffLocalisationProb` *Compute differential localisation probabilities from ms-based experiments using the bandle method*

Description

These functions implement helper functions for the bandle method

Usage

```
diffLocalisationProb(params)

bootstrapdiffLocprob(params, top = 20, Bootsample = 5000, decreasing = TRUE)

binomialDiffLocProb(params, top = 20, nsample = 5000, decreasing = TRUE)
```

Arguments

`params`	An instance of `bandleParams`
`top`	The number of proteins for which to sample from the binomial distribution
`Bootsample`	Number of Bootstramp samples. Default is 5000
`decreasing`	Starting at protein most likely to be differentially localization
`nsample`	how many samples to return from the binomial distribution

Value

returns a named vector of differential localisation probabilities

returns a matrix of size Bootsample * top containing bootstrap

returns a list containing empirical binomial samples

Examples

```
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mcmc1 <- bandle(objectCond1 = control1, objectCond2 = treatment1, gpParams = gpParams,
                                  fcol = "markers", numIter = 10L, burnin = 1L, thin = 2L,
                                      numChains = 1, BPPARAM = SerialParam(RNGseed = 1))
mcmc1 <- bandleProcess(mcmc1)
dp <- diffLocalisationProb(mcmc1)

library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
gpParams <- lapply(tansim$lopitrep,
function(x) fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mcmc1 <- bandle(objectCond1 = control1, objectCond2 = treatment1, gpParams = gpParams,
                                  fcol = "markers", numIter = 10L, burnin = 1L, thin = 2L,
                                      numChains = 1, BPPARAM = SerialParam(RNGseed = 1))
mcmc1 <- bandleProcess(mcmc1)
bdp <- bootstrapdiffLocprob(mcmc1)
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
gpParams <- lapply(tansim$lopitrep,
function(x) fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mcmc1 <- bandle(objectCond1 = control1, objectCond2 = treatment1, gpParams = gpParams,
                                  fcol = "markers", numIter = 10L, burnin = 1L, thin = 2L,
                                      numChains = 1, BPPARAM = SerialParam(RNGseed = 1))
mcmc1 <- bandleProcess(mcmc1)
dp <- binomialDiffLocProb(mcmc1)
```

EFDR *Compute the expected False Discovery Rate*

Description

The EFDR for a given threshold is equal to the sum over all proteins that exceed that threshold of one minus the posterior probability of differential localisations, divides by the total number of proteins with probabilities of differential localisation greater than that threshold.

Usage

```
EFDR(prob, threshold = 0.9)
```

Arguments

prob	A numeric indicating probabilities of differential localisation
threshold	A numeric indicating the probability threshold. The default is 0.90.

Value

The expected false discovery rate for a given threshold

Examples

```
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mcmc1 <- bandle(objectCond1 = control1, objectCond2 = treatment1, gpParams = gpParams,
                                  fcol = "markers", numIter = 10L, burnin = 1L, thin = 2L,
                                      numChains = 1, BPPARAM = SerialParam(RNGseed = 1))
mcmc1 <- bandleProcess(mcmc1)
dp <- diffLocalisationProb(mcmc1)
EFDR(dp, threshold = 0.5)
```

fitGP *Fit a Gaussian process to spatial proteomics data*

Description

The fitGP function is a helper function to fit GPs with squared exponential co-variances, maximum marginal likelihood

The fitGPmaternPC function is a helper function to fit matern GPs to data with penalised complexity priors on the hyperparameters.

The fitGPmatern function fits matern GPs to data.

