

Package ‘BPRMeth’

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Type Package

Title Model higher-order methylation profiles

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Description The BPRMeth package is a probabilistic method to quantify explicit features of methylation profiles, in a way that would make it easier to formally use such profiles in downstream modelling efforts, such as predicting gene expression levels or clustering genomic regions or cells according to their methylation profiles.

LinkingTo Rcpp, RcppArmadillo

Depends R (>= 3.5.0), GenomicRanges

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bernoulli_data *Synthetic Bernoulli data*

Description

A synthetic dataset containinig 300 entries from Bernoulli probit regression observations (e.g. single cell methylation data).

Usage

bernoulli_data

Format

A list with 300 elements, where each element element is an L x 2 matrix of observations, where:

1st column locations of obseravtions

2nd column methylation level, 0 - unmethylated, 1 - methylated

Value

Synthetic Bernoulli methylation data.

See Also

[binomial_data](#), [beta_data](#), [gaussian_data](#)

beta_data *Synthetic Beta data*

Description

A synthetic dataset containinig 300 entries from Beta probit regression observations (e.g. Beta values from array methylation data).

Usage

beta_data

Format

A list with 300 elements, where each element element is an L x 2 matrix of observations, where:

1st column locations of obseravtions

2nd column methylation level

Value

Synthetic Beta methylation data.

Details

The beta regression model is based on alternative parameterization of the beta density in terms of the mean and dispersion parameter:<https://cran.r-project.org/web/packages/betareg/>.

See Also

[binomial_data](#), [bernoulli_data](#), [gaussian_data](#)

binomial_data

Synthetic Binomial data

Description

A synthetic dataset containinig 300 entries from Binomial probit regression observations (e.g. bulk methylation data).

Usage

```
binomial_data
```

Format

A list with 300 elements, where each element element is an L x 3 matrix of observations, where:

1st column locations of obseravtions

2nd column total trials

3rd column number of successes

Value

Synthetic Binomial methylation data.

See Also

[bernoulli_data](#), [beta_data](#), [gaussian_data](#)

boxplot_cluster_expr *Boxplot of clustered expression levels*

Description

Create a boxplot of clustered gene expression levels which depend on the clustered methylation profiles. Each colour denotes a different cluster.

Usage

```
boxplot_cluster_expr(cluster_obj, expr, anno, title = "Expression levels")
```

Arguments

| | |
|-------------|--|
| cluster_obj | The output from cluster_profiles_vb or cluster_profiles_mle functions. |
| expr | The expression data object. |
| anno | The annotation data object. |
| title | Plot title |

Value

A ggplot2 object.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[plot_cluster_profiles](#), [plot_infer_profiles](#), [plot_predicted_expr](#)

Examples

```
# Cluster methylation profiles using 3 RBFs
basis <- create_rbf_object(M = 3)
# Perform clustering
cl_obj <- cluster_profiles_vb(X = encode_met$met, K = 3, model = "binomial",
                             basis = basis, vb_max_iter = 5)
# Create plot
g <- boxplot_cluster_expr(cluster_obj = cl_obj, expr = encode_expr,
                          anno = encode_met$anno)
```

BPRMeth

BPRMeth: *Extracting higher order methylation features*

Description

Higher order methylation features for clustering and prediction in epigenomic studies

Usage

```
.datatable.aware
```

Format

An object of class `logical` of length 1.

Value

BPRMeth main package documentation.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

bpr_cluster_wrap

(DEPRECATED) Cluster methylation profiles

Description

(DEPRECATED) `bpr_cluster_wrap` is a wrapper function that clusters methylation profiles using the EM algorithm. Initially, it performs parameter checking, and initializes main parameters, such as mixing proportions, basis function coefficients, then the EM algorithm is applied and finally model selection metrics are calculated, such as BIC and AIC.

Usage

```
bpr_cluster_wrap(  
  x,  
  K = 3,  
  pi_k = NULL,  
  w = NULL,  
  basis = NULL,  
  em_max_iter = 100,  
  epsilon_conv = 1e-04,  
  lambda = 1/2,  
  opt_method = "CG",  
  opt_itnmax = 100,  
)
```

```

    init_opt_itnmax = 100,
    is_parallel = TRUE,
    no_cores = NULL,
    is_verbose = FALSE
)

```

Arguments

| | |
|-----------------|---|
| x | The binomial distributed observations, which has to be a list of elements of length N, where each element is an L x 3 matrix of observations, where 1st column contains the locations. The 2nd and 3rd columns contain the total trials and number of successes at the corresponding locations, respectively. See process_haib_caltech_wrap on a possible way to get this data structure. |
| K | Integer denoting the number of clusters K. |
| pi_k | Mixing proportions. |
| w | A MxK matrix, where each column consists of the basis function coefficients for each corresponding cluster. |
| basis | A 'basis' object. E.g. see create_rbf_object . |
| em_max_iter | Integer denoting the maximum number of EM iterations. |
| epsilon_conv | Numeric denoting the convergence parameter for EM. |
| lambda | The complexity penalty coefficient for ridge regression. |
| opt_method | The optimization method to be used. See optim for possible methods. Default is "CG". |
| opt_itnmax | Optional argument giving the maximum number of iterations for the corresponding method. See optim for details. |
| init_opt_itnmax | Optimization iterations for obtaining the initial EM parameter values. |
| is_parallel | Logical, indicating if code should be run in parallel. |
| no_cores | Number of cores to be used, default is max_no_cores - 2. |
| is_verbose | Logical, print results during EM iterations. |

Value

A 'bpr_cluster' object which, in addition to the input parameters, consists of the following variables:

- pi_k: Fitted mixing proportions.
- w: A MxK matrix with the fitted coefficients of the basis functions for each cluster k.
- NLL: The Negative Log Likelihood after the EM algorithm has finished.
- r_nk: Posterior probabilities of each promoter region belonging to each cluster.
- labels: Hard clustering assignments of each observation/promoter region.
- BIC: Bayesian Information Criterion metric.
- AIC: Akaike Information Criterion metric.
- ICL: Integrated Complete Likelihood criterion metric.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

Examples

```
ex_data <- meth_data
data_clust <- bpr_cluster_wrap(x = ex_data, em_max_iter = 3, opt_itnmax = 3,
                             init_opt_itnmax = 5, is_parallel = FALSE)
```

bpr_log_likelihood *Compute observation model log-likelihood*

Description

These functions evaluate the model log-likelihood and gradient for different observation models. Available models are "bpr" (i.e. "bernoulli" or "binomial"), "beta" and "lr" (i.e. "gaussian"). There are also functions to compute the sum and weighted sum of the observation model likelihoods, e.g. required for the EM algorithm. These functions are written in C++ for efficiency.

Usage

```
bpr_log_likelihood(w, X, H, lambda, is_nll)

bpr_gradient(w, X, H, lambda, is_nll)

betareg_log_likelihood(w, X, H, lambda, is_nll)

betareg_gradient(w, X, H, lambda, is_nll)

sum_weighted_bpr_lik(w, X_list, H_list, r_nk, lambda, is_nll)

sum_weighted_bpr_grad(w, X_list, H_list, r_nk, lambda, is_nll)

sum_weighted_betareg_lik(w, X_list, H_list, r_nk, lambda, is_nll)

sum_weighted_betareg_grad(w, X_list, H_list, r_nk, lambda, is_nll)

lr_log_likelihood(w, X, H, lambda = 0.5, is_nll = FALSE)
```

Arguments

w A vector of parameters (i.e. coefficients of the basis functions)

X An L X C matrix, where L are the total number of observations. The first column contains the input observations x (i.e. CpG locations). If "binomial" model then C=3, and 2nd and 3rd columns contain total number of trials and number of successes respectively. If "bernoulli" or "gaussian" model, then C=2 containing

| | |
|---------------------|--|
| | the output y (e.g. methylation level). if "beta" model, then $C=3$, where 2nd column contains output y and 3rd column the dispersion parameter. Each row corresponds to each row of the design matrix H . |
| H | The $L \times M$ matrix design matrix, where L is the number of observations and M the number of basis functions. |
| λ | The complexity penalty coefficient for penalized regression. |
| <code>is_nll</code> | Logical, indicating if the Negative Log Likelihood should be returned. |
| <code>X_list</code> | A list of elements of length N , where each element is an $L \times K$ matrix of observations X . |
| <code>H_list</code> | A list of elements of length N , where each element contains the $L \times M$ design matrices H . |
| <code>r_nk</code> | A vector of length N containing the posterior probabilities (i.e. responsibilities) for each element of <code>X_list</code> . |

Value

Returns the log likelihood or gradient of the observation model.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[eval_functions](#), [infer_profiles_mle](#)

`bpr_optimize` *(DEPRECATED) Optimize BPR negative log likelihood function*

Description

(DEPRECATED) The function `bpr_optimize` minimizes the negative log likelihood of the BPR function. Since it cannot be evaluated analytically, an optimization procedure is used. The `optim` packages is used for performing optimization.

Usage

```
bpr_optim(x, ...)

## S3 method for class 'list'
bpr_optim(
  x,
  w = NULL,
  basis = NULL,
  lambda = 1/2,
  opt_method = "CG",
```

```

    opt_itnmax = 100,
    is_parallel = TRUE,
    no_cores = NULL,
    ...
)

## S3 method for class 'matrix'
bpr_optim(
  x,
  w = NULL,
  basis = NULL,
  lambda = 1/2,
  opt_method = "CG",
  opt_itnmax = 100,
  ...
)

```

Arguments

| | |
|-------------|--|
| x | The input object, either a matrix or a list . |
| ... | Additional parameters. |
| w | A vector of parameters (i.e. coefficients of the basis functions) |
| basis | A 'basis' object. E.g. see create_rbf_object . |
| lambda | The complexity penalty coefficient for ridge regression. |
| opt_method | The optimization method to be used. See optim for possible methods. Default is "CG". |
| opt_itnmax | Optional argument giving the maximum number of iterations for the corresponding method. See optim for details. |
| is_parallel | Logical, indicating if code should be run in parallel. |
| no_cores | Number of cores to be used, default is <code>max_no_cores - 2</code> . |

Value

Depending on the input object x:

- If x is a [list](#): An object containing the following elements:
 - `W_opt`: An $N \times (M+1)$ matrix with the optimized parameter values. Each row of the matrix corresponds to each element of the list x. The columns are of the same length as the parameter vector w (i.e. number of basis functions).
 - `Mus`: An $N \times M$ matrix with the RBF centers if basis object is [create_rbf_object](#), otherwise NULL.
 - `basis`: The basis object.
 - `w`: The initial values of the parameters w.
- If x is a [matrix](#): An object containing the following elements:
 - `w_opt`: Optimized values for the coefficient vector w. The length of the result is the same as the length of the vector w.

