

Package ‘MethScope’

June 16, 2026

Title Ultra-Fast Analysis of Sparse DNA Methylome via Recurrent
Pattern Encoding

Version 1.0.3

Description Methods for analyzing DNA methylation data via Most Recurrent Methylation Patterns (MRMPs). Supports cell-type annotation, spatial deconvolution, unsupervised clustering, and cancer cell-of-origin inference. Includes C-backed summaries for YAME “.cg/.cm” files (overlap counts, log2 odds ratios, beta/depth aggregation), an XGBoost classifier, NNLS deconvolution, and plotting utilities. Scales to large spatial and single-cell methylomes and is robust to extreme sparsity.

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.3.2

Imports xgboost, dplyr, utils, tidyr, stringr, caret, doParallel,
parallel, ggplot2, uwot, magrittr, FNN, data.table, nnls

Suggests knitr, rmarkdown, spelling, testthat

VignetteBuilder knitr

Depends R (>= 4.0)

SystemRequirements zlib

NeedsCompilation yes

Maintainer Hongxiang Fu <fhx@seas.upenn.edu>

Language en-US

Author Hongxiang Fu [aut, cre] (ORCID:
<<https://orcid.org/0000-0002-9873-8606>>),
Wanding Zhou [cph, fnd],
The SAMtools/HTSlib authors [ctb, cph] (BGZF components; see
inst/COPYRIGHTS),
Attractive Chaos [ctb, cph] (Author and copyright holder of khash.h
(klib, MIT license))

Repository CRAN

Date/Publication 2026-06-16 07:00:16 UTC

Contents

confidence_score	2
confidence_score_top95	3
filter_cell	3
GenerateInput	4
GenerateReference	4
imputeRowMean	5
Input_training	5
Liu2021_MouseBrain_P1000	6
nnls_deconv	7
PlotConfusion	7
PlotF1	8
PlotUMAP	8
PlotUMAP_fixedwindow	9
PredictCellType	9
smooth_matrix	10
Zhou2025_HumanAtlas_P1000	11
Index	12

confidence_score	<i>Produce confidence score for XGBoost prediction</i>
------------------	--

Description

Produce confidence score for XGBoost prediction

Usage

confidence_score(vec)

Arguments

vec A vector of predicted probability for each cell type

Value

A numeric confidence score from 0 to 1.

confidence_score_top95	<i>Produce confidence score based on top 95 percent for XGBoost prediction</i>
------------------------	--

Description

Produce confidence score based on top 95 percent for XGBoost prediction

Usage

```
confidence_score_top95(vec)
```

Arguments

vec A vector of predicted probability for each cell type

Value

A numeric confidence score from 0 to 1.

filter_cell	<i>Filter final prediction to reduce noise</i>
-------------	--

Description

Filter final prediction to reduce noise

Usage

```
filter_cell(pred_result, knn_res, KNeighbor = 5)
```

Arguments

pred_result The prediction result from XGBoost
knn_res knn graph from smooth_matrix
KNeighbor Number of knn neighbors to use for smoothing (Default: 5)

Value

The final prediction result after dropping few cell types

GenerateInput	<i>Generate pattern level data for cell type annotation</i>
---------------	---

Description

Generate pattern level data for cell type annotation

Usage

```
GenerateInput(query_fn, knowledge_fn)
```

Arguments

query_fn	File path to query .cg
knowledge_fn	File path to pattern file .cm

Value

A cell by pattern matrix.

Examples

```
qry <- system.file("extdata", "toy.cg", package = "MethScope")
msk <- system.file("extdata", "toy.cm", package = "MethScope")
res <- GenerateInput(qry, msk)
```

GenerateReference	<i>Generate reference pattern labels (no default writing)</i>
-------------------	---

Description

Generate reference pattern labels (no default writing)

Usage

```
GenerateReference(binary_file, min_CG = 50, output_path = NULL)
```

Arguments

binary_file	Path to the pattern strings file (one string per line).
min_CG	Minimum CpG count a pattern must have to keep its own ID (default: 50). Patterns with frequency <= 'min_CG' are grouped as "Pna".
output_path	Optional file path to write the resulting labels. If 'NULL' (default), nothing is written and the labels are only returned.

Value

A character vector of pattern labels (same length/order as the input file).

Examples

```
## Not run:
# DO write only to a temp location in examples/vignettes/tests:
tmp_out <- file.path(tempdir(), "patterns.txt")
labs <- GenerateReference("path/to/pattern_strings.txt", min_CG = 50, output_path = tmp_out)
# Or skip writing and just get the vector:
labs <- GenerateReference("path/to/pattern_strings.txt", min_CG = 50)

## End(Not run)
```

imputeRowMean	<i>Impute missing value for 100K window matrix</i>
---------------	--

Description

Impute missing value for 100K window matrix

Usage

```
imputeRowMean(mtx, na_percent = 30)
```

Arguments

- mtx A cell by 100K window data frame with missing values
- na_percent A na percent threshold to be filterd (Default: 30)

Value

A cell by 100K window data frame with imputed values

Input_training	<i>Train XGBoost model to predict cell type</i>
----------------	---

Description

Train XGBoost model to predict cell type

Usage

```
Input_training(
  summary_results,
  cell_type_label,
  number_patterns = 1000,
  cross_validation = FALSE,
  xgb_parameters = list()
)
```

Arguments

`summary_results` a wide cell by pattern matrix generated from `GenerateInput` function

`cell_type_label` a vector of the corresponding cell type label for each row of the summary results

`number_patterns` a numeric value to indicate number of patterns to be used (Default: 1000)

`cross_validation` a boolean variable whether to perform `cross_validation` to obtain the best hyper parameters for the model

`xgb_parameters` an optional list for xgb model parameters provided by the user

Value

A `MethScopeModel` object containing the trained XGBoost booster and metadata.