The plotGPmatern function plots matern GPs

Usage

```
fitGP(object = object, fcol = "markers")

fitGPmaternPC(
  object = object,
  fcol = "markers",
  materncov = TRUE,
  nu = 2,
  hyppar = matrix(c(10, 60, 250), nrow = 1)
)

fitGPmatern(object = object, fcol = "markers", materncov = TRUE, nu = 2)

plotGPmatern(object = object, params = params, fcol = "markers")
```

Arguments

object	A instance of class MSnSet
fcol	feature column to indicate markers. Default is "markers".
materncov	logical indicating whether matern covariance is used.
nu	matern smoothness parameter. Default is 2.
hyppar	The vector of penalised complexity hyperparameters, you must provide a matrix with 3 columns and 1 row. The order is hyperparameters on length-scale, amplitude, variance.
params	The output of running fitGPmatern, fitGPmaternPC or fitGP which is of class gpParams

Details

This set of functions allow users to fit GPs to their data. The fitGPmaternPC function allows users to pass a vector of penalised complexity hyperparameters using the hyppar argument. You must provide a matrix with 3 columns and 1 row. The order of these 3 columns represent the

hyperparameters length-scale, amplitude, variance. We have found that the `matrix(c(10, 60, 250), nrow = 1)` worked well for the spatial proteomics datasets tested in Crook et al (2021). This was visually assessed by passing these values and visualising the GP fit using the `plotGPmatern` function (please see vignette for an example of the output). Generally, (1) increasing the lengthscale parameter (the first column of the `hyppar` matrix) increases the spread of the covariance i.e. the similarity between points, (2) increasing the amplitude parameter (the second column of the `hyppar` matrix) increases the maximum value of the covariance and lastly (3) decreasing the variance (third column of the `hyppar` matrix) reduces the smoothness of the function to allow for local variations. We strongly recommend users start with the recommended parameters and change and assess them as necessary for their dataset by visually evaluating the fit of the GPs using the `plotGPmatern` function. Please see the vignettes for more details and examples.

Value

Returns an object of class `gpParams` which stores the posterior predictive means, standard deviations, variances and also the MAP hyperparamters for the GP.

The functions `plotGPmatern` plot the posterior predictives overlayed with the markers for each subcellular class.

Examples

```
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
gpParams <- lapply(tansim$lopitrep, function(x) fitGP(x))

## ====== fitGPmaternPC =====
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
## Please note that hyppar should be chosen carefully and tested
## by checking the GP fit with the plotGPmatern function
## (please see details above)
gpParams <- lapply(tansim$lopitrep,
function(x) fitGPmaternPC(x, hyppar = matrix(c(10, 60, 100), nrow = 1)))

## ====== fitGPmatern =====
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
gpParams <- lapply(tansim$lopitrep, function(x) fitGPmaternPC(x))
```

```
## ====== plotGPmatern =====
## generate example data
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
## fit a GP
gpParams <- lapply(tansim$lopitrep, function(x) fitGP(x))

## Overlay posterior predictives onto profiles
## Dataset1 1
par(mfrow = c(2, 3))
plotGPmatern(tansim$lopitrep[[1]], gpParams[[1]])

## Dataset 2, etc.
par(mfrow = c(2, 3))
plotGPmatern(tansim$lopitrep[[2]], gpParams[[2]])
```

---

gpParams-class *Container for GP results*

Description

The gpParams infrastructure is used to store and process the GP results for output from using the fitGP functions in bandle

Details

Objects of the gpParams class are created with the fitGP, fitGPmaternPC or fitGPmatern functions

These objects a list of posterior predictive means and standard deviations. As well as maximum marginal likelihood for the GP

Slots

method character indicating the GP method used

M A list of the posterior predictive means for each K components of GPs fitted to the data

sigma A numeric of length K standard deviations fitted to the data

V A list of the variance fitted to the data

params A matrix array of the MAP hyperparameters for the GP

gradientGP *Compute GP gradient*

Description

Internal R function to pass R to C++, not for external use.

Internal R function to pass R to C++, not for external use.