- basis: The basis object.
- If calling bpr_optim_fast just the optimal weight matrix W_{opt} .

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_basis](#), [eval_functions](#)

Examples

```
# Example of optimizing parameters for synthetic data using default values
data <- meth_data
out_opt <- bpr_optim(x = data, is_parallel = FALSE, opt_itnmax = 3)

#-----

# Example of optimizing parameters for synthetic data using 3 RBFs
ex_data <- meth_data
basis <- create_rbf_object(M=3)
out_opt <- bpr_optim(x = ex_data, is_parallel = FALSE, basis = basis,
                    opt_itnmax = 3)

#-----

# Example of of specific promoter region using 2 RBFs
basis <- create_rbf_object(M=2)
w <- c(0.1, 0.1, 0.1)
data <- meth_data[[1]]
out_opt <- bpr_optim(x = data, w = w, basis = basis, fit_feature = "NLL",
                    opt_itnmax = 3)
```

bpr_predict_wrap

(DEPRECATED) Predict gene expression from methylation profiles

Description

(DEPRECATED) bpr_predict_wrap is a function that wraps all the necessary subroutines for performing prediction on gene expression levels. Initially, it optimizes the parameters of the basis functions so as to learn the methylation profiles. Then, uses the learned parameters / coefficients of the basis functions as input features for performing regression in order to predict the corresponding gene expression levels.

Usage

```

bpr_predict_wrap(
  formula = NULL,
  x,
  y,
  model_name = "svm",
  w = NULL,
  basis = NULL,
  train_ind = NULL,
  train_perc = 0.7,
  fit_feature = "RMSE",
  cov_feature = TRUE,
  opt_method = "CG",
  opt_itnmax = 100,
  is_parallel = TRUE,
  no_cores = NULL,
  is_summary = TRUE
)

```

Arguments

| | |
|-------------|---|
| formula | An object of class formula , e.g. see lm function. If NULL, the simple linear regression model is used. |
| x | The binomial distributed observations, which has to be a list of elements of length N, where each element is an L x 3 matrix of observations, where 1st column contains the locations. The 2nd and 3rd columns contain the total trials and number of successes at the corresponding locations, respectively. See process_haib_caltech_wrap on a possible way to get this data structure. |
| y | Corresponding gene expression data for each element of the list x. |
| model_name | A string denoting the regression model. Currently, available models are: "svm", "randomForest", "r1m", "mars" and "1m". |
| w | Optional vector of initial parameter / coefficient values. |
| basis | Optional basis function object, default is an 'rbf' object, see create_rbf_object . |
| train_ind | Optional vector containing the indices for the train set. |
| train_perc | Optional parameter for defining the percentage of the dataset to be used for training set, the remaining will be the test set. |
| fit_feature | Return additional feature on how well the profile fits the methylation data. Either NULL for ignoring this feature or one of the following: 1) "RMSE" for returning the fit of the profile using the RMSE as measure of error or 2) "NLL" for returning the fit of the profile using the Negative Log Likelihood as measure of error. |
| cov_feature | Logical, whether to return an additional feature for the CpG coverage across the promoter region. |
| opt_method | The optimization method to be used. See optim for possible methods. Default is "CG". |

cluster_profiles_mle *Cluster methylation profiles using EM*

Description

General purpose functions for clustering latent profiles for different observation models using maximum likelihood estimation (MLE) and the EM algorithm. Initially, it performs parameter checking, and initializes main parameters, such as mixing proportions, basis function coefficients, then the EM algorithm is applied and finally model selection metrics are calculated, such as BIC and AIC.

Usage

```
cluster_profiles_mle(
  X,
  K = 3,
  model = NULL,
  basis = NULL,
  H = NULL,
  pi_k = NULL,
  lambda = 0.5,
  beta_dispersion = 5,
  gaussian_sigma = rep(0.2, K),
  w = NULL,
  em_max_iter = 50,
  epsilon_conv = 1e-04,
  opt_method = "CG",
  opt_itnmax = 50,
  init_opt_itnmax = 30,
  is_parallel = FALSE,
  no_cores = NULL,
  is_verbose = FALSE,
  ...
)
```

Arguments

- | | |
|-------|--|
| X | The input data, which has to be a list of elements of length N, where each element is an L X C matrix, where L are the total number of observations. The first column contains the input observations x (i.e. CpG locations). If "binomial" model then C=3, and 2nd and 3rd columns contain total number of trials and number of successes respectively. If "bernoulli" or "gaussian" model, then C=2 containing the output y (e.g. methylation level). If "beta" model, then C=3, where 2nd column contains output y and 3rd column the dispersion parameter. |
| K | Integer denoting the total number of clusters K. |
| model | Observation model name as character string. It can be either 'bernoulli', 'binomial', 'beta' or 'gaussian'. |

| | |
|-----------------|---|
| basis | A 'basis' object. E.g. see create_basis . If NULL, will an RBF object will be created. |
| H | Optional, design matrix of the input data X. If NULL, H will be computed inside the function. |
| pi_k | Vector of length K, denoting the mixing proportions. |
| lambda | The complexity penalty coefficient for ridge regression. |
| beta_dispersion | Dispersion parameter, only used for Beta distribution and will be the same for all observations. |
| gaussian_sigma | Initial standard deviation of the noise term, only used when having "gaussian" observation model. |
| w | Optional, an (M+1)xK matrix of the initial parameters, where each column consists of the basis function coefficients for each corresponding cluster k. If NULL, will be assigned with default values. |
| em_max_iter | Integer denoting the maximum number of EM iterations. |
| epsilon_conv | Numeric denoting the convergence threshold for EM. |
| opt_method | The optimization method to be used. See optim for possible methods. Default is "CG". |
| opt_itnmax | Optional argument giving the maximum number of iterations for the corresponding method. See optim for details. |
| init_opt_itnmax | Optimization iterations for obtaining the initial EM parameter values. |
| is_parallel | Logical, indicating if code should be run in parallel. |
| no_cores | Number of cores to be used, default is max_no_cores - 1. |
| is_verbose | Logical, print results during EM iterations. |
| ... | Additional parameters. |

Value

An object of class `cluster_profiles_mle_"obs_model"` with the following elements:

- `W`: An (M+1) X K matrix with the optimized parameter values for each cluster. Each column of the matrix corresponds a different cluster k. M are the number of basis functions.
- `pi_k`: Mixing proportions.
- `r_nk`: An (N X K) responsibility matrix of each observations being explained by a specific cluster.
- `basis`: The basis object.
- `nll`: The negative log likelihood vector.
- `labels`: Cluster assignment labels.
- `bic`: Bayesian Information Criterion metric.
- `aic`: Akaike Information Criterion metric.
- `icl`: Integrated Complete Likelihood criterion metric.
- `gaussian_sigma`: Optimized standard deviation for gaussian observation model.

Details

The beta regression model is based on alternative parameterization of the beta density in terms of the mean and dispersion parameter: <https://cran.r-project.org/web/packages/betareg/>. For modelling details for Binomial/Bernoulli observation model check the paper for BPRMeth: <https://academic.oup.com/bioinformatics/article/32/17/i405/2450762>.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_basis](#), [cluster_profiles_vb](#) [infer_profiles_vb](#), [infer_profiles_mle](#), [infer_profiles_gibbs](#), [create_region_object](#)

Examples

```
# Example of optimizing parameters for synthetic data using 3 RBFs

basis <- create_rbf_object(M=3)
out <- cluster_profiles_mle(X = binomial_data, model = "binomial",
  basis=basis, em_max_iter = 5, opt_itnmax = 5, init_opt_itnmax=5,
  is_parallel = FALSE)

#-----

basis <- create_rbf_object(M=3)
out <- cluster_profiles_mle(X = gaussian_data, model = "gaussian",
  basis=basis, em_max_iter = 5, opt_itnmax = 5, init_opt_itnmax=5,
  is_parallel = FALSE)
```

cluster_profiles_vb *Cluster methylation profiles using VB*

Description

General purpose functions for clustering latent profiles for different observation models using Variational Bayes (VB) EM-like algorithm.