Liu2021_MouseBrain_P1000

Load the Liu et al. mouse brain pretrained model

Description

Load the Liu et al. mouse brain pretrained model

Usage

```
Liu2021_MouseBrain_P1000()
```

Value

A `MethScopeModel` object for use with [PredictCellType](#).

nnls_deconv	<i>Estimate cell type relative proportion</i>
-------------	---

Description

Estimate cell type relative proportion

Usage

```
nnls_deconv(ref, mixture_matrix, number_patterns = 1000, var_threshold = 0.01)
```

Arguments

ref	An imputed wide cell by pattern matrix generated from GenerateInput function using reference Pseudobulk
mixture_matrix	An imputed wide cell by pattern matrix generated from GenerateInput function
number_patterns	a numeric value to indicate number of patterns to be used (Default: 1000)
var_threshold	a numeric value to indicate variance that should filter the patterns (Default: 0.1)

Value

A cell type by cell matrix showing the relative cell type proportion estimate for each cells

PlotConfusion	<i>Generate confusion table for the final prediction</i>
---------------	--

Description

Generate confusion table for the final prediction

Usage

```
PlotConfusion(prediction_result, actual_label, log2 = FALSE)
```

Arguments

prediction_result	Prediction result from PredictCellType
actual_label	Ground truth cell label
log2	Log scale count (Default: False)

Value

A ggplot2 confusion table object.

PlotF1	<i>Generate F1 score barplot for each class</i>
--------	---

Description

Generate F1 score barplot for each class

Usage

```
PlotF1(prediction_result, actual_label)
```

Arguments

prediction_result	Prediction result from PredictCellType
actual_label	Ground truth cell label

Value

A ggplot2 object.

PlotUMAP	<i>Generate UMAP for the final prediction based on cell patterns</i>
----------	--

Description

Generate UMAP for the final prediction based on cell patterns

Usage

```
PlotUMAP(predictMatrix, prediction_result, n_component = 30, seed = 123, ...)
```

Arguments

predictMatrix	a wide cell by pattern matrix generated from GenerateInput function
prediction_result	Prediction result from PredictCellType
n_component	Number of PCA components to use (Default: 30)
seed	A number for random seed (Default: 123)
...	Additional arguments passed to 'uwot::umap' (e.g., 'n_neighbors', 'metric').

Value

A list of two ggplot2 UMAP object.

PlotUMAP_fixedwindow	<i>Generate UMAP for the final prediction based on fixed window eg.100kb bin widows</i>
----------------------	---

Description

Generate UMAP for the final prediction based on fixed window eg.100kb bin widows

Usage

```
PlotUMAP_fixedwindow(
  query_fn,
  knowledge_fn,
  prediction_result,
  n_component = 30,
  seed = 123,
  ...
)
```

Arguments

query_fn	File path to query .cg
knowledge_fn	File path to 100bk bins window or reference pattern
prediction_result	Prediction result from PredictCellType
n_component	Number of PCA components to use (Default: 30)
seed	A number for random seed (Default: 123)
...	Additional arguments passed to 'uwot::umap' (e.g., 'n_neighbors', 'metric').

Value

A list of two ggplot2 UMAP object.

PredictCellType	<i>Predict cell type annotation from the trained model</i>
-----------------	--

Description

Predict cell type annotation from the trained model

Usage

```
PredictCellType(bst_model, predictMatrix, smooth = FALSE, KNeighbor = 5)
```

Arguments

bst_model	The boosting model trained from ModelTrain
predictMatrix	A wide cell by pattern matrix generated from GenerateInput function
smooth	A Boolean variable to indicate whether smooth the matrix (Default: FALSE)
KNeighbor	number of knn neighbors to use for smoothing (Default: 5)

Value

A cell by cell type matrix with confidence score and labeled cell type.

Examples

```
qry <- system.file("extdata", "toy.cg", package = "MethScope")
msk <- system.file("extdata", "toy.cm", package = "MethScope")
res <- GenerateInput(qry, msk)
## Not run:
model <- Liu2021_MouseBrain_P1000()
prediction <- PredictCellType(model, res)

## End(Not run)
```

smooth_matrix

Smooth cell by pattern matrix to reduce noise

Description

Smooth cell by pattern matrix to reduce noise

Usage

```
smooth_matrix(predictMatrix, KNeighbor = 5)
```

Arguments

predictMatrix	A wide cell by pattern matrix generated from GenerateInput function
KNeighbor	Number of knn neighbors to use for smoothing (Default: 5)

Value

A wide cell by pattern matrix after smoothing and knn graph

`Zhou2025_HumanAtlas_P1000`*Load the Zhou et al. human atlas pretrained model*

Description

Load the Zhou et al. human atlas pretrained model

Usage

```
Zhou2025_HumanAtlas_P1000()
```

Value

A MethScopeModel object for use with [PredictCellType](#).

Index

confidence_score, [2](#)
confidence_score_top95, [3](#)

filter_cell, [3](#)

GenerateInput, [4](#)
GenerateReference, [4](#)

imputeRowMean, [5](#)
Input_training, [5](#)

Liu2021_MouseBrain_P1000, [6](#)

nnls_deconv, [7](#)

PlotConfusion, [7](#)
PlotF1, [8](#)
PlotUMAP, [8](#)
PlotUMAP_fixedwindow, [9](#)
PredictCellType, [6](#), [9](#), [11](#)

smooth_matrix, [10](#)

Zhou2025_HumanAtlas_P1000, [11](#)