Function to perform Metropolis-Hastings for GP hyperparameters with different priors

Usage

```
gradientGP(Xk, tau, h, nk, D)

gradientGPmatern(Xk, tau, h, nk, D, materncov, nu)

posteriorgradientGPmatern(Xk, tau, h, nk, D, materncov, nu, hyppar)

gradientlogprior(h, hyppar)

likelihoodGP(Xk, tau, h, nk, D)

likelihoodGPmatern(Xk, tau, h, nk, D, materncov, nu)

posteriorGPmatern(Xk, tau, h, nk, D, materncov, nu, hyppar)

Gumbel(x, lambda, log = TRUE)

PCrhomvar(rho, a, lambda1, lambda2, log = TRUE)

metropolisGP(
  inith,
  X,
  tau,
  nk,
  D,
  niter,
  hyperMean = c(0, 0, 0),
  hyperSd = c(1, 1, 1)
)

metropolisGPmatern(
  inith,
  X,
  tau,
  nk,
  D,
```

```
  niter,
  nu = 2,
  hyppar = c(1, 1, 1),
  propSd = c(0.3, 0.1, 0.1)
)

Gumbel(x, lambda, log = TRUE)

PCrhomvar(rho, a, lambda1, lambda2, log = TRUE)
```

Arguments

Xk	The data
tau	The indexing parameters
h	GP hyperparameters
nk	Number of observations
D	number of samples
materncov	logical indicating whether matern covariance is used
nu	Smoothness of the matern covariance
hyppar	A vector indicating the penalised complexity prior hyperparameters. Default is c(1,1,1)
x	observation
lambda	scale parameter of the type-2 Gumbel distribution
log	logical indicating whether to return log. Default is TRUE
rho	length-scale parameter
a	amplitude
lambda1	first parameter of distribution
lambda2	second parameter of distribution
inith	initial hyperparamters
X	The data
niter	Number of MH iteractions
hyperMean	A vector indicating the log-normal means. Default is c(0,0,0).
hyperSd	A vector indicating the log-normal standard deviations. Default is c(1,1,1)
propSd	The proposal standard deviation. Default is c(0.3,0.1,0.1). Do not change unless you know what you are doing.

Value

Returns gp gradient

Returns gp gradient

Returns the gradient of the posterior

return the gradient of the log prior, length-scale, aamplitude and noise

Returns gp negative log likelihood

Returns gp negative log likelihood

Returns the negative log posterior of the GP

Returns the likelihood of the type-2 GUmbel distribution

Returns the likelihood of the bivariate penalised complexity prior

Returns new hyperparamters and the acceptance rate

Returns the likelihood of the type-2 GUmbel distribution

Returns the likelihood of the bivariate penalised complexity prior

Examples

```
Gumbel(3, lambda = 1)
```

`kldirpg` *Computes the Kullback-Leibler divergence between Polya-Gamma and Dirichlet priors*

Description

Computes the Kullback-Leibler divergence between Polya-Gamma and Dirichlet priors

Compute the KL divergence between two Dirichlet distributions

A function to compute the prior predictive distribution of the Dirichlet prior.

A function to compute the prior predictive distribution of the Polya-Gamma prior.

Usage

```
kldirpg(sigma = diag(1, 1, 1), mu = c(0, 0, 0), alpha = c(1))

kldir(alpha, beta)

prior_pred_dir(object, fcol = "markers", iter = 5000, dirPrior = NULL, q = 15)

prior_pred_pg(
  objectCond1,
  objectCond2,
  fcol = "markers",
  tau = 0.2,
  lambda = 0.01,
  mu_prior = NULL,
  iter = 10000,
  q = 15
)
```

Arguments

sigma	the sigma parameter of the Polya-Gamma prior. A positive-definite symmetric matrix.
mu	the mu parameter of the Polya-Gamma prior. A vector of means
alpha	The concentration parameter of the first Dirichlet distribution
beta	The concentration parameter of the second Dirichlet distribution
object	An instance of class MSnSet
fcol	The feature column indiating the markers. Default is "markers"
iter	Number of sample to use from prior predictive distribution. Default is 10000
dirPrior	The Dirichlet prior used. If NULL (default) will generate a a default Dirichlet prior. This should be a matrix with the same dimensions as the number of subcellular niches. The diagonal terms correspond to the prior probability of not differentially localising. The (i,j) term corresponds to prior probability of differntially localising between niche i and j.
q	The upper tail value. That is the prior probability of having more than q differential localisations. Default is 15.
objectCond1	An instance of class MSnSet, usually the control dataset
objectCond2	An instance of class MSnSet, usually the treatment dataset
tau	The tau parameter of the Polya-Gamma prior. Default is 0.2.
lambda	The lambda ridge parameter used for numerical stability. Default is 0.01
mu_prior	The mean of the Polya-Gamma prior. Default is NULL which generates a default Polya-Gamma prior.