Usage

```
cluster_profiles_vb(
  X,
  K = 3,
  model = NULL,
  basis = NULL,
  H = NULL,
```



```

    delta_0 = NULL,
    w = NULL,
    gaussian_l = 50,
    alpha_0 = 0.5,
    beta_0 = 0.1,
    vb_max_iter = 100,
    epsilon_conv = 1e-04,
    is_verbose = FALSE,
    ...
)

```

Arguments

| | |
|--------------|---|
| X | The input data, which has to be a list of elements of length N, where each element is an L X C matrix, where L are the total number of observations. The first column contains the input observations x (i.e. CpG locations). If "binomial" model then C=3, and 2nd and 3rd columns contain total number of trials and number of successes respectively. If "bernoulli" or "gaussian" model, then C=2 containing the output y (e.g. methylation level). |
| K | Integer denoting the total number of clusters K. |
| model | Observation model name as character string. It can be either 'bernoulli', 'binomial', 'beta' or 'gaussian'. |
| basis | A 'basis' object. E.g. see create_basis . If NULL, will an RBF object will be created. |
| H | Optional, design matrix of the input data X. If NULL, H will be computed inside the function. |
| delta_0 | Parameter vector of the Dirichlet prior on the mixing proportions pi. |
| w | Optional, an (M+1)xK matrix of the initial parameters, where each column consists of the basis function coefficients for each corresponding cluster k. If NULL, will be assigned with default values. |
| gaussian_l | Noise precision parameter, only used when having "gaussian" observation model. |
| alpha_0 | Hyperparameter: shape parameter for Gamma distribution. A Gamma distribution is used as prior for the precision parameter tau. |
| beta_0 | Hyperparameter: rate parameter for Gamma distribution. A Gamma distribution is used as prior for the precision parameter tau. |
| vb_max_iter | Integer denoting the maximum number of VB iterations. |
| epsilon_conv | Numeric denoting the convergence threshold for VB. |
| is_verbose | Logical, print results during VB iterations. |
| ... | Additional parameters. |

Value

An object of class `cluster_profiles_vb_"obs_model"` with the following elements:

- W: An (M+1) X K matrix with the optimized parameter values for each cluster, M are the number of basis functions. Each column of the matrix corresponds a different cluster k.

- `W_Sigma`: A list with the covariance matrices of the posterior parameter `W` for each cluster `k`.
- `r_nk`: An $(N \times K)$ responsibility matrix of each observations being explained by a specific cluster.
- `delta`: Optimized Dirichlet parameter for the mixing proportions.
- `alpha`: Optimized shape parameter of Gamma distribution.
- `beta`: Optimized rate parameter of the Gamma distribution
- `basis`: The basis object.
- `lb`: The lower bound vector.
- `labels`: Cluster assignment labels.
- `pi_k`: Expected value of mixing proportions.

Details

The modelling and mathematical details for clustering profiles using mean-field variational inference are explained here: <http://rpubs.com/cakapourani/>. More specifically:

- For Binomial/Bernoulli observation model check: <http://rpubs.com/cakapourani/vb-mixture-bpr>
- For Gaussian observation model check: <http://rpubs.com/cakapourani/vb-mixture-lr>

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_basis](#), [cluster_profiles_mle](#), [infer_profiles_vb](#), [infer_profiles_mle](#), [infer_profiles_gibbs](#), [create_region_object](#)

Examples

```
# Example of optimizing parameters for synthetic data using 3 RBFs
basis <- create_rbf_object(M=3)
out <- cluster_profiles_vb(X = binomial_data, model = "binomial",
  basis=basis, vb_max_iter = 10)

#-----

basis <- create_rbf_object(M=3)
out <- cluster_profiles_vb(X = gaussian_data, model = "gaussian",
  basis=basis, vb_max_iter = 10)
```

create_anno_region *Create annotation regions*

Description

create_anno_region creates annotation regions from annotation data, using the central point of the annotation features as ground truth labels we create genomic regions N bp upstream and M bp downstream of central location.

Usage

```
create_anno_region(  
  anno,  
  chrom_size = NULL,  
  is_centre = FALSE,  
  is_window = TRUE,  
  upstream = -5000,  
  downstream = 5000  
)
```

Arguments

| | |
|------------|--|
| anno | A GRanges object containing the annotation data, this normally would be the output from read_anno function. |
| chrom_size | Object containing genome chromosome sizes, normally would be the output of read_chrom_size function. |
| is_centre | Logical, whether 'start' and 'end' locations are pre-centred. If TRUE, the mean of the locations will be chosen as centre. If FALSE, the 'start' will be chosen as the center; e.g. for genes the 'start' denotes the TSS and we use this as centre to obtain K-bp upstream and downstream of TSS. |
| is_window | Whether to consider a predefined window region around centre. If TRUE, then 'upstream' and 'downstream' parameters are used, otherwise we consider the whole region from start to end location. |
| upstream | Integer defining the length of bp upstream of 'centre' for creating the genomic region. If is_window = FALSE, this parameter is ignored. |
| downstream | Integer defining the length of bp downstream of 'centre' for creating the genomic region. If is_window = FALSE, this parameter is ignored. |

Value

A GRanges object containing the genomic regions.

The GRanges object contains two or three additional metadata column:

- id: Genomic region id.
- centre: Central location of each genomic region.

- name: (Optional) Genomic region name.

This column can be accessed as follows: `granges_object$tss`

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_region_object](#), [read_anno](#)

Examples

```
# Obtain the path to files
file <- system.file("extdata", "dummy_anno.bed", package = "BPRMeth")
anno_dt <- read_anno(file, is_anno_region = FALSE)
# Create genomic region
gen_region <- create_anno_region(anno_dt)
# Extract ID
id <- gen_region$id
```

create_basis

Create basis objects

Description

These functions create different basis objects, which can be used as input to complex functions in order to perform computations depending on the class of the basis function.

Usage

```
create_rbf_object(
  M = 2,
  gamma = NULL,
  mus = NULL,
  eq_spaced_mus = TRUE,
  whole_region = TRUE
)

create_polynomial_object(M = 1)

create_fourier_object(M = 2, period = 2)
```

Arguments

| | |
|---------------|--|
| M | The number of the basis functions. In case of Fourier basis, this number should be even, since we need to have pairs of sines and cosines and the constant term is added by default. |
| gamma | Inverse width of radial basis function. |
| mus | Optional centers of the RBF. |
| eq_spaced_mus | Logical, if TRUE, equally spaced centers are created, otherwise centers are created using kmeans algorithm. |
| whole_region | Logical, indicating if the centers will be evaluated equally spaced on the whole region, or between the min and max of the observation values. |
| period | The period, that is the basis functions are periodic on a specific interval. Best choice is the range of the points used for regression. |

Value

A basis object of class 'rbf', 'polynomial' or 'fourier'.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[eval_functions](#), [design_matrix](#)

Examples

```
(obj <- create_rbf_object(M = 2))
#-----
(obj <- create_polynomial_object(M = 2))
(obj <- create_fourier_object(M = 2, period = 1))
```

create_region_object *Create genomic region data*

Description

create_region_object creates genomic regions (e.g. forms methylation regions data) using as input methylation and annotation data with genomic regions of interest.

Usage

```
create_region_object(
  met_dt,
  anno_dt,
  cov = 5,
  sd_thresh = 0.1,
  ignore_strand = TRUE,
  filter_empty_region = TRUE,
  fmin = -1,
  fmax = 1
)
```

Arguments

| | |
|---------------------|---|
| met_dt | A GRanges object with methylation data, whose format should be similar to read_met function. |
| anno_dt | A GRanges object with annotation data, whose format should be similar to read_anno . |
| cov | Integer defining the minimum coverage of CpGs that each region must contain. |
| sd_thresh | Optional numeric defining the minimum standard deviation of the methylation change in a region. This is used to filter regions with no methylation variability. |
| ignore_strand | Logical, whether or not to ignore strand information. |
| filter_empty_region | Logical, whether to discard genomic regions that have no CpG coverage or do not pass filtering options. |
| fmin | Minimum range value for location scaling. Under this version, it should be left to its default value -1. |
| fmax | Maximum range value for location scaling. Under this version, it should be left to its default value 1. |

Value

A list object containing the two elements:

- met: A list containing methylation region data, where each entry in the list is an $L_i \times D$ dimensional matrix, where L_i denotes the number of CpGs found in region i . The columns contain the following information:
 1. 1st column: Contains the locations of CpGs relative to centre. Note that the actual locations are scaled to the (fmin, fmax) region.
 2. 2nd column: If "bulk" data (i.e. binomial) it contains the total number of reads at each CpG location, otherwise the methylation level.
 3. 3rd column: If "bulk" data, the methylated reads at each CpG location, otherwise this $D = 2$ and this column is absent.
 . Rownames of each matrix contain the actual CpG genomic coordinates as <chr>:<location>.
- anno: The annotation object.

Note: The lengths of met and anno should match.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[read_met](#), [read_anno](#)

Examples

```
## Not run:
# Download the files and change the working directory to that location
met_dt <- read_met("name_of_met_file")
anno_dt <- read_anno("name_of_anno_file")

obj <- create_region_object(met_dt, anno_dt)

# Extract methylation regions
met <- obj$met

## End(Not run)
```

design_matrix

Generic function for creating design matrices

Description

These functions call the appropriate methods depending on the class of the object obj to create RBF, polynomial or Fourier design matrices.

Usage

```
design_matrix(obj, ...)

## Default S3 method:
design_matrix(obj, ...)

## S3 method for class 'polynomial'
design_matrix(obj, obs, ...)

## S3 method for class 'rbf'
design_matrix(obj, obs, ...)

## S3 method for class 'fourier'
design_matrix(obj, obs, ...)
```

Arguments

obj A basis function object.
... Additional parameters.
obs A vector of observations.

Value

A design matrix object

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_basis](#), [eval_functions](#)

Examples

```
obj <- create_polynomial_object(M=2)
obs <- c(0,.2,.5)
poly <- design_matrix(obj, obs)
```

```
#-----
```

```
obj <- create_rbf_object(M=2)
obs <- c(0,.2,.5)
rbf <- design_matrix(obj, obs)
```

```
#-----
```

```
obj <- create_fourier_object(M=2)
obs <- c(0,.2,.5)
fourier <- design_matrix(obj, obs)
```

encode_expr

Processed ENCODE expression data

Description

Small subset of ENCODE expression data already in pre-processed format, which are used as a case study for the vignette.

Usage

```
encode_expr
```


Format

Expression data in format as the output of [read_expr](#) function, i.e. a `data.table` with two columns: "id", "expr".

Value

Encode expression data

See Also

[create_region_object](#), [read_met](#), [read_anno](#), [read_expr](#)

encode_met

Processed ENCODE methylation data

Description

Small subset of ENCODE methylation data already in pre-processed format, which are used as a case study for the vignette.

