

# Package ‘blase’

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**Title** Bulk Linking Analysis for Single-cell Experiments

**Version** 1.1.2

**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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annotate\_sce *Annotate a SCE with BLASE Mappings*

**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**

- sce The [SingleCellExperiment::SingleCellExperiment](#) to annotate.
- blase\_results A list of [MappingResult](#) to use for the annotation.
- annotation\_col String. The name of the metadata column in which to store the new annotations.
- include\_stats Boolean. Whether or not to include metadata columns containing the correlation of the best matching bin, and whether that mapping was strong.

**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
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 all bulks to bin
results <- map_all_best_bins(blase_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.BlaseData

*Conversion to BlaseData*


---

**Description**

Conversion to BlaseData

**Usage**

```
as.BlaseData(x, ...)
```

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

### Arguments

**x** An object to take counts from

**...** additional arguments passed to object-specific methods.

**pseudotime\_slot** String or vector of strings. The `SingleCellExperiment::SingleCellExperiment` slot(s) containing pseudotime values for each cell to be passed to `assign_pseudotime_bins()`.

**n\_bins** Integer. The number of bins to create, passed to `assign_pseudotime_bins()`.

**split\_by** String. The `split_by` method to be passed on to `assign_pseudotime_bins()`. Must be one of `pseudotime_range` or `cells`.

### 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 or Vector of Strings. The name of the <code>SingleCellExperiment::SingleCellExperiment</code> slot(s) 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.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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

---

best_bin	<i>Get best bin of a BLASE Mapping Results object.</i>
----------	--

---

### 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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"
```

---

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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

---

```
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

**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)
```

---

```
bins<-
```

*Set genes of a BLASE Data object.*

---

**Description**

Set genes of a BLASE Data object.

**Usage**

```
bins(x) <- value

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

**Arguments**

x                    a [BlaseData](#) object  
 value                Vector of integers The new value for bins slot

**Value**

Nothing

---

BlaseData-class            *Blase Data Object*

---

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

---

## 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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"
```

---

bulk\_name

*Get name of bulk of a BLASE Mapping Results object.*

---

## 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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

---

```
bulk_name<-          Set name of bulk of a BLASE Mapping Results object.
```

---

### Description

Set name of bulk of a BLASE Mapping Results object.

### Usage

```
bulk_name(x) <- value

## S4 replacement method for signature 'MappingResult'
bulk_name(x) <- value
```

### Arguments

x                    a [MappingResult](#) object  
value                String. The name of the bulk used to map against.

### 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)
```

---

```
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	<a href="#">SingleCellExperiment::SingleCellExperiment</a> 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 <a href="#">BiocParallel::BiocParallelParam</a> for parallelisation. Defaults to <a href="#">BiocParallel::SerialParam</a> .

**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"]
  )

```

---

evaluate\_parameters     *Evaluate n\_bins and n\_genes for bin mapping*

---

### 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 <a href="#">BlaseData</a> object to use.
<code>bootstrap_iterations</code>	Integer. Iterations for bootstrapping when calculating strong mappings.
<code>BPPARAM</code>	The <a href="#">BiocParallel::BiocParallelParam</a> configuration. Defaults to <a href="#">BiocParallel::SerialParam</a>
<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.
- "strong\_mapping\_pct" decimal from 0-1. The percent of mappings for this setup which were annotated as strong 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 strong mappings.
BPPARAM	The <a href="#">BiocParallel::BiocParallelParam</a> . Defaults to <a href="#">BiocParallel::SerialParam</a>
...	params to be passed to child functions, see <a href="#">as.BlaseData()</a>

**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
- `strong_mapping_pct`: Decimal. The percent of bins which were strongly 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 strongly 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**

association_test_results	Dataframe. The association test results data frame to take the genes from. Generated by <code>tradeSeq::associationTest</code> .
n_genes	Integer. The number of genes to return. Defaults to 40.
lineage	The Lineage to use. The Defaults to NA, which assumes the test was run with Lineages=False.
p_cutoff	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,
  strong_mapping,
  history,
  bootstrap_iterations,
  metric = "spearman"
)
```

**Arguments**

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

**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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

---

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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

---

map\_all\_best\_bins      *Map many bulk samples in the same dataframe*

---

## 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(),

```

```
metric = "spearman"
)
```

### Arguments

<code>blase_data</code>	The <a href="#">BlaseData</a> holding the bins and pseudobulks.
<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 0.9, or 90%.
<code>BPPARAM</code>	The <a href="#">BiocParallel::BiocParallelParam</a> for multithreading if desired. Defaults to <a href="#">BiocParallel::SerialParam()</a>
<code>metric</code>	Character. The metric to use to compare mappings. One of: 'spearman', 'pearson', 'kendall', 'cosine_similarity', 'euclidean', 'manhattan.'