Value

returns a numeric indicating the KL divergence

a numeric indicating the KL divergence

A list contain the prior predictive distribution of differential localisations, the mean number of differential localised proteins and the probability than more than q are differentially localised

A list contain the prior predictive distribution of differential localisations, the mean number of differential localised proteins and the probability than more than q are differentially localised

Examples

```
kldirpg(sigma = diag(c(1,1,1)), mu = c(0,0,0), alpha = 1)

kldir(c(1,1), c(3,1))

library(pRolocdata)
data("tan2009r1")

out <- prior_pred_dir(object = tan2009r1)

library(pRolocdata)
```

```
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
out <- prior_pred_pg(objectCond1 = control1[[1]],
objectCond2 = treatment1[[1]])
```

`mcmc_plot_probs` *Generate a violin plot showing the probabilitiy of protein localisation to different organelles*

Description

These functions implement plotting functions for bandle objects

Usage

```
mcmc_plot_probs(
  params,
  fname,
  cond = 1,
  n = 1,
  bw = 0.05,
  scale = "width",
  trim = TRUE
)
```

Arguments

`params`	An instance of class `bandleParams`
`fname`	The name of the protein to plot
`cond`	Which conditions do we want to plot. Must be `1` or `2`. Default is `1`
`n`	The chain from which we plot the probability distribution. Default is 1.
`bw`	The bandwidth use in probability distribution smoothing of geom_violin Default is 0.05.
`scale`	Scaling of geom_violin. Defaults to width.
`trim`	trim parameter of geom_violin. Defaults to true.

Value

returns a named vector of differential localisation probabilities

Examples

```
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 6L,
                     numDyn = 100L)
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mcmc1 <- bandle(objectCond1 = control1,
 objectCond2 = treatment1, gpParams = gpParams,
 fcol = "markers", numIter = 5L, burnin = 1L, thin = 2L,
 numChains = 1, BPPARAM = SerialParam(RNGseed = 1))
mcmc_plot_probs(params = mcmc1, fname = rownames(tan2009r1)[1])
```

---

meanOrganelle *Computes Organelle means and variances using markers*

Description

Computes Organelle means and variances using markers

Usage

```
meanOrganelle(object, fcol = "markers")
```

Arguments

object	a instance of class MSnset
fcol	a feature column indicating which feature define the markers

Value

returns a list of means and variances for each

Examples

```
library(pRolocdata)
data("tan2009r1")
meanOrganelle(object = tan2009r1)
```

plotConvergence *Generates a histogram of ranks (a rank plot) for convergence*

Description

Produces a rank plot to analyse convergence of MCMC algorithm

Usage

```
plotConvergence(params)
```

Arguments

params	An instance of class bandleParams

Value

Returns the ranks of the number of outliers in each chain. The side effect returns rank plots. Number of rank plots is equal to the number of chains

Examples

```
## Generate some example data
library("pRolocdata")
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 4L,
                      numDyn = 100L)
data <- tansim$lopitrep
control <- data[1:2]
treatment <- data[3:4]

## fit GP params
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))

## run bandle
res <- bandle(objectCond1 = control,
              objectCond2 = treatment,
              gpParams = gpParams,
              fcol = "markers",
              numIter = 5L,
              burnin = 1L,
              thin = 2L,
              numChains = 2,
              BPPARAM = SerialParam(RNGseed = 1),
              seed = 1)

## Process bandle results
```

```
bandleres <- bandleProcess(res)

## Convergence plots
par(mfrow = c(1, 2))
plotConvergence(bandleres)
```

