

Package ‘blase’

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Title Bulk Linking Analysis for Single-cell Experiments

Version 1.1.0

Description BLASE is a method for finding where bulk RNA-seq data lies on a single-cell pseudotime trajectory. It uses a fast and understandable approach based on Spearman correlation, with bootstrapping to provide confidence. BLASE can be used to ``date" bulk RNA-seq data, annotate cell types in scRNA-seq, and help correct for developmental phenotype differences in bulk RNA-seq experiments.

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Contents

annotate_sce	3
as.BlaseData	4
assign_pseudotime_bins	5
best_bin	7
best_correlation	9
bins	10
bins<-	11
BlaseData-class	12
bootstrap_iterations	12
bulk_name	14
calculate_gene_peakedness	15
confident_mapping	17
evaluate_parameters	18
evaluate_top_n_genes	20
find_best_params	21
genes	23
genes<-	24
gene_peakedness_spread_selection	24
get_bins_as_bulk	26
get_top_n_genes	27
MappingResult	28
mapping_history	30
map_all_best_bins	31
map_best_bin	33
MCA_PF_SCE	35
painter_microarray	36
plot_bin_population	36
plot_find_best_params_results	38
plot_gene_peakedness	39
plot_mapping_result	41
plot_mapping_result_corr	42

<code>annotate_sce</code>	3
---------------------------	---

<code>plot_mapping_result_heatmap</code>	43
<code>PRIVATE_ci</code>	45
<code>PRIVATE_spearman.ci</code>	46
<code>pseudobulk_bins</code>	47
<code>pseudobulk_bins<-</code>	47
<code>show,BlaseData-method</code>	48
<code>show,MappingResult-method</code>	49
<code>smooth_gene</code>	50
<code>top_2_distance</code>	52
<code>tradeSeq_BLASE_example_sce</code>	53
<code>zhang_2021_heat_shock_bulk</code>	54

Index	55
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<code>annotate_sce</code>	<i>Annotate a SCE with BLASE Mappings</i>
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Description

Annotates an SCE with the names of bulk samples that best match each pseudotime bin. For each pseudotime bin, we find the highest correlation with a bulk sample that was mapped against it. Because of this approach, a bulk which mapped best to another pseudotime bin may be the best correlation with the current pseudotime bin of interest.

Usage

```
annotate_sce(  
  sce,  
  blase_results,  
  annotation_col = "BLASE_Annotation",  
  include_stats = FALSE  
)
```

Arguments

- | | |
|-----------------------------|--|
| <code>sce</code> | The SingleCellExperiment::SingleCellExperiment to annotate. |
| <code>blase_results</code> | A list of MappingResult to use for the annotation. |
| <code>annotation_col</code> | String. The name of the metadata column in which to store the new annotations. |
| <code>include_stats</code> | Boolean. Whether or not to include metadata columns containing the correlation of the best matching bin, and whether that mapping was confident. |

Value

A [SingleCellExperiment::SingleCellExperiment](#) with annotations added to metadata (in a column defined by `annotation_col`), and the correlations in `BLASE_Annotation_Correlation` if `include_stats` is enabled.

Examples

```
counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blast_data <- as.BlastData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blast_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map all bulks to bin
results <- map_all_best_bins(blast_data, bulk_counts)

sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)

# Annotate SC from existing bulk
sce <- annotate_sce(sce, results)
table(sce$BLASE_Annotation)
```

as.BlastData

Conversion to BlastData

Description

Conversion to BlastData

Usage

```
as.BlastData(x, ...)

## S4 method for signature 'SingleCellExperiment'
as.BlastData(
  x,
  pseudotime_slot = "slingPseudotime_1",
  n_bins = 20,
  split_by = "pseudotime_range"
)
```

Arguments

<code>x</code>	An object to take counts from
<code>...</code>	additional arguments passed to object-specific methods.
<code>pseudotime_slot</code>	The <code>SingleCellExperiment::SingleCellExperiment</code> slot containing pseudotime values for each cell to be passed to <code>assign_pseudotime_bins()</code> .
<code>n_bins</code>	Integer. The number of bins to create, passed to <code>assign_pseudotime_bins()</code> .
<code>split_by</code>	String. The <code>split_by</code> method to be passed on to <code>assign_pseudotime_bins()</code> . Must be one of <code>pseudotime_range</code> or <code>cells</code> .

Value

An `BlaseData` object

Examples

```
counts <- matrix(rpois(100, lambda = 10), ncol = 10, nrow = 10)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(normcounts = counts)
)
sce$pseudotime <- seq_len(10) - 1
data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 3)
genes(data) <- as.character(seq_len(10))

genes(data)
```

assign_pseudotime_bins

Assign Pseudotime Bins to a source object's metadata

Description

Assign Pseudotime Bins to a source object's metadata

Usage

```
assign_pseudotime_bins(
  x,
  split_by = "pseudotime_range",
  n_bins = 20,
  pseudotime_slot = "slingPseudotime_1",
  ...
)

## S4 method for signature 'SingleCellExperiment'
assign_pseudotime_bins(
```

```

    x,
    split_by,
    n_bins,
    pseudotime_slot = "slingPseudotime_1"
  )

## S4 method for signature 'data.frame'
assign_pseudotime_bins(
  x,
  split_by,
  n_bins,
  pseudotime_slot = "slingPseudotime_1"
)

## S4 method for signature 'Seurat'
assign_pseudotime_bins(
  x,
  split_by,
  n_bins,
  pseudotime_slot = "slingPseudotime_1"
)

```

Arguments

<code>x</code>	An object to add metadata to.
<code>split_by</code>	String. The technique used to split the bins. The default <code>pseudotime_range</code> picks the bin for a cell based on a constant range of pseudotime. <code>cells</code> picks the bin for a cell based on an even number of cells per bin.
<code>n_bins</code>	Integer. The number of bins to split the cells into.
<code>pseudotime_slot</code>	String. The name of the SingleCellExperiment::SingleCellExperiment slot containing the pseudotime values for each cell.
<code>...</code>	For arguments passed to other functions. Unused.

Value

A copy of `x` where cells are annotated with their pseudotime bin.

Examples

```

counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))

```

```

sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BladeData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

best_bin

Get best bin of a BLASE Mapping Results object.

Description

Get best bin of a BLASE Mapping Results object.

Usage

```
best_bin(x)
```

```
## S4 method for signature 'MappingResult'
best_bin(x)
```

Arguments

x a [MappingResult](#) object

Value

Integer. The best bin ID of this mapping

Examples

```
counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")
```

```
# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
```

best_correlation	<i>Get best correlation of a BLASE Mapping Results object.</i>
------------------	--

Description

Get best correlation of a BLASE Mapping Results object.

Usage

```
best_correlation(x)

## S4 method for signature 'MappingResult'
best_correlation(x)
```

Arguments

x a [MappingResult](#) object

Value

Decimal. The highest correlation value of this mapping

Examples

```
counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
```

```

rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

bins

Get bins of a BLASE Data object.