### 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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"
```

---

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,
  metric = "spearman",
  log_data = FALSE
)
```

**Arguments**

<code>blase_data</code>	The <a href="#">BlaseData</a> 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%.
<code>metric</code>	Character. The metric to use to compare mappings. One of: 'spearman', 'pearson', 'kendall', 'cosine_similarity', 'euclidean', 'manhattan.'
<code>log_data</code>	Boolean. When true, bulk and bin values are log2 transformed

**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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"
```

---

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/>

---

 metric

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


---

### Description

Get the mapping history for a BLASE Mapping Results object.

### Usage

```
metric(x)

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

### Arguments

x                    a [MappingResult](#) object

### Value

a String, the metric used to calculate the result.

### 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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"
```

---

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 *Plot the populations of a bin*

---

### 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

x	An object to plot on.
bin	Integer. The pseudotime bin to plot
...	additional arguments passed to object-specific methods.
group_by_slot	String. The metadata column in the <a href="#">SingleCellExperiment::SingleCellExperiment</a> 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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

---

```
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"]
)

```

**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 <a href="#">MappingResult</a> object to plot
...	additional arguments passed to object-specific methods.
group_by_slot	String. The metadata column in the <a href="#">SingleCellExperiment::SingleCellExperiment</a> to be used as the coloring for the output plot. Passed to <a href="#">scater::plotUMAP()</a> 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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

---

```
plot_mapping_result_heatmap
```

*Plot a mapping result heatmap*

---

### Description

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

### Usage

```

plot_mapping_result_heatmap(
  mapping_result_list,
  heatmap_fill_scale = NULL,
  annotate_strong = 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_strong`  
Boolean. Whether to annotate the heatmap with strong 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 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.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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"
```

---

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_correlation.ci`*Confidence interval of a correlation coefficient*

---

**Description**

Computes the confidence interval of a correlation coefficient by bootstrapping. Adapted from the implementation of `spearman.ci` in RVAidemoire Version 0.9-83-7.

**Usage**

```
PRIVATE_correlation.ci(  
  var1,  
  var2,  
  nrep = 1000,  
  conf.level = 0.95,  
  metric = "spearman"  
)
```

**Arguments**

<code>var1</code>	numeric vector (first variable).
<code>var2</code>	numeric vector (second variable).
<code>nrep</code>	number of replicates for bootstrapping.
<code>conf.level</code>	confidence level of the interval.
<code>metric</code>	character from "pearson", "spearman", "kendall", the correlation method to use.

**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` of correlation coefficient.  
`conf.int` confidence interval.

---

PRIVATE\_cosine\_similarity.ci  
*Confidence interval of cosine similarity*

---

**Description**

Computes the confidence interval of a cosine similarity coefficient by bootstrapping. Adapted from the implementation of spearman.ci in RVAidemoire Version 0.9-83-7.

**Usage**

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

**Arguments**

var1	numeric vector (first variable).
var2	numeric vector (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.

---

PRIVATE\_distance.ci    *Confidence interval of a distance metric*

---

**Description**

Computes the confidence interval of a Spearman's rank correlation coefficient by bootstrapping. Adapted from the implementation of spearman.ci in RVAidemoire Version 0.9-83-7.

**Usage**

```
PRIVATE_distance.ci(  
  var1,  
  var2,  
  nrep = 1000,  
  conf.level = 0.95,  
  metric = "euclidean"  
)
```

**Arguments**

var1	numeric vector (first variable).
var2	numeric vector (second variable).
nrep	number of replicates for bootstrapping.
conf.level	confidence level of the interval.
metric	character from "euclidean", "manhattan", the distance method to use.

**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 calculated distance (as a negative, so that there is consistency with other methods where a higher value indicates more similarity).  
 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

<code>x</code>	a <a href="#">BlaseData</a> object
<code>value</code>	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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

**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	<a href="#">SingleCellExperiment::SingleCellExperiment</a> to do the calculations on.
gene	String. The name of the gene to smooth
pseudotime_slot	String. The slot in the <a href="#">SingleCellExperiment::SingleCellExperiment</a> 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"]
)

```

---

strong\_mapping

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


---

### Description

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

### Usage

```
strong_mapping(x)
```

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

**Arguments**

x                    a [MappingResult](#) object

**Value**

Boolean. TRUE if the result is strong, 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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

---

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)
strong_mapping(result)
mapping_history(result)
bootstrap_iterations(result)
metric(result)

# Setters
bulk_name(result) <- "New Name"

```

---

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>

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