`plotTable` *Generates a table for visualising changes in localisation between two conditions/datasets*

Description

Produces a table summarising differential localisation results

Usage

```
plotTable(params, all = FALSE, fcol)
```

Arguments

`params`	An instance of class `bandleParams` or an instance of class `MSnSetList` of length 2.
`all`	A logical specifying whether to count all proteins or only show those that have changed in location between conditions. Default is `FALSE`.
`fcol`	If `params` is a `list` of `MSnSets`. Then `fcol` must be defined. This is a `character` vector of length 2 to set different labels for each dataset. If only one label is specified, and the `character` is of length 1 then this single label will be used to identify the annotation column in both datasets.

Value

Returns a summary table of translocations of proteins between conditions.

Examples

```
## Generate some example data
library("pRolocdata")
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 4L,
                      numDyn = 100L)
data <- tansim$lopitrep
control <- data[1:2]
treatment <- data[3:4]

## fit GP params
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))
```

```
## run bandle
res <- bandle(objectCond1 = control,
              objectCond2 = treatment,
              gpParams = gpParams,
              fcol = "markers",
              numIter = 5L,
              burnin = 1L,
              thin = 2L,
              numChains = 2,
              BPPARAM = SerialParam(RNGseed = 1),
              seed = 1)

## Process bandle results
bandleres <- bandleProcess(res)

## Tabulate results
plotTable(bandleres)
```

`plotTranslocations` *Generates a chord diagram or alluvial plot for visualising changes in localisation between two conditions/datasets*

Description

Produces a chord diagram (circos plot) or an alluvial plot (also known as a Sankey diagram) to show changes in location between two conditions or datasets.

Usage

```
plotTranslocations(
  params,
  type = "alluvial",
  all = FALSE,
  fcol,
  col,
  labels = TRUE,
  labels.par = "adj",
  cex = 1,
  spacer = 4,
  ...
)
```

Arguments

`params`	An instance of class `bandleParams` or an instance of class `MSnSetList` of length 2.
`type`	A `character` specifying the type of visualisation to plot. One of `"alluvial"` (default) or `"chord"`.

all	A logical specifying whether to count all proteins or only show those that have changed in location between conditions. Default is FALSE.
fcol	If params is a list of MSnSets. Then fcol must be defined. This is a character vector of length 2 to set different labels for each dataset. If only one label is specified, and the character is of length 1 then this single label will be used to identify the annotation column in both datasets.
col	A list of colours to define the classes in the data. If not defined then the default pRoloc colours in getStockCol() are used.
labels	Logical indicating whether to display class/organelle labels for the chord segments or alluvial stratum. Default is TRUE.
labels.par	If type is "alluvial". Label style can be specified as one of "adj", "repel". Default is "adj".
cex	Text size. Default is 1.
spacer	A numeric. Default is 4. Controls the white space around the circos plotting region.
...	Additional arguments passed to the chordDiagram function.

Value

Returns a directional circos/chord diagram showing the translocation of proteins between conditions. If type = "alluvial" ouput is a ggplot object.

Examples

```
## Generate some example data
library("pRolocdata")
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 4L,
                      numDyn = 100L)
data <- tansim$lopitrep
control <- data[1:2]
treatment <- data[3:4]

## fit GP params
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))

## run bandle
res <- bandle(objectCond1 = control,
              objectCond2 = treatment,
              gpParams = gpParams,
              fcol = "markers",
              numIter = 5L,
              burnin = 1L,
              thin = 2L,
              numChains = 1,
              BPPARAM = SerialParam(RNGseed = 1),
```

```
              seed = 1)

## Process the results
bandleres <- bandleProcess(res)

## plot the results
plotTranslocations(bandleres)
plotTranslocations(bandleres, type = "chord")
```

`proteinAllocation` *sample allocations, probabilities and compute loglikilihoods*