Usage

```
encode_met
```

Format

A list object containing methylation regions and annotation data. This in general would be the output of the [create_region_object](#) function. It has the following two objects:

- met: A list containing the methylation regions, each element of the list is a different genomic region.
- anno: Corresponding annotation data.

Value

Encode methylation data

See Also

[create_region_object](#), [read_met](#), [read_anno](#), [read_expr](#)

eval_functions *Evaluate basis functions*

Description

Method for evaluating an M basis function model with observation data `obs` and coefficients `w`.

Usage

```
eval_probit_function(obj, ...)  
  
eval_function(obj, ...)  
  
## S3 method for class 'rbf'  
eval_function(obj, obs, w, ...)  
  
## S3 method for class 'polynomial'  
eval_function(obj, obs, w, ...)  
  
## S3 method for class 'fourier'  
eval_function(obj, obs, w, ...)
```

Arguments

| | |
|------------------|---|
| <code>obj</code> | The basis function object. |
| <code>...</code> | Optional additional parameters |
| <code>obs</code> | Observation data. |
| <code>w</code> | Vector of length M, containing the coefficients of an M^{th} -order basis function. |

Value

The evaluated function values.

NOTE that the `eval_probit_function` computes the probit transformed basis function values.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_basis](#), [design_matrix](#)

Examples

```

# Evaluate the probit transformed basis function values
obj <- create_rbf_object(M=2)
obs <- c(1,2,3)
w <- c(0.1, 0.3, -0.6)
out <- eval_probit_function(obj, obs, w)

# -----

# Evaluate the RBF basis function values
obj <- create_rbf_object(M=2, mus = c(2,2.5))
obs <- c(1,2,3)
w <- c(0.1, 0.3, -0.6)
out <- eval_function(obj, obs, w)

# -----

# Evaluate the Polynomial basis function values
obj <- create_polynomial_object(M=2)
obs <- c(1,2,3)
w <- c(0.1, 0.3, -0.6)
out <- eval_function(obj, obs, w)

# -----

# Evaluate the Fourier basis function values
obj <- create_fourier_object(M=2)
obs <- c(1,2,3)
w <- c(0.1, 0.3, -0.6)
out <- eval_function(obj, obs, w)

```

gaussian_data

Synthetic Gaussian data

Description

A synthetic dataset containing 300 entries from Gaussian (i.e. linear) regression observations (e.g. M-values from array methylation data).

Usage

```
gaussian_data
```

Format

A list with 300 elements, where each element element is an L x 2 matrix of observations, where:

1st column locations of obseravtions

2nd column methylation level

Value

Synthetic Bernoulli methylation data.

See Also

[binomial_data](#), [beta_data](#), [bernoulli_data](#)

gex_data

Synthetic expression data

Description

Corresponding gene expression data for the [meth_data](#)

Usage

gex_data

Format

A vector of length 600

Value

Synthetic gene expression data

See Also

[meth_data](#), [bernoulli_data](#), [binomial_data](#), [beta_data](#), [gaussian_data](#)

impute_bulk_met

Impute/predict bulk methylation states

Description

Make predictions of missing methylation states, i.e. perform imputation using BPRmeth. This requires keeping a subset of data as a held out test set during BPRMeth inference or providing a different file that contains chromosome and CpG locations.

Usage

```
impute_bulk_met(obj, anno, test_data = NULL, return_test = FALSE)
```

Arguments

| | |
|-------------|--|
| obj | Output of BPRMeth inference object. |
| anno | A GRanges object with annotation data, whose format should be similar to read_anno . |
| test_data | Test data to evaluate performance. |
| return_test | Whether or not to return a list with the predictions. |

Value

A list containing two vectors, the true methylation state and the predicted/imputed methylation states.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[partition_bulk_dataset](#)

Examples

```
# Extract synthetic data
dt <- encode_met

# Partition to train and test set
dt <- partition_bulk_dataset(dt)

# Create basis object
basis_obj <- create_rbf_object(M = 3)

# Run BPRMeth
fit <- infer_profiles_mle(X = dt$met, model = "binomial",
  basis = basis_obj, is_parallel = FALSE, opt_itnmax = 10)

# Perform imputation
imputation_obj <- impute_bulk_met(obj = fit, anno = dt$anno,
  test_data = dt$met_test)
```

infer_profiles_gibbs *Infer methylation profiles using Gibbs sampling*

Description

General purpose functions for inferring latent profiles for different observation models using Gibbs sampling. Currently implemented observation models are: 'bernoulli' and 'binomial' and the auxiliary variable approach is used.

Usage

```
infer_profiles_gibbs(
  X,
  model = NULL,
  basis = NULL,
  H = NULL,
  w = NULL,
  mu_0 = NULL,
  cov_0 = NULL,
  gibbs_nsim = 500,
  gibbs_burn_in = 100,
  store_gibbs_draws = FALSE,
  is_parallel = FALSE,
  no_cores = NULL,
  ...
)
```

Arguments

| | |
|-------------------|---|
| X | The input data, either a matrix or a list of elements of length N, where each element is an L X C matrix, where L are the total number of observations. The first column contains the input observations x (i.e. CpG locations). If "binomial" model then C=3, and 2nd and 3rd columns contain total number of trials and number of successes respectively. If "bernoulli" then C=2 containing the output y (e.g. methylation level). |
| model | Observation model name as character string. It can be either 'bernoulli' or 'binomial'. |
| basis | A 'basis' object. E.g. see create_basis . If NULL, will an RBF object will be created. |
| H | Optional, design matrix of the input data X. If NULL, H will be computed inside the function. |
| w | A vector of initial parameters (i.e. coefficients of the basis functions). If NULL, it will be initialized inside the function. |
| mu_0 | The prior mean hyperparameter vector for w. |
| cov_0 | The prior covariance hyperparameter matrix for w. |
| gibbs_nsim | Total number of simulations for the Gibbs sampler. |
| gibbs_burn_in | Burn in period of the Gibbs sampler. |
| store_gibbs_draws | Logical indicating if we should keep the whole MCMC chain for further analysis. |
| is_parallel | Logical, indicating if code should be run in parallel. |
| no_cores | Number of cores to be used, default is max_no_cores - 1. |
| ... | Additional parameters. |

Value

An object of class `infer_profiles_gibbs_"obs_model"` with the following elements:

- `W`: An $N \times (M+1)$ matrix with the posterior mean of the parameters w . Each row of the matrix corresponds to each element of the list `X`; if `X` is a matrix, then $N = 1$. The columns are of the same length as the parameter vector w (i.e. number of basis functions).
- `W_sd`: An $N \times (M+1)$ matrix with the posterior standard deviation (sd) of the parameters W .
- `basis`: The basis object.
- `nll_feat`: NLL fit feature.
- `rmse_feat`: RMSE fit feature.
- `coverage_feat`: CpG coverage feature.
- `W_draws`: Optional, draws of the Gibbs sampler.

Details

The modelling and mathematical details for inferring profiles using Gibbs sampling are explained here: <http://rpubs.com/cakapourani/> . More specifically:

- For Binomial observation model check: <http://rpubs.com/cakapourani/bayesian-bpr-model>
- For Bernoulli observation model check: <http://rpubs.com/cakapourani/bayesian-bpr-model>

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_basis](#), [infer_profiles_mle](#), [infer_profiles_vb](#), [create_region_object](#)

Examples

```
# Example of inferring parameters for synthetic data using 3 RBFs
basis <- create_rbf_object(M=3)
out <- infer_profiles_gibbs(X = binomial_data, model = "binomial",
  basis = basis, is_parallel = FALSE, gibbs_nsim = 10, gibbs_burn_in = 5)

#-----
```

infer_profiles_mle *Infer methylation profiles using MLE*

Description

General purpose functions for inferring latent profiles for different observation models using maximum likelihood estimation (MLE). Current observation models are: 'bernoulli', 'binomial', 'beta' or 'gaussian'. For most models we cannot obtain an analytically tractable solution, hence an optimization procedure is used. The `optim` package is used for performing optimization.

Usage

```
infer_profiles_mle(
  X,
  model = NULL,
  basis = NULL,
  H = NULL,
  lambda = 0.5,
  w = NULL,
  beta_dispersion = 5,
  opt_method = "CG",
  opt_itnmax = 100,
  is_parallel = FALSE,
  no_cores = NULL,
  ...
)
```

Arguments

| | |
|--------|---|
| X | The input data, either a <code>matrix</code> or a <code>list</code> of elements of length N, where each element is an L X C matrix, where L are the total number of observations. The first column contains the input observations x (i.e. CpG locations). If "binomial" model then C=3, and 2nd and 3rd columns contain total number of trials and number of successes respectively. If "bernoulli" or "gaussian" model, then C=2 containing the output y (e.g. methylation level). If "beta" model, then C=3, where 2nd column contains output y and 3rd column the dispersion parameter. |
| model | Observation model name as character string. It can be either 'bernoulli', 'binomial', 'beta' or 'gaussian'. |
| basis | A 'basis' object. E.g. see <code>create_basis</code> . If NULL, will an RBF object will be created. |
| H | Optional, design matrix of the input data X. If NULL, H will be computed inside the function. |
| lambda | The complexity penalty coefficient for ridge regression. |
| w | A vector of initial parameters (i.e. coefficients of the basis functions). |

| | |
|-----------------|---|
| beta_dispersion | Dispersion parameter, only used for Beta distribution and will be the same for all observations. |
| opt_method | The optimization method to be used. See <code>optim</code> for possible methods. Default is "CG". |
| opt_itnmax | Optional argument giving the maximum number of iterations for the corresponding method. See <code>optim</code> for details. |
| is_parallel | Logical, indicating if code should be run in parallel. |
| no_cores | Number of cores to be used, default is <code>max_no_cores - 1</code> . |
| ... | Additional parameters. |

Value

An object of class `infer_profiles_mle_"obs_model"` with the following elements:

- `W`: An $N \times (M+1)$ matrix with the optimized parameter values. Each row of the matrix corresponds to each element of the list `X`; if `X` is a matrix, then $N = 1$. The columns are of the same length as the parameter vector `w` (i.e. number of basis functions).
- `basis`: The basis object.
- `nll_feat`: NLL fit feature.
- `rmse_feat`: RMSE fit feature.
- `coverage_feat`: CpG coverage feature.