Description

Get bins of a BLASE Data object.

Usage

```

bins(x)

## S4 method for signature 'BlaseData'
bins(x)

```

Arguments

x a [BlaseData](#) object

`bins<-`

11

Value

vector of integers. The bin names in the BLASE Data object.

Examples

```
counts <- matrix(rpois(100, lambda = 10), ncol = 10, nrow = 10)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(normcounts = counts)
)
sce$pseudotime <- seq_len(10) - 1
data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 3)
genes(data) <- as.character(seq_len(10))

genes(data)
```

<code>bins<-</code>	<i>Set genes of a BLASE Data object.</i>
------------------------	--

Description

Set genes of a BLASE Data object.

Usage

```
bins(x) <- value

## S4 replacement method for signature 'BlaseData'
bins(x) <- value
```

Arguments

<code>x</code>	a BlaseData object
<code>value</code>	Vector of integers The new value for bins slot

Value

Nothing

BlaseData-class	<i>Blase Data Object</i>
-----------------	--------------------------

Description

For creation details, see [as.BlaseData\(\)](#)

Value

A [BlaseData](#) object

Slots

pseudobulk_bins list of [data.frames](#). Each item is a normalised count matrix representing a bin, where a column is a cell in the bin and each row is a gene.

bins list. A list of bin names for each timepoint.

genes list. A list of the genes selected for discriminating timepoints.

Examples

```
counts <- matrix(rpois(100, lambda = 10), ncol = 10, nrow = 10)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(normcounts = counts)
)
sce$pseudotime <- seq_len(10) - 1
data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 3)
genes(data) <- as.character(seq_len(10))

genes(data)
```

bootstrap_iterations	<i>Get the number of bootstrap iterations performed for a BLASE Mapping Results object.</i>
----------------------	---

Description

Get the number of bootstrap iterations performed for a BLASE Mapping Results object.

Usage

```
bootstrap_iterations(x)

## S4 method for signature 'MappingResult'
bootstrap_iterations(x)
```

Arguments

x a [MappingResult](#) object

Value

Integer. The number of iterations performed for this mapping.

Examples

```
counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
```

```

top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

bulk_name	<i>Get name of bulk of a BLASE Mapping Results object.</i>
-----------	--

Description

Get name of bulk of a BLASE Mapping Results object.

Usage

```

bulk_name(x)

## S4 method for signature 'MappingResult'
bulk_name(x)

```

Arguments

x a [MappingResult](#) object

Value

String. The name of the bulk used to map against.

Examples

```

counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)

```

```

result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

```

calculate_gene_peakedness
      calculate_gene_peakedness

```

Description

Calculate the peakedness of a gene. The power is the ratio of the mean of reads 5% either side of the smoothed peak of the gene's expression over pseudotime against the mean of the reads outside of this.

This function can take some time to complete, please be patient.

Usage

```

calculate_gene_peakedness(
  sce,
  window_pct = 10,
  pseudotime_slot = "slingPseudotime_1",
  knots = 10,
  BPPARAM = BiocParallel::SerialParam()
)

```

Arguments

sce	SingleCellExperiment::SingleCellExperiment to do the calculations on.
window_pct	Decimal between 0-100. The size of the window to consider, as a percentage of the maximum pseudotime value.
pseudotime_slot	String. The name of the metadata column in the SCE object containing pseudotime
knots	Integer. The number of knots to use when fitting the GAM
BPPARAM	The BiocParallel::BiocParallelParam for parallelisation. Defaults to BiocParallel::SerialParam .

Value

Dataframe, where each row is a gene, and the following columns: mean_expression_in_window (decimal), mean_expression_out_window (decimal), ratio (decimal)

Examples

```
ncells <- 70
ngenes <- 100
# Each gene should have mean around its gene number
counts <- c()
for (i in seq_len(ngenes)) {
  counts <- c(counts, dnorm(seq_len(ncells), mean = (ncells / i), sd = 1))
}

counts_matrix <- matrix(
  counts,
  ncol = ncells,
  nrow = ngenes
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  counts = counts_matrix * 3,
  normcounts = counts_matrix,
  logcounts = log(counts_matrix)
))
colnames(sce) <- paste0("cell", seq_len(ncells))
rownames(sce) <- paste0("gene", seq_len(ngenes))
sce$cell_type <- c(
  rep("celltype_1", ncells / 2),
  rep("celltype_2", ncells / 2)
)

sce$pseudotime <- seq_len(ncells) - 1
genelist <- rownames(sce)

# calculate_gene_peakedness
gene_peakedness <- calculate_gene_peakedness(
  sce,
  pseudotime_slot = "pseudotime"
```

```

)

head(gene_peakedness)

# plot_gene_peakedness
plot_gene_peakedness(sce, gene_peakedness, "gene20",
  pseudotime_slot = "pseudotime"
)

# smooth_gene
smoothed_gene20 <- smooth_gene(
  sce, "gene20",
  pseudotime_slot = "pseudotime"
)
head(smoothed_gene20)

# Select best spread of genes
genes_to_use <- gene_peakedness_spread_selection(sce, gene_peakedness,
  genes_per_bin = 2, n_gene_bins = 1, pseudotime_slot = "pseudotime"
)

print(genes_to_use)
plot(
  x = gene_peakedness[
    gene_peakedness$gene %in% genes_to_use, "peak_pseudotime"
  ],
  y = gene_peakedness[gene_peakedness$gene %in% genes_to_use, "ratio"]
)

```

confident_mapping

Get if the result is confident for a BLASE Mapping Results object.

Description

Get if the result is confident for a BLASE Mapping Results object.