Description

Internal sampling function, not for outside use documented for completness

Usage

```
proteinAllocation(loglikelihoods, currentweights, alloctemp, cond)

outlierAllocationProbs(
  outlierlikelihood,
  loglikelihoods,
  epsilon,
  alloctemp,
  cond
)

sampleOutlier(allocoutlierprob)

covOrganelle(object, fcol = "markers")

pg_prior(object_cond1, object_cond2, K, pgPrior = NULL, fcol = "markers")

sample_weights_pg(nk_mat, pgPrior, w, K, tau = 0.2)

sample_weights_dir(nk_mat, dirPrior)
```

Arguments

`loglikelihoods`	the log likelihoods
`currentweights`	the current allocations weights
`alloctemp`	the current protein allocations
`cond`	the control = 1, treatment = 2
`outlierlikelihood`	the outlier log likelihoods

epsilon	the outlier component weight
allocoutlierprob	the outlier probabilities
object	An instance of class MSnSet
fcol	The feature column containing the markers.
object_cond1	A list of instance of class MSnSets usually control
object_cond2	A list of instance of class MSnSets usually treatment
K	The number of organelle classes
pgPrior	The Polya-Gamma prior
nk_mat	The summary matrix of allocations
w	The Polya-Gamma auxiliary variable
tau	The empirical bayes parameter for the Polya-Gamma variable. Defaults to 0.2.
dirPrior	The Dirichlet prior

Value

returns samples for protein allocations, log likelihoods and probabilities

returns outlier probabilities

returns outlier allocations

returns covariance of organelles using marker proteins

returns the Polya-Gamma prior

returns A sample of the weights using Polya-Gamma priors.

returns A sample of the weights using Dirichlet prior.

Examples

```
library(pRolocdata)
data("tan2009r1")
covOrganelle(object = tan2009r1)


library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                    numRep = 6L,
                   numDyn = 100L)
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
out <- pg_prior(object_cond1 = control1,
 object_cond2 = treatment1, K = 11)
```

`robustMahalanobis` *robust Mahalanobis distance*

Description

These function implement the MR method of Itzhak et al

Usage

```
robustMahalanobis(delta)

reprodScore(x, y, method = c("pearson"))

mrMethod(objectCond1, objectCond2, method = "2017")
```

Arguments

`delta`	The difference profile to compute the squared mahalanobis distance
`x`	Numeric vector to compute reproducibility score
`y`	Numeric vector to compute reproducibility score
`method`	Correlation method. Default is Pearson
`objectCond1`	A list of `MSnbase::MSnSet`s where each is an experimental replicate for the first condition, usually a control
`objectCond2`	A list of `MSnbase::MSnSet`s where each is an experimental replicate for the second condition, usually a treatment

Value

The squared Mahalanobis distance

The R score

The MR score of the Ithzak et al. 2016/2017

Examples

```
## Generate some example data
library("pRolocdata")
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 4L,
                      numDyn = 100L)
data <- tansim$lopitrep
control <- data[1:2]
treatment <- data[3:4]

## compute delta matrix
```

```
deltaMatrix <- exprs(control[[1]]) - exprs(treatment[[1]])
res <- bandle:::robustMahalanobis(deltaMatrix)
##' @examples
## Generate some example data
library("pRolocdata")
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 4L,
                      numDyn = 100L)
data <- tansim$lopitrep
control <- data[1:2]
treatment <- data[3:4]

## compute delta matrix
deltaMatrix1 <- exprs(control[[1]]) - exprs(treatment[[1]])
deltaMatrix2 <- exprs(control[[2]]) - exprs(treatment[[2]])
mr_score <- bandle:::reprodScore(deltaMatrix1, deltaMatrix2)
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                    numRep = 6L,
                   numDyn = 100L)
d1 <- tansim$lopitrep
control1 <- d1[1:3]
treatment1 <- d1[4:6]
mr1 <- mrMethod(objectCond1 = control1, objectCond2 = treatment1)
plot(mr1$Mscore, mr1$Rscore, pch = 21,
     xlab = "MScore", ylab = "RScore")
```