Details

The beta regression model is based on alternative parameterization of the beta density in terms of the mean and dispersion parameter: <https://cran.r-project.org/web/packages/betareg/>. For modelling details for Binomial/Bernoulli observation model check the paper for BPRMeth: <https://academic.oup.com/bioinformatics/article/32/17/i405/2450762>.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_basis](#), [infer_profiles_vb](#), [infer_profiles_gibbs](#), [create_region_object](#)

Examples

```
# Example of optimizing parameters for synthetic data using 3 RBFs
basis <- create_rbf_object(M=3)
out <- infer_profiles_mle(X = binomial_data, model = "binomial",
  basis = basis, is_parallel = FALSE, opt_itnmax = 10)

#-----

basis <- create_rbf_object(M=3)
```

```

out <- infer_profiles_mle(X = beta_data, model = "beta",
  basis = basis, is_parallel = FALSE, opt_itnmax = 10)

#-----

basis <- create_rbf_object(M=3)
out <- infer_profiles_mle(X = gaussian_data[[1]], model = "gaussian",
  basis = basis, is_parallel = FALSE, opt_itnmax = 10)

```

infer_profiles_vb *Infer methylation profiles using VB*

Description

General purpose functions for inferring latent profiles for different observation models using Variational Bayes (VB). Current observation models are: 'bernoulli', 'binomial' or 'gaussian'.

Usage

```

infer_profiles_vb(
  X,
  model = NULL,
  basis = NULL,
  H = NULL,
  w = NULL,
  gaussian_l = 50,
  alpha_0 = 0.5,
  beta_0 = 0.1,
  vb_max_iter = 100,
  epsilon_conv = 1e-05,
  is_parallel = FALSE,
  no_cores = NULL,
  is_verbose = FALSE,
  ...
)

```

Arguments

| | |
|-------|--|
| X | The input data, either a matrix or a list of elements of length N, where each element is an L X C matrix, where L are the total number of observations. The first column contains the input observations x (i.e. CpG locations). If "binomial" model then C=3, and 2nd and 3rd columns contain total number of trials and number of successes respectively. If "bernoulli" or "gaussian" model, then C=2 containing the output y (e.g. methylation level). |
| model | Observation model name as character string. It can be either 'bernoulli', 'binomial', 'beta' or 'gaussian'. |

| | |
|--------------|---|
| basis | A 'basis' object. E.g. see create_basis . If NULL, will an RBF object will be created. |
| H | Optional, design matrix of the input data X. If NULL, H will be computed inside the function. |
| w | A vector of initial parameters (i.e. coefficients of the basis functions). If NULL, it will be initialized inside the function. |
| gaussian_l | Noise precision parameter, only used when having "gaussian" observation model. |
| alpha_0 | Hyperparameter: shape parameter for Gamma distribution. A Gamma distribution is used as prior for the precision parameter tau. |
| beta_0 | Hyperparameter: rate parameter for Gamma distribution. A Gamma distribution is used as prior for the precision parameter tau. |
| vb_max_iter | Integer denoting the maximum number of VB iterations. |
| epsilon_conv | Numeric denoting the convergence threshold for VB. |
| is_parallel | Logical, indicating if code should be run in parallel. |
| no_cores | Number of cores to be used, default is max_no_cores - 1. |
| is_verbose | Logical, print results during VB iterations. |
| ... | Additional parameters. |

Value

An object of class `infer_profiles_vb_"obs_model"` with the following elements:

- `W`: An $N \times (M+1)$ matrix with the optimized parameter values. Each row of the matrix corresponds to each element of the list `X`; if `X` is a matrix, then $N = 1$. The columns are of the same length as the parameter vector `w` (i.e. number of basis functions).
- `W_Sigma`: A list with covariance matrices for each element row in `W`.
- `basis`: The basis object.
- `nll_feat`: NLL fit feature.
- `rmse_feat`: RMSE fit feature.
- `coverage_feat`: CpG coverage feature.
- `lb_feat`: Lower Bound feature.

Details

The modelling and mathematical details for inferring profiles using mean-field variational inference are explained here: <http://rpubs.com/cakapourani/>. More specifically:

- For Binomial/Bernoulli observation model check: <http://rpubs.com/cakapourani/variational-bayes-bpr>
- For Gaussian observation model check: <http://rpubs.com/cakapourani/variational-bayes-lr>

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_basis](#), [infer_profiles_mle](#), [predict_expr](#), [create_region_object](#)

Examples

```
# Example of inferring parameters for synthetic data using 3 RBFs
basis <- create_rbf_object(M=3)
out <- infer_profiles_vb(X = binomial_data, model = "binomial",
  basis = basis, is_parallel = FALSE, vb_max_iter = 10)

#-----

basis <- create_rbf_object(M=3)
out <- infer_profiles_vb(X = gaussian_data, model = "gaussian",
  basis = basis, is_parallel = FALSE, vb_max_iter = 10)
```

inner_predict_model_expr

(INNER) Predict expression

Description

This functions makes predictions of gene expression levels using a model trained on methylation features extracted from genomic regions.

Usage

```
inner_predict_model_expr(model, test, is_summary = TRUE)
```

Arguments

| | |
|------------|--|
| model | The fitted regression model, i.e. the output of inner_train_model_expr . |
| test | The testing data. |
| is_summary | Logical, print the summary statistics. |

Value

A list containing the following elements:

- test_pred: The predicted values for the test data.
- test_errors: The test error metrics.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also[predict_expr](#)**Examples**

```
# Create synthetic data
train_data <- data.frame(x = rnorm(20), y=rnorm(20, 1, 4))
test_data <- data.frame(x = rnorm(40), y=rnorm(20, 1, 3))

# Train the model
train_model <- inner_train_model_expr(formula = y~., model_name="svm",
                                     train = train_data)

# Make predictions
res <- inner_predict_model_expr(model = train_model$model, test = test_data)
```

`inner_train_model_expr`*(INNER) Train expression model from methylation profiles*

Description

This function trains a regression model for predicting gene expression levels by taking as input the higher order methylation features extracted from specific genomic regions.

Usage

```
inner_train_model_expr(  
  formula = NULL,  
  model_name = "lm",  
  train,  
  is_summary = TRUE  
)
```

Arguments

| | |
|-------------------------|--|
| <code>formula</code> | An object of class formula , e.g. see lm function. If NULL, the simple linear model is used. |
| <code>model_name</code> | A string denoting the regression model. Currently, available models are: "svm", "randomForest", "r1m", "mars", "gp", and "lm". |
| <code>train</code> | The training data. |
| <code>is_summary</code> | Logical, print the summary statistics. |

Value

A list containing the following elements:

- `formula`: The formula that was used.
- `gex_model`: The fitted model.
- `train_pred`: The predicted values for the training data.
- `train_errors`: The training error metrics.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[predict_expr](#)

Examples

```
# Create synthetic data
train_data <- data.frame(x = rnorm(20), y=rnorm(20, 1, 4))
res <- inner_train_model_expr(formula = y~., train = train_data)

# Using a different model
res <- inner_train_model_expr(model_name = "randomForest",
                             train = train_data)
```

meth_data

Synthetic bulk methylation data

Description

A synthetic dataset containing 600 entries.

Usage

```
meth_data
```

Format

A list with 600 elements, where each element is an L x 3 matrix of observations, where:

1st column locations of observations

2nd column total trials

3rd column number of successes

Value

Synthetic bulk methylation data

See Also

[gex_data](#), [bernoulli_data](#), [binomial_data](#), [beta_data](#), [gaussian_data](#)

old_boxplot_cluster_gex

(DEPRECATED) Boxplot of clustered expression levels

Description

(DEPRECATED) `boxplot_cluster_gex` creates a boxplot of clustered gene expression levels which depend on the clustered methylation profiles. Each colour denotes a different cluster.

Usage

```
old_boxplot_cluster_gex(  
  bpr_cluster_obj,  
  gex,  
  main_lab = "Gene expression levels"  
)
```

Arguments

| | |
|------------------------------|--|
| <code>bpr_cluster_obj</code> | The output of the <code>bpr_cluster_wrap</code> function. |
| <code>gex</code> | The vector of gene expression data for each promoter region. |
| <code>main_lab</code> | The title of the plot |

Value

The figure to be plotted in the device.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[old_plot_cluster_prof](#), [old_plot_fitted_profiles](#)

Examples

```
# Cluster methylation profiles using 4 RBFs
obs <- meth_data
basis <- create_rbf_object(M = 4)
res <- bpr_cluster_wrap(x = obs, K = 3, em_max_iter = 2, opt_itnmax = 3,
                       init_opt_itnmax = 2, is_parallel = FALSE)

# Create the plot
old_boxplot_cluster_gex(bpr_cluster_obj = res, gex = gex_data)
```

old_plot_cluster_prof (*DEPRECATED*) *Plot of clustered methylation profiles*

Description

(DEPRECATED) `plot_cluster_prof` creates a plot of cluster methylation profiles, where each colour denotes a different cluster.