Usage

```

confident_mapping(x)

## S4 method for signature 'MappingResult'
confident_mapping(x)

```

Arguments

x a [MappingResult](#) object

Value

Boolean. TRUE if the result is confident, otherwise FALSE

Examples

```

counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

Description

Will use the `n_bins` and `n_genes` implied by the `sce` and `pseudotime_bins_top_n_genes_df` parameters and return quality metrics and an optional chart.

Usage

```
evaluate_parameters(
  blase_data,
  bootstrap_iterations = 200,
  BPPARAM = BiocParallel::SerialParam(),
  make_plot = FALSE,
  plot_columns = 4
)
```

Arguments

<code>blase_data</code>	The BlaseData object to use.
<code>bootstrap_iterations</code>	Integer. Iterations for bootstrapping when calculating confident mappings.
<code>BPPARAM</code>	The BiocParallel::BiocParallelParam configuration. Defaults to BiocParallel::SerialParam
<code>make_plot</code>	Boolean. Whether or not to render the plot showing the correlations for each pseudobulk bin when we try to map the given bin.
<code>plot_columns</code>	Integer. How many columns to use in the plot.

Value

A vector of length 3:

- "worst top 2 distance" decimal containing the lowest difference between the absolute values of the top 2 most correlated bins for each bin. Higher is better for differentiating.
- "mean top 2 distance" decimal containing the mean top 2 distance across the entire set of genes and bins. Higher is better for differentiation, but it should matter less than the worst value.
- "confident_mapping_pct" decimal from 0-1. The percent of mappings for this setup which were annotated as confident by BLASE.

Examples

```
ncells <- 70
ngenes <- 100
counts_matrix <- matrix(
  c(seq_len(3500) / 10, seq_len(3500) / 5),
  ncol = ncells,
  nrow = ngenes
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(ncells)
```

```

rownames(sce) <- as.character(seq_len(ngenes))
sce$cell_type <- c(
  rep("celltype_1", ncells / 2),
  rep("celltype_2", ncells / 2)
)

sce$pseudotime <- seq_len(ncells) - 1
genelist <- as.character(seq_len(ngenes))

# Evaluating created BlaseData
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 10)
genes(blase_data) <- genelist[1:20]

# Check convexity of parameters
evaluate_parameters(blase_data, make_plot = TRUE)

```

evaluate_top_n_genes *Evaluate Top Genes*

Description

Shows plots over bins of expression of the top n genes. This is designed to help identify if you have selected genes that vary over the pseudotime you have chosen bins to exist over. Uses the normcounts of the SCE.

Usage

```
evaluate_top_n_genes(blase_data, n_genes_to_plot = 16, plot_columns = 4)
```

Arguments

blase_data	The BlaseData to get bins and expression from.
n_genes_to_plot	Integer. The number of genes to plot.
plot_columns	Integer. The number of columns to plot the grid with. Best as a divisor of n_genes_to_plot.

Value

A [ggplot2::ggplot2](#) plot showing the normalised expression of the top genes over pseudotime bins.

Examples

```

ncells <- 70
ngenes <- 100
counts_matrix <- matrix(
  c(seq_len(3500) / 10, seq_len(3500) / 5),
  ncol = ncells,
  nrow = ngenes
)

```

```

)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- paste0("cell", seq_len(ncells))
rownames(sce) <- paste0("gene", seq_len(ngenes))
sce$cell_type <- c(
  rep("celltype_1", ncells / 2),
  rep("celltype_2", ncells / 2)
)

sce$pseudotime <- seq_len(ncells) - 1
genelist <- rownames(sce)

# Evaluating created BlaseData
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 10)
genes(blase_data) <- genelist[1:20]

# Check gene expression over pseudotime
evaluate_top_n_genes(blase_data)

```

find_best_params

Identify the Best Parameters For Your Dataset

Description

Identify the Best Parameters For Your Dataset

Usage

```

find_best_params(
  x,
  genelist,
  bins_count_range = c(5, 10, 20, 40),
  gene_count_range = c(10, 20, 40, 80),
  bootstrap_iterations = 200,
  BPPARAM = BiocParallel::SerialParam(),
  ...
)

```

Arguments

x	The object to create ‘BlaseData‘ from
genelist	Vector of strings. The list of genes to use (ordered by descending goodness)
bins_count_range	Integer vector. The n_bins list to try out
gene_count_range	Integer vector. The n_genes list to try out

bootstrap_iterations Integer. Iterations for bootstrapping when calculating confident mappings.

BPPARAM The [BiocParallel::BiocParallelParam](#). Defaults to [BiocParallel::SerialParam](#)

... params to be passed to child functions, see [as.BlaseData\(\)](#)

Value

A dataframe of the results.

- bin_count: Integer. The bin count for this attempt
- gene_count: Integer. The top n genes to use for this attempt
- min_convexity: Decimal. The worst convexity for these parameters
- mean_convexity: Decimal. The mean convexity for these parameters
- confident_mapping_pct: Decimal. The percent of bins which were confidently mapped to themselves for these parameters. If this value is low, then it is likely that in real use, few or no results will be confidently mapped.

See Also

[plot_find_best_params_results\(\)](#) for plotting the results of this function.

Examples

```
ncells <- 70
ngenes <- 100
counts_matrix <- matrix(
  c(seq_len(3500) / 10, seq_len(3500) / 5),
  ncol = ncells,
  nrow = ngenes
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- paste0("cell", seq_len(ncells))
rownames(sce) <- paste0("gene", seq_len(ngenes))
sce$cell_type <- c(
  rep("celltype_1", ncells / 2),
  rep("celltype_2", ncells / 2)
)

sce$pseudotime <- seq_len(ncells) - 1
genelist <- rownames(sce)

# Finding the best params for the BlaseData
best_params <- find_best_params(
  sce, genelist,
  bins_count_range = c(2, 3),
  gene_count_range = c(20, 50),
  pseudotime_slot = "pseudotime",
  split_by = "pseudotime_range"
```

```
)
best_params
plot_find_best_params_results(best_params)
```

genes

Get genes of a BLASE Data object.

Description

Get genes of a BLASE Data object.

Usage

```
genes(x)

## S4 method for signature 'BlaseData'
genes(x)
```

Arguments

x a [BlaseData](#) object

Value

The vector of genes a BLASE object will use for mappings.

Examples

```
counts <- matrix(rpois(100, lambda = 10), ncol = 10, nrow = 10)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(normcounts = counts)
)
sce$pseudotime <- seq_len(10) - 1
data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 3)
genes(data) <- as.character(seq_len(10))

genes(data)
```

```
genes<-
```

Set genes of a BLASE Data object.

Description

Set genes of a BLASE Data object.

Usage

```
genes(x) <- value
```

```
## S4 replacement method for signature 'BlaseData'
genes(x) <- value
```

Arguments

x a [BlaseData](#) object

value Vector of strings. The new value for genes slot

Value

Nothing

Examples