`sim_dynamic` *Generate a dynamic spatial proteomics experiment*

Description

A function to simulate dynamic spatial proteomics data using a bootstrap method

Usage

```
sim_dynamic(
  object,
  subsample = NULL,
  knn_par = 10L,
  fcol = "markers",
  numRep = 6L,
  method = "wild",
  batch = FALSE,
  frac_perm = FALSE,
```

```
  nu = 2,
  numDyn = 20L
)
```

Arguments

object	A instance of class MSnSet from which to generate a spatial proteomics dataset.
subsample	how many proteins to subsample to speed up analysis. Default is NULL.
knn_par	the number of nearest neighbours to use in KNN classification to simulate dataset. Default is 10
fcol	feature column to indicate markers. Default is "markers". Proteins with unknown localisations must be encoded as "unknown".
numRep	The total number of datasets to generate. Default is 6. An integer must be provided
method	The bootstrap method to use to simulate dataset. Default is "wild". refer to BANDLE paper for more details.
batch	Whether or not to include batch effects. Default is FALSE.
frac_perm	whether or not to permute the fractions. Default is FALSE
nu	parameter to generate residual inflated noise. Default is 2. See BANDLE paper for more details
numDyn	An integer number of protein to simulate dynamic transitions. Default is 20

Value

returns simulate dynamic lopit datasets and the name of the relocalated protein.

Examples

```
library(pRolocdata)
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1, numRep = 6L, numDyn = 100L)
```

---

spatial2D *Generate a PCA plot with smoothed probability contours*

Description

Generate a PCA plot with smoothed probability contours

Usage

```
spatial2D(
  object,
  params,
  fcol = "markers",
  dims = c(1, 2),
  cov.function = NULL,
  theta = 2,
  derivative = 2,
  k = 1,
  cond = 1,
  n = 1,
  breaks = c(0.99, 0.95, 0.9, 0.85, 0.8, 0.75, 0.7),
  aspect = 0.5
)
```

Arguments

object	An instance of class MSnSet to provide the pca coordinates
params	An instance of class bandleParams
fcol	Feature columns that defines the markers. Defaults to "markers".
dims	The PCA dimensions to plot. Defaults to c(1,2)
cov.function	The covariance function for the smoothing kernel. Defaults to wendland.cov
theta	The theta parameter of the wendland.cov. Defaults to 2.
derivative	The derivative paramter of the wendland.cov. Defaults to 2.
k	The k parameter of the wendland.cov
cond	Which conditions do we want to plot. Must be 1 or 2. Default is 1
n	The chain from which we plot the probability distribution. Default is 1.
breaks	The levels at which to plot the contours. Defaults to c(0.99, 0.95, 0.9, 0.85, 0.8, 0.75, 0.7)
aspect	The aspect ratio of the pca plots. Defaults to 0.5.

Value

returns a named vector of differential localisation probabilities

Examples

```
 ## Not run:
## Generate some example data
library("pRolocdata")
data("tan2009r1")
set.seed(1)
tansim <- sim_dynamic(object = tan2009r1,
                      numRep = 4L,
                      numDyn = 100L)
```

```
data <- tansim$lopitrep
control <- data[1:2]
treatment <- data[3:4]

## fit GP params
gpParams <- lapply(tansim$lopitrep, function(x)
fitGPmaternPC(x, hyppar = matrix(c(0.5, 1, 100), nrow = 1)))

## run bandle
res <- bandle(objectCond1 = control,
              objectCond2 = treatment,
              gpParams = gpParams,
              fcol = "markers",
              numIter = 5L,
              burnin = 1L,
              thin = 2L,
              numChains = 1,
              BPPARAM = SerialParam(RNGseed = 1),
              seed = 1)

## Process the results
bandleres <- bandleProcess(res)

## plot the results
spatial2D(control[[1]], bandleres)

## End(Not run)
```

`StatStratum` *inherits StatSratum*

Description

inherits StatSratum

Usage

```
StatStratum
```

Format

An object of class `StatStratum` (inherits from `Stat`, `ggproto`, `gg`) of length 5.

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