Usage

```
old_plot_cluster_prof(
  bpr_cluster_obj,
  main_lab = "Clustered methylation profiles"
)
```

Arguments

| | |
|------------------------------|---|
| <code>bpr_cluster_obj</code> | The output of the <code>bpr_cluster_wrap</code> function. |
| <code>main_lab</code> | The title of the plot |

Value

The figure to be plotted in the device.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[old_plot_fitted_profiles](#), [old_boxplot_cluster_gex](#)

Examples

```
# Cluster methylation profiles using 4 RBFs
obs <- meth_data
basis <- create_rbf_object(M = 4)
res <- bpr_cluster_wrap(x = obs, K = 3, em_max_iter = 2, opt_itnmax = 3,
                       init_opt_itnmax = 2, is_parallel = FALSE)

# Create the plot
old_plot_cluster_prof(bpr_cluster_obj = res)
```

old_plot_fitted_profiles

(DEPRECATED) Plot the fit of methylation profiles across a region

Description

(DEPRECATED) `plot_fitted_profiles` is a simple function for plotting the methylation data across a give region, together with the fit of the methylation profiles.

Usage

```
old_plot_fitted_profiles(  
  region,  
  X,  
  fit_prof,  
  fit_mean = NULL,  
  title = "Gene promoter",  
  ...  
)
```

Arguments

| | |
|-----------------------|-------------------------------|
| <code>region</code> | Promoter region number |
| <code>X</code> | Methylation data observations |
| <code>fit_prof</code> | Fitted profile |
| <code>fit_mean</code> | Fitted mean function |
| <code>title</code> | Title of the plot |
| <code>...</code> | Additional parameters |

Value

The figure to be plotted in the device.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also[old_plot_cluster_prof](#)**Examples**

```
# Fit methylation profiles using 3 RBFs
obs <- meth_data
y <- gex_data
basis <- create_rbf_object(M = 3)
out <- bpr_predict_wrap(x = obs, y = y, basis = basis,
                       is_parallel = FALSE, opt_itnmax = 5)

# Create the plot
old_plot_fitted_profiles(region = 16, X = meth_data, fit_prof = out)
```

partition_bulk_dataset

Partition bulk methylation dataset to training and test set

Description

Partition bulk methylation dataset to training and test set

Usage

```
partition_bulk_dataset(dt_obj, cpg_train_prcg = 0.5)
```

Arguments

dt_obj BPRMeth data 'region_object' object
cpg_train_prcg Fraction of CpGs in each genomic region to keep for training set.

Value

The BPRMeth data 'region_object' object with the following changes. The 'met' element will now contain only the 'training' data. An additional element called 'met_test' will store the data that will be used during testing to evaluate the imputation performance. These data will not be seen from BPRMeth during inference.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[create_region_object](#), [read_met](#), [impute_bulk_met](#)

Examples

```
# Partition the synthetic data from BPRMeth package
dt <- partition_bulk_dataset(encode_met)
```

plot_cluster_profiles *Plot clustered methylation profiles across a region*

Description

Function for plotting the clustered methylation profiles across a given region where each colour denotes a different cluster.

Usage

```
plot_cluster_profiles(
  cluster_obj,
  title = "Clustered profiles",
  x_axis = "genomic region",
  y_axis = "met level",
  x_labels = c("Upstream", "", "Centre", "", "Downstream"),
  ...
)
```

Arguments

| | |
|-------------|--|
| cluster_obj | Clustered profiles object, i.e. output from cluster_profiles_vb or cluster_profiles_mle functions. |
| title | Plot title |
| x_axis | x axis label |
| y_axis | x axis label |
| x_labels | x axis ticks labels |
| ... | Additional parameters |

Value

A ggplot2 object.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[plot_infer_profiles](#), [plot_predicted_expr](#), [boxplot_cluster_expr](#)

Examples

```
# Cluster methylation profiles using 3 RBFs
basis <- create_rbf_object(M = 3)
# Perform clustering
cl_obj <- cluster_profiles_vb(X = encode_met$met, K = 3, model = "binomial",
                             basis = basis, vb_max_iter = 5)
# Create plot
g <- plot_cluster_profiles(cluster_obj = cl_obj)
```

plot_infer_profiles *Plot inferred methylation profiles across a region*

Description

Function for plotting the inferred methylation profiles across a given region, and optionally the mean methylation rate together with the observed methylation data, using [ggplot2](#).

Usage

```
plot_infer_profiles(
  region = 1,
  obj_prof,
  obj_mean = NULL,
  obs = NULL,
  title = "Inferred profiles",
  x_axis = "genomic region",
  y_axis = "met level",
  x_labels = c("Upstream", "", "Centre", "", "Downstream"),
  ...
)
```

Arguments

| | |
|----------|--|
| region | Genomic region number |
| obj_prof | Inferred profile, i.e. output from infer_profiles_vb or infer_profiles_mle |
| obj_mean | Inferred mean function, i.e. output from infer_profiles_vb or infer_profiles_mle |
| obs | Methylation data observations, if a list, will extract the specific region, if a matrix will plot directly its observations. |
| title | Plot title |
| x_axis | x axis label |
| y_axis | x axis label |
| x_labels | x axis ticks labels |
| ... | Additional parameters |

Value

A ggplot2 object.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[plot_predicted_expr](#), [plot_cluster_profiles](#), [boxplot_cluster_expr](#)

Examples

```
# Fit methylation profiles using 5 RBFs
basis <- create_rbf_object(M = 5)
prof <- infer_profiles_vb(X = encode_met$met, model = "binomial",
  basis = basis, is_parallel = FALSE, vb_max_iter = 5)
# Create the plot
g <- plot_infer_profiles(region = 16, obj_prof = prof, obs = encode_met$met)
```

plot_predicted_expr *Scatter plot of predicted vs measured gene expression levels*

Description

plot_predicted_expr creates a scatter plot of predicted gene expression values on the x-axis versus the measured gene expression values on the y-axis.

Usage

```
plot_predicted_expr(
  pred_obj,
  title = "Predicted expression",
  is_margins = FALSE
)
```

Arguments

| | |
|------------|--|
| pred_obj | The output of the predict_expr function. |
| title | The title of the plot. |
| is_margins | Use specified margins or not. |

Value

A ggplot2 object.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[plot_infer_profiles](#), [plot_cluster_profiles](#), [boxplot_cluster_expr](#)

Examples

```
# Fit methylation profiles using 5 RBFs
basis <- create_rbf_object(M = 5)
prof <- infer_profiles_vb(X = encode_met$met, model = "binomial",
  basis = basis, is_parallel = FALSE, vb_max_iter = 5)
# Predict expression
pred_obj <- predict_expr(prof_obj = prof, expr = encode_expr,
  anno = encode_met$anno, model_name = "lm", is_summary = FALSE)
# Create plot
g <- plot_predicted_expr(pred_obj = pred_obj)
```

pool_bs_seq_rep *(DEPRECATED) Read and pool replicates from BS-Seq data*

Description

(DEPRECATED) pool_bs_seq_rep reads and pools replicate methylation data from BS-Seq experiments that are either in Encode RRBS or Bismark Cov format. Read the Important section below on when to use this function.

Usage

```
pool_bs_seq_rep(files, file_format = "encode_rrbs", chr_discarded = NULL)
```

Arguments

| | |
|---------------|---|
| files | A vector of filenames containing replicate experiments. This can also be just a single replicate. |
| file_format | A string denoting the file format that the BS-Seq data are stored. Current version allows "encode_rrbs" or "bismark_cov" formats. |
| chr_discarded | A vector with chromosome names to be discarded. |

Value

A GRanges object. The GRanges object contains two additional metadata columns:

- total_reads: total reads mapped to each genomic location.
- meth_reads: methylated reads mapped to each genomic location.

These columns can be accessed as follows: `granges_object$total_reads`

Important

Unless you want to create a different workflow when processing the BS-Seq data, you should NOT call this function, since this is a helper function. Instead you should call the [preprocess_bs_seq](#) function.

Information about the file formats can be found in the following links:

Encode RRBS format: http://rohsdb.cmb.usc.edu/GBshape/cgi-bin/hgTables?db=hg19&hgta_group=regulation&hgta_track=wgEncodeHaibMethylRrbs&hgta_table=wgEncodeHaibMethylRrbsBcbreast02&hgta_doSchema=describe+table+schema

Bismark Cov format: <http://rnbeads.mpi-inf.mpg.de/data/RnBeads.pdf>

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[read_bs_encode_haib](#), [preprocess_bs_seq](#)

Examples

```
# Obtain the path to the file
bs_file1 <- system.file("extdata", "rrbs.bed", package = "BPRMeth")
bs_file2 <- system.file("extdata", "rrbs.bed", package = "BPRMeth")

# Concatenate the files
bs_files <- c(bs_file1, bs_file2)
# Pool the replicates
pooled_data <- pool_bs_seq_rep(bs_files)
```

predict_expr

Predict gene expression from methylation profiles

Description

bpr_predict_wrap is a function that wraps all the necessary subroutines for performing prediction on gene expression levels. Initially, it optimizes the parameters of the basis functions so as to learn the methylation profiles. Then, uses the learned parameters / coefficients of the basis functions as input features for performing regression in order to predict the corresponding gene expression levels.