```
counts <- matrix(rpois(100, lambda = 10), ncol = 10, nrow = 10)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(normcounts = counts)
)
sce$pseudotime <- seq_len(10) - 1
data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 3)
genes(data) <- as.character(seq_len(10))

genes(data)
```

```
gene_peakedness_spread_selection
```

Gene Peakedness Spread Selection

Description

This function selects genes with peaks evenly distributed from a pseudotime trajectory. It does this by splitting pseudotime into evenly spread regions of pseudotime, and then selecting genes with the highest peakedness ratio with a peak inside that region of pseudotime. The number of regions and genes per region can be tuned.

Usage

```
gene_peakedness_spread_selection(
  sce,
  gene_peakedness_df,
  genes_per_bin = 10,
  n_gene_bins = 10,
  pseudotime_slot = "slingPseudotime_1"
)
```

Arguments

`sce` [SingleCellExperiment::SingleCellExperiment](#) to obtain pseudotime values from

`gene_peakedness_df` Gene peakedness DF generated by [calculate_gene_peakedness\(\)](#)

`genes_per_bin` Integer. Number of genes to select per gene bin.

`n_gene_bins` Integer. Number of gene bins to create over pseudotime. We recommend around 1-2x the number of pseudotime bins you want to use.

`pseudotime_slot` String. The name of the pseudotime column in the SCE metadata.

Value

A list of gene IDs with the highest ratios across regions of pseudotime.

Examples

```
ncells <- 70
ngenes <- 100
# Each gene should have mean around its gene number
counts <- c()
for (i in seq_len(ngenes)) {
  counts <- c(counts, dnorm(seq_len(ncells), mean = (ncells / i), sd = 1))
}

counts_matrix <- matrix(
  counts,
  ncol = ncells,
  nrow = ngenes
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  counts = counts_matrix * 3,
  normcounts = counts_matrix,
  logcounts = log(counts_matrix)
))
colnames(sce) <- paste0("cell", seq_len(ncells))
rownames(sce) <- paste0("gene", seq_len(ngenes))
sce$cell_type <- c(
  rep("celltype_1", ncells / 2),
  rep("celltype_2", ncells / 2)
)
```

```

sce$pseudotime <- seq_len(ncells) - 1
genelist <- rownames(sce)

# calculate_gene_peakedness
gene_peakedness <- calculate_gene_peakedness(
  sce,
  pseudotime_slot = "pseudotime"
)

head(gene_peakedness)

# plot_gene_peakedness
plot_gene_peakedness(sce, gene_peakedness, "gene20",
  pseudotime_slot = "pseudotime"
)

# smooth_gene
smoothed_gene20 <- smooth_gene(
  sce, "gene20",
  pseudotime_slot = "pseudotime"
)
head(smoothed_gene20)

# Select best spread of genes
genes_to_use <- gene_peakedness_spread_selection(sce, gene_peakedness,
  genes_per_bin = 2, n_gene_bins = 1, pseudotime_slot = "pseudotime"
)

print(genes_to_use)
plot(
  x = gene_peakedness[
    gene_peakedness$gene %in% genes_to_use, "peak_pseudotime"
  ],
  y = gene_peakedness[gene_peakedness$gene %in% genes_to_use, "ratio"]
)

```

get_bins_as_bulk

Get a pseudobulk of bins with at least 2 replicates

Description

This function will try to create a pseudobulked count matrix for the bins. When a replicate has too few cells, it is discounted. If only one exists, then we sample from it twice to create the pseudobulks.

Usage

```

get_bins_as_bulk(
  pseudotime_sce,

```

```

    min_cells_for_bulk = 50,
    replicate_slot = "replicate"
  )

```

Arguments

pseudotime_sce The [SingleCellExperiment::SingleCellExperiment](#) object to get the bins from

min_cells_for_bulk Integer. The minimum cells to look for per replicate and bin.

replicate_slot String. The name of the metadata column in the Single Cell Experiment that contains replicate information

Value

A dataframe containing the pseudobulked counts matrix.

Examples

```

library(SingleCellExperiment, quietly = TRUE)
library(blase)
counts <- matrix(rpois(1000, lambda = 10), ncol = 100, nrow = 10)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(normcounts = counts, counts = counts / 2)
)
sce$pseudotime <- seq_len(100) - 1
colnames(sce) <- seq_len(100)
rownames(sce) <- as.character(seq_len(10))
sce <- assign_pseudotime_bins(sce,
  n_bins = 5,
  pseudotime_slot = "pseudotime", split_by = "cells"
)
sce$replicate <- rep(c(1, 2), 50)
result <- get_bins_as_bulk(
  sce,
  min_cells_for_bulk = 1,
  replicate_slot = "replicate"
)
result

```

get_top_n_genes

Get Top Genes From An AssociationTestResult

Description

Pulls the genes with the highest wald statistic from an association test result, with a p value cutoff.

Usage

```
get_top_n_genes(
  association_test_results,
  n_genes = 40,
  lineage = NA,
  p_cutoff = 0.05
)
```

Arguments

<code>association_test_results</code>	Dataframe. The association test results data frame to take the genes from. Generated by tradeSeq::associationTest .
<code>n_genes</code>	Integer. The number of genes to return. Defaults to 40.
<code>lineage</code>	The Lineage to use. The Defaults to NA, which assumes the test was run with Lineages=False.
<code>p_cutoff</code>	Decimal. The maximum P value cutoff to use. Defaults to 0.05.

Value

A vector of strings. The names of the genes that best describe a lineage's trajectory.

Examples

```
assoRes <- data.frame(
  row.names = c("A", "B", "C", "D"),
  waldStat = c(25, 50, 100, 10),
  pvalue = c(0.01, 0.5, 0.005, 0.13)
)
get_top_n_genes(assoRes, n_genes = 2)
```

MappingResult

Blase Mapping Result

Description

Created by [map_best_bin\(\)](#)

Usage

```
MappingResult(
  bulk_name,
  best_bin,
  best_correlation,
  top_2_distance,
  confident_mapping,
  history,
  bootstrap_iterations
)
```

Arguments

bulk_name	String. The name of the bulk sample being mapped.
best_bin	Integer. The bin that best matched the bulk sample.
best_correlation	Decimal. The spearman's rho that the test geneset had between the winning bin and the bulk.
top_2_distance	Decimal. The absolute difference between the best and second best mapping buckets. Higher indicates a less doubtful mapping.
confident_mapping	Boolean. TRUE when the mapped bin's lower bound is higher than the maximum upper bound of the other bins.
history	A dataframe of the correlation score (decimal) and confidence bounds (decimal pairs) for each bin. Access with mapping_history()
bootstrap_iterations	Integer. The number of iterations used during the bootstrap.

Value

A MappingResult object

See Also

[map_best_bin\(\)](#)

Examples

```
counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result
```

```
# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
```

mapping_history*Get the mapping history for a BLASE Mapping Results object.*

Description

Get the mapping history for a BLASE Mapping Results object.

Usage

```
mapping_history(x)

## S4 method for signature 'MappingResult'
mapping_history(x)
```

Arguments

x a [MappingResult](#) object

Value

The mapping history of this mapping, in a data frame.

Examples

```

counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

Description

Map many bulk samples in the same dataframe

Usage

```
map_all_best_bins(
  blase_data,
  bulk_data,
  bootstrap_iterations = 200,
  confidence_level = 0.9,
  BPPARAM = BiocParallel::SerialParam()
)
```

Arguments

blase_data	The BlaseData holding the bins and pseudobulks.
bulk_data	Dataframe. The whole bulk read matrix as a dataframe. Each row should represent a gene, and each column a sample.
bootstrap_iterations	Integer. The number of bootstrapping iterations to run.
confidence_level	Decimal between 0-1. The confidence interval to calculate for mappings. Defaults to 0.9, or 90%.
BPPARAM	The BiocParallel::BiocParallelParam for multithreading if desired. Defaults to BiocParallel::SerialParam()

Value

A vector of [MappingResult](#) objects.

See Also

[map_best_bin\(\)](#)

Examples

```
counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
```

```

genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

map_best_bin

Map the best matching SC bin for a bulk sample

Description

Map the best matching SC bin for a bulk sample

Usage

```

map_best_bin(
  blase_data,
  bulk_id,
  bulk_data,
  bootstrap_iterations = 200,
  confidence_level = 0.9
)

```

Arguments

<code>blase_data</code>	The BlaseData holding the bins.
<code>bulk_id</code>	String. The sample id of the bulk to analyse.
<code>bulk_data</code>	Dataframe. The whole bulk read matrix as a dataframe. Each row should represent a gene, and each column a sample.
<code>bootstrap_iterations</code>	Integer. The number of bootstrapping iterations to run.
<code>confidence_level</code>	Decimal between 0-1. The confidence interval to calculate for mappings. Defaults to 90%.

Value

A [MappingResult](#) object.

Examples

```
counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
```

```
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
```

MCA_PF_SCE

*Malaria Cell Atlas Plasmodium falciparum for BLASE Vignette***Description**

Data from the Malaria Cell Atlas, with the following additional processing:

1. Genes renamed to match bulk samples in vignette
2. Subset to 2500 cells
3. Normalised
4. Highly variable genes identified
5. Pseudotime calculated
6. Genes subset to include a spread of those found to have high ratios by BLASE's "Gene Peakedness" measure.

Usage

```
MCA_PF_SCE
```

Format

An object of class SingleCellExperiment with 1746 rows and 2500 columns.

Source

<https://www.malariacellatlas.org/atlas/plasmodium-falciparum-atlas/>

painter_microarray	<i>Painter 2018 Plasmodium falciparum 48h asexual lifecycle microarray data</i>
--------------------	---

Description

Data originally from <https://doi.org/10.1038/s41467-018-04966-3>. Used as generated in the BLASE reproducibility documents available at <https://zenodo.org/records/16615703>, however genes have been subset to reduce file size.

Usage

```
painter_microarray
```

Format

An object of class `data.frame` with 1731 rows and 48 columns.

Source

<https://zenodo.org/records/16615703>

plot_bin_population	<i>Plot the populations of a bin</i>
---------------------	--------------------------------------

Description

Plot the populations of a bin

Usage

```
plot_bin_population(x, bin, ...)

## S4 method for signature 'SingleCellExperiment'
plot_bin_population(x, bin, group_by_slot)
```

Arguments

<code>x</code>	An object to plot on.
<code>bin</code>	Integer. The pseudotime bin to plot
<code>...</code>	additional arguments passed to object-specific methods.
<code>group_by_slot</code>	String. The metadata column in the SingleCellExperiment::SingleCellExperiment to be used as the cell type labels.

Value

A ggplot2 object of a plot of population in the given object for this bin.

Examples

```
counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
```

```
plot_find_best_params_results
```

Plot the results of the search for good parameters

Description

Plot the results of the search for good parameters

Usage

```
plot_find_best_params_results(
  find_best_params_results,
  bin_count_colors = viridis::scale_color_viridis(option = "viridis"),
  gene_count_colors = viridis::scale_color_viridis(option = "magma")
)
```

Arguments

```
find_best_params_results
    Dataframe. Results dataframe from find\_best\_params\(\)
bin_count_colors
    Optional, custom bin count scale color scheme.
gene_count_colors
    Optional, custom gene count scale color scheme.
```

Value

A plot showing how convexity changes as n_bins and n_genes are changed. See [find_best_params\(\)](#) for details on how to interpret.

See Also

[find_best_params\(\)](#)

Examples

```
ncells <- 70
ngenes <- 100
counts_matrix <- matrix(
  c(seq_len(3500) / 10, seq_len(3500) / 5),
  ncol = ncells,
  nrow = ngenes
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- paste0("cell", seq_len(ncells))
rownames(sce) <- paste0("gene", seq_len(ngenes))
```

```

sce$cell_type <- c(
  rep("celltype_1", ncells / 2),
  rep("celltype_2", ncells / 2)
)

sce$pseudotime <- seq_len(ncells) - 1
genelist <- rownames(sce)

# Finding the best params for the BlaseData
best_params <- find_best_params(
  sce, genelist,
  bins_count_range = c(2, 3),
  gene_count_range = c(20, 50),
  pseudotime_slot = "pseudotime",
  split_by = "pseudotime_range"
)
best_params
plot_find_best_params_results(best_params)

```

plot_gene_peakedness *plot_gene_peakedness*

Description

plot_gene_peakedness

Usage

```

plot_gene_peakedness(
  sce,
  gene_peakedness_df,
  gene,
  pseudotime_slot = "slingPseudotime_1"
)

```

Arguments

sce	SingleCellExperiment::SingleCellExperiment to plot gene from. Must contain pseudotime, and normcounts
gene_peakedness_df	The DataFrame Result of calculate_gene_peakedness
gene	String. The name of the gene to plot. Must be present in the SCE and gene_peakedness_df
pseudotime_slot	String. The pseudotime column in the SingleCellExperiment::SingleCellExperiment object metadata.

Value

A `ggplot2::ggplot2` plot showing: in black points, expression of the gene over pseudotime, in a green line, the fitted expression of the gene over pseudotime, the inside and outside of window means of smoothed expression (red and blue dotted horizontal lines respectively), and the bounds of the window (in black dotted vertical lines).

Examples