Usage

```
predict_expr(
  formula = NULL,
  prof_obj,
  expr,
  anno,
  model_name = "lm",
  train_ind = NULL,
  train_perc = 0.7,
  fit_feature = "RMSE",
  cov_feature = TRUE,
  is_summary = TRUE
)
```

Arguments

| | |
|-------------|--|
| formula | An object of class <code>formula</code> , e.g. see <code>lm</code> function. If NULL, the simple linear regression model is used. |
| prof_obj | Inferred profiles object. This in general will be the output of <code>'infer_profiles_'</code> (<code>inference_meth</code>) function. |
| expr | Gene expression data with two columns in <code>data.frame</code> or <code>data.table</code> format. 1st column will have gene IDs and should have column name "id", 2nd column will have expression levels. |
| anno | Annotation data as a <code>GRanges</code> object. |
| model_name | A string denoting the regression model. Currently, available models are: "svm", "randomForest", "r1m", "mars", "gp", and "lm". |
| train_ind | Optional vector containing the indices for the train set. |
| train_perc | Optional parameter for defining the percentage of the dataset to be used for training set, the remaining will be the test set. |
| fit_feature | Use additional feature of how well the profile fits the methylation data. Either NULL for ignoring this feature or one of the following: 1) "RMSE" or 2) "NLL" which will be used as input features for predicting expression. |
| cov_feature | Logical, whether to use coverage as input feature for predictions. |
| is_summary | Logical, print the summary statistics. |

Value

A `'predict_expr'` object which consists of the following variables:

- `train`: The training data.
- `test`: The test data.
- `model`: The fitted regression model.
- `train_pred`: The predicted values for the training data.
- `test_pred`: The predicted values for the test data.
- `train_errors`: The training error metrics.
- `test_errors`: The test error metrics.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[infer_profiles_mle](#), [infer_profiles_vb](#), [infer_profiles_gibbs](#), [create_basis](#),

Examples

```
# Fit methylation profiles using 5 RBFs
basis <- create_rbf_object(M = 5)
prof <- infer_profiles_vb(X = encode_met$met, model = "binomial",
  basis = basis, is_parallel = FALSE, vb_max_iter = 5)
# Predict expression
pred_obj <- predict_expr(prof_obj = prof, expr = encode_expr,
  anno = encode_met$anno, model_name = "lm", is_summary = FALSE)
```

preprocess_bs_seq *(DEPRECATED) Pre-process BS-Seq data in any given format*

Description

(DEPRECATED) preprocess_bs_seq is a general function for reading and preprocessing BS-Seq data. If a vector of files is given, these are considered as replicates and are pooled together. Finally, noisy reads are discarded.

Usage

```
preprocess_bs_seq(
  files,
  file_format = "encode_rrbs",
  chr_discarded = NULL,
  min_bs_cov = 4,
  max_bs_cov = 1000
)
```

Arguments

| | |
|---------------|---|
| files | A vector of filenames containing replicate experiments. This can also be just a single replicate. |
| file_format | A string denoting the file format that the BS-Seq data are stored. Current version allows "encode_rrbs" or "bismark_cov" formats. |
| chr_discarded | A vector with chromosome names to be discarded. |
| min_bs_cov | The minimum number of reads mapping to each CpG site. CpGs with less reads will be considered as noise and will be discarded. |
| max_bs_cov | The maximum number of reads mapping to each CpG site. CpGs with more reads will be considered as noise and will be discarded. |

Value

A GRanges object. The GRanges object contains two additional metadata columns:

- total_reads: total reads mapped to each genomic location.
- meth_reads: methylated reads mapped to each genomic location.

These columns can be accessed as follows: `granges_object$total_reads`

Additional Info

Information about the file formats can be found in the following links:

Encode RRBS format: http://rohshdb.cmb.usc.edu/GBshape/cgi-bin/hgTables?db=hg19&hgta_group=regulation&hgta_track=wgEncodeHaibMethylRrbs&hgta_table=wgEncodeHaibMethylRrbsBcbreast02&hgta_doSchema=describe+table+schema

Bismark Cov format: <http://rnbeads.mpi-inf.mpg.de/data/RnBeads.pdf>

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[read_bs_encode_haib](#) [pool_bs_seq_rep](#)

Examples

```
# Obtain the path to the files
bs_file <- system.file("extdata", "rrbs.bed", package = "BPRMeth")
bs_data <- preprocess_bs_seq(bs_file, file_format = "encode_rrbs")
```

preprocess_final_HTS_data

(DEPRECATED) Pre-process final HTS data for downstream analysis

Description

(DEPRECATED) `preprocess_final_HTS_data` performs a final filtering and preprocessing on the data for use in downstream analysis. These include, removing noisy gene expression data, removing or not un-expressed genes and log₂-transforming of the FPKM values.

Usage

```
preprocess_final_HTS_data(  
  methyl_region,  
  prom_reg,  
  rna_data,  
  gene_log2_transf = TRUE,  
  gene_outl_thresh = TRUE,  
  gex_outlier = 300  
)
```

Arguments

| | |
|-------------------------------|--|
| <code>methyl_region</code> | Methylation region data, which are the output of the "create_region_object" function. |
| <code>prom_reg</code> | A GRanges object containing corresponding annotated promoter regions for each entry of the methyl_region list. |
| <code>rna_data</code> | A GRanges object containing corresponding RNA-Seq data for each entry of the methyl_region list. This is the output of the "read_rna_encode_caltech" function. |
| <code>gene_log2_transf</code> | Logical, whether or not to log2 transform the gene expression data. |
| <code>gene_outl_thresh</code> | Logical, whether or not to remove outlier gene expression data. |
| <code>gex_outlier</code> | Numeric, denoting the threshold above of which the gene expression data (before the log2 transformation) are considered as noise. |

Value

An object which contains following information:

- `methyl_region`: The subset of promoter methylation region data after the filtering process.
- `gex`: A vectoring storing only the corresponding gene expression values for each promoter region.
- `rna_data`: The corresponding gene expression data stored as a GRanges object.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[read_rna_encode_caltech](#) [process_haib_caltech_wrap](#)

Examples

```

# Obtain the path to the BS file and then read it
bs_file <- system.file("extdata", "rrbs.bed", package = "BPRMeth")
bs_data <- read_bs_encode_haib(bs_file)

# Create promoter regions
rnaseq_file <- system.file("extdata", "rnaseq.bed", package = "BPRMeth")
annot_data <- read_rna_encode_caltech(rnaseq_file)
prom_region <- create_anno_region(annot_data)

# Create methylation regions
methyl_reg <- create_region_object(bs_data, prom_region,
  filter_empty_region = FALSE)

# Keep only covered genomic regions
cov_ind <- which(!is.na(methyl_reg))
methyl_reg <- methyl_reg[cov_ind]
prom_region <- prom_region[cov_ind, ]
annot_data <- annot_data[cov_ind, ]

# Finally preprocess the HTS data
res <- preprocess_final HTS_data(methyl_reg, prom_region, annot_data)

```

```
process_haib_caltech_wrap
```

(DEPRECATED) Wrapper for processing ENCODE HAIB and Caltech HTS

Description

(DEPRECATED) process_haib_caltech_wrap is a wrapper method for processing HTS data and returning the methylation promoter regions and the corresponding gene expression data for those promoter regions. Note that the format of BS-Seq data should be in the Encode Haib bed format and for the RNA-Seq data in Encode Caltech bed format.

Usage

```

process_haib_caltech_wrap(
  bs_files,
  rna_files,
  chrom_size_file = NULL,
  chr_discarded = NULL,
  upstream = -7000,
  downstream = 7000,
  min_bs_cov = 4,
  max_bs_cov = 1000,
  cpkg_density = 10,

```

```

sd_thresh = 0.1,
ignore_strand = TRUE,
gene_log2_transf = TRUE,
gene_outl_thresh = TRUE,
gex_outlier = 300,
fmin = -1,
fmax = 1
)

```

Arguments

| | |
|------------------|--|
| bs_files | Filename (or vector of filenames if there are replicates) of the BS-Seq '.bed' formatted data to read values from. |
| rna_files | Filename of the RNA-Seq '.bed' formatted data to read values from. Currently, this version does not support pooling RNA-Seq replicates. |
| chrom_size_file | Optional filename containing genome chromosome sizes. |
| chr_discarded | A vector with chromosome names to be discarded. |
| upstream | Integer defining the length of bp upstream of TSS for creating the promoter region. |
| downstream | Integer defining the length of bp downstream of TSS for creating the promoter region. |
| min_bs_cov | The minimum number of reads mapping to each CpG site. CpGs with less reads will be considered as noise and will be discarded. |
| max_bs_cov | The maximum number of reads mapping to each CpG site. CpGs with more reads will be considered as noise and will be discarded. |
| cpg_density | Optional integer defining the minimum number of CpGs that have to be in a methylated region. Regions with less than n CpGs are discarded. |
| sd_thresh | Optional numeric defining the minimum standard deviation of the methylation change in a region. This is used to filter regions with no methylation change. |
| ignore_strand | Logical, whether or not to ignore strand information. |
| gene_log2_transf | Logical, whether or not to log2 transform the gene expression data. |
| gene_outl_thresh | Logical, whether or not to remove outlier gene expression data. |
| gex_outlier | Numeric, denoting the threshold above of which the gene expression data (before the log2 transformation) are considered as noise. |
| fmin | Optional minimum range value for region location scaling. Under this version, this parameter should be left to its default value. |
| fmax | Optional maximum range value for region location scaling. Under this version, this parameter should be left to its default value. |

Value

A processHTS object which contains following information:

- methyl_region: A list containing methylation data, where each entry in the list is an $L_i \times 3$ dimensional matrix, where L_i denotes the number of CpGs found in region i . The columns contain the following information:
 1. 1st column: Contains the locations of CpGs relative to TSS. Note that the actual locations are scaled to the (fmin, fmax) region.
 2. 2nd column: Contains the total reads of each CpG in the corresponding location.
 3. 3rd column: Contains the methylated reads each CpG in the corresponding location.
- gex: A vector containing the corresponding gene expression levels for each entry of the methyl_region list.
- prom_region: A GRanges object containing corresponding annotated promoter regions for each entry of the methyl_region list. The GRanges object has one additional metadata column named tss, which stores the TSS of each promoter.
- rna_data: A GRanges object containing the corresponding RNA-Seq data for each entry of the methyl_region list. The GRanges object has three additional metadata columns which are explained in [read_rna_encode_caltech](#)
- upstream: Integer defining the length of bp upstream of TSS.
- downstream: Integer defining the length of bp downstream of TSS.
- cpq_density: Integer defining the minimum number of CpGs that have to be in a methylated region. Regions with less than n CpGs are discarded.
- sd_thresh: Numeric defining the minimum standard deviation of the methylation change in a region. This is used to filter regions with no methylation change.
- fmin: Minimum range value for region location scaling.
- fmax: Maximum range value for region location scaling.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

Examples

```
# Obtain the path to the files
rrbs_file <- system.file("extdata", "rrbs.bed", package = "BPRMeth")
rnaseq_file <- system.file("extdata", "rnaseq.bed", package = "BPRMeth")
proc_data <- process_haib_caltech_wrap(rrbs_file, rnaseq_file)
```

| | |
|-----------|-----------------------------|
| read_anno | <i>Read annotation file</i> |
|-----------|-----------------------------|

Description

read_anno reads a file containing annotation data, which will be used to select genomic regions of interest for downstream analysis. The annotation file format is the following: "chromosome", "start", "end", "strand", "id", "name" (optional). Read the Important section below for more details.