```
ncells <- 70
ngenes <- 100
# Each gene should have mean around its gene number
counts <- c()
for (i in seq_len(ngenes)) {
  counts <- c(counts, dnorm(seq_len(ncells), mean = (ncells / i), sd = 1))
}

counts_matrix <- matrix(
  counts,
  ncol = ncells,
  nrow = ngenes
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  counts = counts_matrix * 3,
  normcounts = counts_matrix,
  logcounts = log(counts_matrix)
))
colnames(sce) <- paste0("cell", seq_len(ncells))
rownames(sce) <- paste0("gene", seq_len(ngenes))
sce$cell_type <- c(
  rep("celltype_1", ncells / 2),
  rep("celltype_2", ncells / 2)
)

sce$pseudotime <- seq_len(ncells) - 1
genelist <- rownames(sce)

# calculate_gene_peakedness
gene_peakedness <- calculate_gene_peakedness(
  sce,
  pseudotime_slot = "pseudotime"
)

head(gene_peakedness)

# plot_gene_peakedness
plot_gene_peakedness(sce, gene_peakedness, "gene20",
  pseudotime_slot = "pseudotime"
)

# smooth_gene
smoothed_gene20 <- smooth_gene(
  sce, "gene20",
```

```

    pseudotime_slot = "pseudotime"
  )
  head(smoothed_gene20)

  # Select best spread of genes
  genes_to_use <- gene_peakedness_spread_selection(sce, gene_peakedness,
    genes_per_bin = 2, n_gene_bins = 1, pseudotime_slot = "pseudotime"
  )

  print(genes_to_use)
  plot(
    x = gene_peakedness[
      gene_peakedness$gene %in% genes_to_use, "peak_pseudotime"
    ],
    y = gene_peakedness[gene_peakedness$gene %in% genes_to_use, "ratio"]
  )

```

plot_mapping_result *Plot a summary of the mapping result*

Description

Plot a summary of the mapping result

Usage

```

plot_mapping_result(x, y, ...)

## S4 method for signature 'SingleCellExperiment,MappingResult'
plot_mapping_result(x, y, group_by_slot)

```

Arguments

x	An object to plot on.
y	The MappingResult object to plot
...	additional arguments passed to object-specific methods.
group_by_slot	String. The metadata column in the SingleCellExperiment::SingleCellExperiment to be used as the coloring for the output plot. Passed to scater::plotUMAP() as colour_by, and will be used to produce a bar chart of populations in the best mapped bin.

Value

A set of plots describing the mapping.

See Also

[plot_mapping_result_corr\(\)](#), [plot_bin_population\(\)](#)

Examples

```

counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

result <- map_best_bin(blase_data, "B", bulk_counts)

# Plot bin
sce <- scater::runUMAP(sce)
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_mapping_result(sce, result, group_by_slot = "cell_type")

```

plot_mapping_result_corr

Plot a mapping result's correlation

Description

Plots the mapping results correlations with each pseudotime bin

Usage

```
plot_mapping_result_corr(mapping_result)
```

Arguments

`mapping_result` A [MappingResult](#) object to plot the correlations for.

Value

A [ggplot2::ggplot2](#) object of the the line plot

Examples

```

counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

plot_mapping_result_heatmap

Plot a mapping result heatmap

Description

Plots Spearman's Rho as the fill colour, and adds * if the [MappingResult](#) was confidently assigned.

Usage

```
plot_mapping_result_heatmap(
  mapping_result_list,
  heatmap_fill_scale = ggplot2::scale_fill_gradientn(colors = c("blue", "white", "red"),
    limits = c(-1, 1)),
  annotate_confidence = TRUE,
  annotate_correlation = FALSE,
  bin_order = NULL,
  text_background = FALSE
)
```

Arguments

mapping_result_list	A list of MappingResult objects to include in the heatmap.
heatmap_fill_scale	The ggplot2 compatible fill gradient scale to apply to the heatmap.
annotate_confidence	Boolean. Whether to annotate the heatmap with significant results or not, defaults to TRUE.
annotate_correlation	Boolean. Whether to annotate the heatmap with the correlation of bin to each bulk sample. Defaults to FALSE.
bin_order	Vector of integers. A vector of the bin ids in which to plot the pseudotime bins along the x-axis.
text_background	Boolean. Whether to show background on labels or not. Has no effect if no annotations are enabled.

Value

A [ggplot2::ggplot2](#) heatmap showing the correlations of each mapping result across every pseudo-time bin.

Examples

```
counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
```

```

)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

PRIVATE_.ci

.ci

Description

Originally implemented in RVAidemoire Version 0.9-83-7.

Usage

```
PRIVATE_.ci(x, conf.level = 0.95)
```

Arguments

x	data to calculate ci for
conf.level	confidence level to calculate

Value

confidence interval results

PRIVATE_spearman.ci	<i>Confidence interval of a Spearman's rank correlation coefficient</i>
---------------------	---

Description

Computes the confidence interval of a Spearman's rank correlation coefficient by bootstrapping. Originally implemented in RVAidemoire Version 0.9-83-7.

Usage

```
PRIVATE_spearman.ci(var1, var2, nrep = 1000, conf.level = 0.95)
```

Arguments

var1	numeric vector (first variable).
var2	nuermic verctor (second variable).
nrep	number of replicates for bootstrapping.
conf.level	confidence level of the interval.

Value

description method name of the test.
 data.name a character string giving the name(s) of the data.
 conf.level confidence level.
 rep number of replicates.
 estimate Spearman's rank correlation coefficient.
 conf.int confidence interval.

pseudobulk_bins *Get pseudobulk bins of a BLASE Data object.*

Description

Get pseudobulk bins of a BLASE Data object.

Usage

```
pseudobulk_bins(x)

## S4 method for signature 'BlaseData'
pseudobulk_bins(x)
```

Arguments

x a [BlaseData](#) object

Value

List of dataframes. Each dataframe is the normalised counts of cells by genes in each pseudotime bin. List index is the pseudotime bin.

Examples

```
counts <- matrix(rpois(100, lambda = 10), ncol = 10, nrow = 10)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(normcounts = counts)
)
sce$pseudotime <- seq_len(10) - 1
data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 3)
genes(data) <- as.character(seq_len(10))

genes(data)
```

pseudobulk_bins<- *Set genes of a BLASE Data object.*

Description

Set genes of a BLASE Data object.

Usage

```
pseudobulk_bins(x) <- value

## S4 replacement method for signature 'BlaseData'
pseudobulk_bins(x) <- value
```

Arguments

x	a BlaseData object
value	List of dataframes. Each dataframe is the normalised counts of cells by genes in each pseudotime bin. List index is the pseudotime bin.

Value

Nothing

show,BlaseData-method *Show an BlaseData object*

Description

Show an BlaseData object

Usage

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

Arguments

object	a BlaseData object
--------	------------------------------------

Value

A character vector describing the BLASE object

Examples

```
counts <- matrix(rpois(100, lambda = 10), ncol = 10, nrow = 10)
sce <- SingleCellExperiment::SingleCellExperiment(
  assays = list(normcounts = counts)
)
sce$pseudotime <- seq_len(10) - 1
data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 3)
genes(data) <- as.character(seq_len(10))

genes(data)
```

`show, MappingResult-method`*Show an MappingResult object*

Description

Show an MappingResult object

Usage

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

Arguments

object an [MappingResult](#) object

Value

A character vector describing the Mapping Result object

Examples

```
counts_matrix <- matrix(  
  c(seq_len(120) / 10, seq_len(120) / 5),  
  ncol = 48, nrow = 5  
)  
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(  
  normcounts = counts_matrix, logcounts = log(counts_matrix)  
))  
colnames(sce) <- seq_len(48)  
rownames(sce) <- as.character(seq_len(5))  
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))  
  
sce$pseudotime <- seq_len(48) - 1  
blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)  
genes(blase_data) <- as.character(seq_len(5))  
  
bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)  
colnames(bulk_counts) <- c("A", "B", "C")  
rownames(bulk_counts) <- as.character(seq_len(5))  
  
# Map to bin  
result <- map_best_bin(blase_data, "B", bulk_counts)  
result  
  
# Map all bulks to bin  
results <- map_all_best_bins(blase_data, bulk_counts)  
  
# Plot Heatmap
```

```

plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

smooth_gene

smooth_gene

Description

Returns the smoothed expression of the given gene, based on a GAM fit to the normalised expression.

Usage

```
smooth_gene(sce, gene, pseudotime_slot = "slingPseudotime_1", knots = 10)
```

Arguments

sce	SingleCellExperiment::SingleCellExperiment to do the calculations on.
gene	String. The name of the gene to smooth
pseudotime_slot	String. The slot in the SingleCellExperiment::SingleCellExperiment object meta-data containing pseudotime
knots	Integer. The number of knots to use when fitting the GAM

Value

Smoothed Gene Expression over pseudotime

Examples

```

ncells <- 70
ngenes <- 100
# Each gene should have mean around its gene number
counts <- c()
for (i in seq_len(ngenes)) {
  counts <- c(counts, dnorm(seq_len(ncells), mean = (ncells / i), sd = 1))
}

counts_matrix <- matrix(
  counts,
  ncol = ncells,
  nrow = ngenes
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  counts = counts_matrix * 3,
  normcounts = counts_matrix,
  logcounts = log(counts_matrix)
))
colnames(sce) <- paste0("cell", seq_len(ncells))
rownames(sce) <- paste0("gene", seq_len(ngenes))
sce$cell_type <- c(
  rep("celltype_1", ncells / 2),
  rep("celltype_2", ncells / 2)
)

sce$pseudotime <- seq_len(ncells) - 1
genelist <- rownames(sce)

# calculate_gene_peakedness
gene_peakedness <- calculate_gene_peakedness(
  sce,
  pseudotime_slot = "pseudotime"
)

head(gene_peakedness)

# plot_gene_peakedness
plot_gene_peakedness(sce, gene_peakedness, "gene20",
  pseudotime_slot = "pseudotime"
)

# smooth_gene
smoothed_gene20 <- smooth_gene(
  sce, "gene20",
  pseudotime_slot = "pseudotime"
)
head(smoothed_gene20)

# Select best spread of genes
genes_to_use <- gene_peakedness_spread_selection(sce, gene_peakedness,
  genes_per_bin = 2, n_gene_bins = 1, pseudotime_slot = "pseudotime"
)

```

```

)

print(genes_to_use)
plot(
  x = gene_peakedness[
    gene_peakedness$gene %in% genes_to_use, "peak_pseudotime"
  ],
  y = gene_peakedness[gene_peakedness$gene %in% genes_to_use, "ratio"]
)

```

top_2_distance	<i>Get the difference in correlation between the top 2 most correlated bins for a BLASE Mapping Results object.</i>
----------------	---

Description

Get the difference in correlation between the top 2 most correlated bins for a BLASE Mapping Results object.

Usage

```

top_2_distance(x)

## S4 method for signature 'MappingResult'
top_2_distance(x)

```

Arguments

x a [MappingResult](#) object

Value

Decimal. The difference in correlation between the top 2 most correlated bins for this mapping.

Examples

```

counts_matrix <- matrix(
  c(seq_len(120) / 10, seq_len(120) / 5),
  ncol = 48, nrow = 5
)
sce <- SingleCellExperiment::SingleCellExperiment(assays = list(
  normcounts = counts_matrix, logcounts = log(counts_matrix)
))
colnames(sce) <- seq_len(48)
rownames(sce) <- as.character(seq_len(5))
sce$cell_type <- c(rep("celltype_1", 24), rep("celltype_2", 24))

sce$pseudotime <- seq_len(48) - 1

```

```

blase_data <- as.BlaseData(sce, pseudotime_slot = "pseudotime", n_bins = 4)
genes(blase_data) <- as.character(seq_len(5))

bulk_counts <- matrix(seq_len(15) * 10, ncol = 3, nrow = 5)
colnames(bulk_counts) <- c("A", "B", "C")
rownames(bulk_counts) <- as.character(seq_len(5))

# Map to bin
result <- map_best_bin(blase_data, "B", bulk_counts)
result

# Map all bulks to bin
results <- map_all_best_bins(blase_data, bulk_counts)

# Plot Heatmap
plot_mapping_result_heatmap(list(result))

# Plot Correlation
plot_mapping_result_corr(result)

# Plot populations
sce <- assign_pseudotime_bins(
  sce,
  pseudotime_slot = "pseudotime", n_bins = 4
)
plot_bin_population(sce, best_bin(result), group_by_slot = "cell_type")

# Getters
bulk_name(result)
best_bin(result)
best_correlation(result)
top_2_distance(result)
confident_mapping(result)
mapping_history(result)
bootstrap_iterations(result)

```

tradeSeq_BLASE_example_sce

TradeSeq Example SCE for BLASE Vignette

Description

Data from the TradeSeq vignette, with the following additional processing applied:

Usage

```
tradeSeq_BLASE_example_sce
```

Format

An object of class `SingleCellExperiment` with 240 rows and 1565 columns.