Usage

```
read_anno(
  file,
  chrom_size_file = NULL,
  chr_discarded = NULL,
  is_centre = FALSE,
  is_window = TRUE,
  upstream = -5000,
  downstream = 5000,
  is_anno_region = TRUE,
  delimiter = "\t"
)
```

Arguments

| | |
|-----------------|--|
| file | File name. |
| chrom_size_file | Optional file name to read genome chromosome sizes. |
| chr_discarded | Optional vector with chromosomes to be discarded. |
| is_centre | Logical, whether 'start' and 'end' locations are pre-centred. If TRUE, the mean of the locations will be chosen as centre. If FALSE, the 'start' will be chosen as the center; e.g. for genes the 'start' denotes the TSS and we use this as centre to obtain K-bp upstream and downstream of TSS. |
| is_window | Whether to consider a predefined window region around centre. If TRUE, then 'upstream' and 'downstream' parameters are used, otherwise we consider the whole region from start to end location. |
| upstream | Integer defining the length of bp upstream of 'centre' for creating the genomic region. If is_window = FALSE, this parameter is ignored. |
| downstream | Integer defining the length of bp downstream of 'centre' for creating the genomic region. If is_window = FALSE, this parameter is ignored. |
| is_anno_region | Logical, whether or not to create genomic region. It should be set to TRUE, if you want to use the object as input to create_region_object function. |
| delimiter | Delimiter format the columns are splitted. Default is tab. |

Value

A GRanges object.

The GRanges object contains two or three additional metadata columns:

- id: Feature ID, e.g. Ensembl IDs for each gene.
- centre: The central (middle) location of the genomic region. This is required when transforming 'methylation regions' in the (-1, 1) interval, the 'centre' would be at 0.
- name (Optional) the feature name.

These columns can be accessed as follows: `granges_obj$id`

Important

- When having strand information, and we are in the antisense strand ("-"), the 'start' is automatically switched with the 'end' location.
- By default columns are considered in tab delimited format.
- The "name" feature is optional.
- When there is no "strand" info, this can be set to "*".

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[read_met](#), [create_anno_region](#), [create_region_object](#)

Examples

```
# Obtain the path to files
file <- system.file("extdata", "dummy_anno.bed", package = "BPRMeth")
anno_dt <- read_anno(file, chr_discarded = c("X"))

# Extract feature id
anno_ids <- anno_dt$id
```

`read_bs_encode_haib` (DEPRECATED) Read ENCODE HAIB bed formatted BS-Seq file

Description

(DEPRECATED) `read_bs_encode_haib` reads a file containing methylation data from BS-Seq experiments using the [scan](#) function. The BS-Seq file should be in ENCODE HAIB bed format. Read the Important section below on when to use this function.

Usage

```
read_bs_encode_haib(file, chr_discarded = NULL, is_GRanges = TRUE)
```

Arguments

| | |
|---------------|---|
| file | The name of the file to read data values from. |
| chr_discarded | A vector with chromosome names to be discarded. |
| is_GRanges | Logical: if TRUE a GRanges object is returned, otherwise a data.frame object is returned. |

Value

A GRanges object if is_GRanges is TRUE, otherwise a data.table object.

The GRanges object contains two additional metadata columns:

- total_reads: total reads mapped to each genomic location.
- meth_reads: methylated reads mapped to each genomic location.

These columns can be accessed as follows: `granges_object$total_reads`

Important

Unless you want to create a different workflow when processing the BS-Seq data, you should NOT call this function, since this is a helper function. Instead you should call the [preprocess_bs_seq](#) function.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[pool_bs_seq_rep](#), [preprocess_bs_seq](#)

Examples

```
# Obtain the path to the file and then read it
bs_file <- system.file("extdata", "rrbs.bed", package = "BPRMeth")
bs_data <- read_bs_encode_haib(bs_file)
```

| | |
|-----------------|--|
| read_chrom_size | <i>Read genome chromosome sizes file</i> |
|-----------------|--|

Description

read_chrom_size reads a file containing genome chromosome sizes using the [fread](#) function.

Usage

```
read_chrom_size(file, delimiter = "\t")
```

Arguments

| | |
|-----------|--|
| file | File name |
| delimiter | Delimiter format the columns are splitted. Default is tab. |

Value

A [data.table](#) object.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[read_met](#), [read_anno](#)

Examples

```
chr_file <- system.file("extdata", "hg19.chr.sizes", package = "BPRMeth")
chr_data <- read_chrom_size(chr_file)

# Extract the size of chr1
chr_data[1]
```

| | |
|-----------|----------------------------------|
| read_expr | <i>Read expression data file</i> |
|-----------|----------------------------------|

Description

read_expr reads a file containing expression data. It should contain two columns: "id", "expr" and by default columns are considered in tab delimited format.

Usage

```
read_expr(file, log2_transf = FALSE, delimiter = "\t")
```

Arguments

| | |
|-------------|--|
| file | File name |
| log2_transf | Logical, whether to log2 transform the expression data. |
| delimiter | Delimiter format the columns are splitted. Default is tab. |

Value

A [data.table](#) object.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[read_met](#), [read_anno](#)

Examples

```
# Obtain the path to files
file <- system.file("extdata", "dummy_expr.bed", package = "BPRMeth")
expr_dt <- read_expr(file)

# Extract feature id
expr_ids <- expr_dt$id
```

| | |
|----------|------------------------------|
| read_met | <i>Read methylation file</i> |
|----------|------------------------------|

Description

read_met reads a file containing methylation data using the fread function. Since there are different technologies, e.g. array, bulk BS-Seq, scBS-Seq, and still there is no standard file format, different options are available, check the Important section below on the file format for each type you choose. If a file format is not available, you need to read the file and create a GRanges object, where the data are ordered by chromosome and genomic location.

Usage

```
read_met(
  file,
  type = "sc_seq",
  strand_info = FALSE,
  chr_discarded = NULL,
  min_bulk_cov = 4,
  max_bulk_cov = 1000,
  delimiter = "\t"
)
```

Arguments

| | |
|---------------|---|
| file | File name. |
| type | Type of technology as character. Either "bulk_seq", "sc_seq" or "array". Check the Important section below for more details. |
| strand_info | Logical, whether or not the file contains strand information. |
| chr_discarded | Optional vector with chromosomes to be discarded. |
| min_bulk_cov | Minimum number of reads mapping to each CpG site. Used only for "bulk_seq" and CpGs with less reads will be discarded as noise. |
| max_bulk_cov | Maximum number of reads mapping to each CpG site. Used only for "bulk_seq" and CpGs with less reads will be discarded as noise. |
| delimiter | Delimiter format the columns are splitted. Default is tab. |

Value

A GRanges object.

The GRanges object contains one or two additional metadata columns:

- met: Methylation level.
 - For "array" this is the Beta or M-values
 - For "sc_seq" this is either 0 or 1 (unmethylated or methylated)
 - For "bulk_seq" this contains the number of methylated reads for each CpG.

- total: Total number of reads for each CpG. Present only for "bulk_seq" type.

These columns can be accessed as follows: `granges_obj$met`

Important

Depending on technology type we assume different file formats.

- "array" File format: "chromosome", "start", "strand" (optional), "met" .
- "sc_seq" File format: "chromosome", "start", "strand" (optional), "met" . Where "met" should contain only 1s or 0s.
- "bulk_seq" File format: "chromosome", "start", "strand" (optional), "met", "total".

By default columns are considered in tab delimited format.

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[read_anno](#), [read_expr](#), [create_region_object](#)

Examples

```
# Obtain the path to files
file <- system.file("extdata", "dummy_met.bed", package = "BPRMeth")
met_dt <- read_met(file)

# Extract methylation level
met <- met_dt$met
```

`read_rna_encode_caltech`

(DEPRECATED) Read ENCODE Caltech bed formatted RNA-Seq file

Description

(DEPRECATED) `read_rna_encode_caltech` reads a file containing promoter annotation data together with gene expression levels from RNA-Seq experiments using the [scan](#) function. The RNA-Seq file should be in ENCODE Caltech bed format, e.g. use `gtf2bed` tool if your initial file is in `gtf` format.

Usage

```
read_rna_encode_caltech(file, chr_discarded = NULL, is_GRanges = TRUE)
```

Arguments

| | |
|----------------------------|---|
| <code>file</code> | The name of the file to read data values from. |
| <code>chr_discarded</code> | A vector with chromosome names to be discarded. |
| <code>is_GRanges</code> | Logical: if TRUE a GRanges object is returned, otherwise a data.frame object is returned. |

Value

A GRanges object if `is_GRanges` is TRUE, otherwise a `data.table` object.

The GRanges object contains three additional metadata columns:

- `ensembl_id`: Ensembl IDs of each gene promoter.
- `gene_name`: Gene name.
- `gene_fpkm`: Expression level in FPKM.

These columns can be accessed as follows: `granges_object$ensembl_id`

Author(s)

C.A.Kapourani <C.A.Kapourani@ed.ac.uk>

See Also

[read_chrom_size](#), [read_bs_encode_haib](#)

Examples

```
# Obtain the path to the file and then read it
rnaseq_file <- system.file("extdata", "rnaseq.bed", package = "BPRMeth")
rna_data <- read_rna_encode_caltech(rnaseq_file)
```

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