Details

1. Pseudotime calculated
2. TradeSeq applied
3. Log normalised and normalised counts calculated
4. Erythrocyte cell type removed
5. UMAP calculated

Source

<https://bioconductor.org/packages/devel/bioc/vignettes/tradeSeq/inst/doc/tradeSeq.html>

zhang_2021_heat_shock_bulk

Zhang 2021 Plasmodium falciparum heat shock bulk data

Description

Data originally from <https://doi.org/10.1038/s41467-021-24814-1>. Used as generated in the BLASE reproducibility documents available at <https://zenodo.org/records/16615703>, however genes have been subset to reduce file size.

Usage

```
zhang_2021_heat_shock_bulk
```

Format

An object of class `data.frame` with 990 rows and 12 columns.

Source

<https://zenodo.org/records/16615703>

Index

- * **annotation**
 - annotate_sce, 3
 - * **blase-object**
 - as.BlaseData, 4
 - assign_pseudotime_bins, 5
 - bins, 10
 - bins<-, 11
 - BlaseData-class, 12
 - genes, 23
 - genes<-, 24
 - pseudobulk_bins, 47
 - pseudobulk_bins<-, 47
 - show, BlaseData-method, 48
 - * **datasets**
 - MCA_PF_SCE, 35
 - painter_microarray, 36
 - tradeSeq_BLASE_example_sce, 53
 - zhang_2021_heat_shock_bulk, 54
 - * **data**
 - MCA_PF_SCE, 35
 - painter_microarray, 36
 - tradeSeq_BLASE_example_sce, 53
 - zhang_2021_heat_shock_bulk, 54
 - * **gene-selection**
 - calculate_gene_peakedness, 15
 - gene_peakedness_spread_selection, 24
 - get_top_n_genes, 27
 - plot_gene_peakedness, 39
 - smooth_gene, 50
 - * **internal**
 - bins, 10
 - bins<-, 11
 - PRIVATE_.ci, 45
 - PRIVATE_spearman.ci, 46
 - pseudobulk_bins, 47
 - pseudobulk_bins<-, 47
 - * **mapping-result-object**
 - best_bin, 7
 - best_correlation, 9
 - bootstrap_iterations, 12
 - bulk_name, 14
 - confident_mapping, 17
 - mapping_history, 30
 - MappingResult, 28
 - show, MappingResult-method, 49
 - top_2_distance, 52
 - * **mapping_plots**
 - plot_bin_population, 36
 - plot_mapping_result, 41
 - plot_mapping_result_corr, 42
 - plot_mapping_result_heatmap, 44
 - * **mapping**
 - map_all_best_bins, 31
 - map_best_bin, 33
 - * **tuning**
 - evaluate_parameters, 18
 - evaluate_top_n_genes, 20
 - find_best_params, 21
 - plot_find_best_params_results, 38
 - * **util**
 - get_bins_as_bulk, 26
-
- annotate_sce, 3
 - as.BlaseData, 4
 - as.BlaseData(), 12, 22
 - as.BlaseData, SingleCellExperiment-method (as.BlaseData), 4
 - assign_pseudotime_bins, 5
 - assign_pseudotime_bins(), 5
 - assign_pseudotime_bins, data.frame-method (assign_pseudotime_bins), 5
 - assign_pseudotime_bins, Seurat-method (assign_pseudotime_bins), 5
 - assign_pseudotime_bins, SingleCellExperiment-method (assign_pseudotime_bins), 5
 - best_bin, 7

best_bin, MappingResult-method
 (best_bin), 7
 best_correlation, 9
 best_correlation, MappingResult-method
 (best_correlation), 9
 bins, 10
 bins, BlaseData-method (bins), 10
 bins<-, 11
 bins<-, BlaseData-method (bins<-), 11
 BiocParallel::BiocParallelParam, 16, 19,
 22, 32
 BiocParallel::SerialParam, 16, 19, 22
 BiocParallel::SerialParam(), 32
 BlaseData, 5, 10–12, 19, 20, 23, 24, 32, 34,
 47, 48
 BlaseData (BlaseData-class), 12
 BlaseData-class, 12
 bootstrap_iterations, 12
 bootstrap_iterations, MappingResult-method
 (bootstrap_iterations), 12
 bulk_name, 14
 bulk_name, MappingResult-method
 (bulk_name), 14

 calculate_gene_peakedness, 15
 calculate_gene_peakedness(), 25
 confident_mapping, 17
 confident_mapping, MappingResult-method
 (confident_mapping), 17

 data.frame, 12

 evaluate_parameters, 18
 evaluate_top_n_genes, 20

 find_best_params, 21
 find_best_params(), 38

 gene_peakedness_spread_selection, 24
 genes, 23
 genes, BlaseData-method (genes), 23
 genes<-, 24
 genes<-, BlaseData-method (genes<-), 24
 get_bins_as_bulk, 26
 get_top_n_genes, 27
 ggplot2::ggplot2, 20, 40, 42, 44

 map_all_best_bins, 31
 map_best_bin, 33
 map_best_bin(), 28, 29, 32

 mapping_history, 30
 mapping_history, MappingResult-method
 (mapping_history), 30
 MappingResult, 3, 8, 9, 13, 14, 17, 28, 30, 32,
 34, 41, 42, 44, 49, 52
 MappingResult-class (MappingResult), 28
 MCA_PF_SCE, 35

 painter_microarray, 36
 plot_bin_population, 36
 plot_bin_population(), 41
 plot_bin_population, SingleCellExperiment-method
 (plot_bin_population), 36
 plot_find_best_params_results, 38
 plot_find_best_params_results(), 22
 plot_gene_peakedness, 39
 plot_mapping_result, 41
 plot_mapping_result, SingleCellExperiment, MappingResult-met
 (plot_mapping_result), 41
 plot_mapping_result_corr, 42
 plot_mapping_result_corr(), 41
 plot_mapping_result_heatmap, 43
 PRIVATE_.ci, 45
 PRIVATE_spearman.ci, 46
 pseudobulk_bins, 47
 pseudobulk_bins, BlaseData-method
 (pseudobulk_bins), 47
 pseudobulk_bins<-, 47
 pseudobulk_bins<-, BlaseData-method
 (pseudobulk_bins<-), 47

 scater::plotUMAP(), 41
 show, BlaseData-method, 48
 show, MappingResult-method, 49
 SingleCellExperiment::SingleCellExperiment,
 3, 5, 6, 16, 25, 27, 36, 39, 41, 50
 smooth_gene, 50

 top_2_distance, 52
 top_2_distance, MappingResult-method
 (top_2_distance), 52
 tradeSeq::associationTest, 28
 tradeSeq_BLASE_example_sce, 53

 zhang_2021_heat_shock_bulk, 54