

Package ‘spillR’

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Type Package

Title Spillover Compensation in Mass Cytometry Data

Version 1.3.0

Description Channel interference in mass cytometry can cause spillover and may result in miscounting of protein markers. We develop a nonparametric finite mixture model and use the mixture components to estimate the probability of spillover. We implement our method using expectation-maximization to fit the mixture model.

biocViews FlowCytometry, ImmunoOncology, MassSpectrometry, Preprocessing, SingleCell, Software, StatisticalMethod, Visualization, Regression

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Encoding UTF-8

LazyData false

Config/testthat/edition 3

RoxygenNote 7.3.1

Imports dplyr, tibble, tidyselect, stats, ggplot2, tidyr, spatstat.univar, S4Vectors, parallel

Depends R (>= 4.3.0), SummarizedExperiment, CATALYST

Suggests knitr, rmarkdown, cowplot, testthat (>= 3.0.0), BiocStyle, hexbin

VignetteBuilder knitr

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| compCytof | <i>Compute spillover probability and correct for spillover</i> |
|-----------|--|

Description

Compute spillover probability and correct for spillover

Usage

```
compCytof(
  sce,
  sce_bead,
  marker_to_barcode,
  impute_value,
  overwrite = FALSE,
  n_cores = 1,
  naive = FALSE
)
```

Arguments

| | |
|-------------------|---|
| sce | SingleCellExperiment for the real cells |
| sce_bead | SingleCellExperiment for the bead experiment |
| marker_to_barcode | Table that maps the marker to the barcode in the beads experiment |
| impute_value | Imputed value for counts that are declared as spillover |

| | |
|-----------|--|
| overwrite | logical; if TRUE data are overwritten if FALSE data are saved in new columns |
| n_cores | Number of computing cores |
| naive | logical; if TRUE use the naive version |

Value

A [SingleCellExperiment](#) object

Examples

```
library(CATALYST)
library(dplyr)
bc_key <- c(139, 141:156, 158:176)
sce_bead <- prepData(ss_exp)
sce_bead <- assignPrelim(sce_bead, bc_key, verbose = FALSE)
sce_bead <- applyCutoffs(estCutoffs(sce_bead))
sce_bead <- computeSpillmat(sce_bead)
data(mp_cells, package = "CATALYST")
sce <- prepData(mp_cells)
marker_to_barcode <- rowData(sce_bead)[, c("channel_name", "is_bc")] |>
  as_tibble() |>
  filter(is_bc == TRUE) |>
  mutate(barcode = bc_key) |>
  select(marker = channel_name, barcode)
spillR::compCytobf(sce, sce_bead, marker_to_barcode, impute_value = NA)
```

 compensate

Compute spillover probability and correct for spillover

Description

Compute spillover probability and correct for spillover

Usage

```
compensate(
  tb_real,
  tb_bead,
  target_marker,
  spillover_markers,
  impute_value = NA,
  n_iter = 1000
)
```

Arguments

| | |
|-------------------|--|
| tb_real | Data frame or tibble with proteins counts of real experiment |
| tb_bead | Data frame or tibble with proteins counts of bead experiment |
| target_marker | Marker name in real experiment |
| spillover_markers | Marker names in bead experiment |
| impute_value | Value for counts that are declared as spillover |
| n_iter | Maximum number of EM steps |

Value

A list of class `spillr` containing

| | |
|-------------------|----------------------------------|
| tb_compensate | corrected real cells |
| tb_spill_prob | probability curve |
| convergence | covergence table of EM algorithm |
| tb_real | input real cells |
| tb_bead | input bead cells |
| target_marker | input marker in real experiment |
| spillover_markers | input markers in bead experiment |

| | |
|------------------|--|
| compensate_naive | <i>Compute spillover probability and correct for spillover from beads only</i> |
|------------------|--|

Description

Compute spillover probability and correct for spillover from beads only

Usage

```
compensate_naive(
  tb_real,
  tb_bead,
  target_marker,
  spillover_markers,
  impute_value = NA
)
```

Arguments

| | |
|-------------------|--|
| tb_real | Data frame or tibble with proteins counts of real experiment |
| tb_bead | Data frame or tibble with proteins counts of bead experiment |
| target_marker | Marker name in real experiment |
| spillover_markers | Marker names in bead experiment |
| impute_value | Value for counts that are declared as spillover |

Value

A list of class `spillr` containing

| | |
|-------------------|----------------------------------|
| tb_compensate | corrected real cells |
| tb_spill_prob | probability curve |
| convergence | covergence table of EM algorithm |
| tb_real | input real cells |
| tb_bead | input bead cells |
| target_marker | input marker in real experiment |
| spillover_markers | input markers in bead experiment |

| | |
|---------------|--|
| generate_bead | <i>Generate dataset for vignettes and simulation studies</i> |
|---------------|--|

Description

Generate dataset for vignettes and simulation studies

Usage

```
generate_bead()
```

Value

`tibble` data frame

Examples

```
set.seed(23)
generate_bead()
```

generate_real *Generate dataset for vignettes and simulation studies*

Description

Generate dataset for vignettes and simulation studies

Usage

```
generate_real()
```

Value

[tibble](#) data frame

Examples

```
set.seed(23)
generate_real()
```

plotDiagnostics *Compute spillover probability and correct for spillover*

Description

Compute spillover probability and correct for spillover

Usage

```
plotDiagnostics(sce, ch)
```

Arguments

sce A [SingleCellExperiment](#) object
ch Character string specifying the channel to plot

Value

A list of [ggplot2](#) plots

Examples

```
library(CATALYST)
library(dplyr)
bc_key <- c(139, 141:156, 158:176)
sce_bead <- prepData(ss_exp)
sce_bead <- assignPrelim(sce_bead, bc_key, verbose = FALSE)
sce_bead <- applyCutoffs(estCutoffs(sce_bead))
sce_bead <- computeSpillmat(sce_bead)
data(mp_cells, package = "CATALYST")
sce <- prepData(mp_cells)
marker_to_barcode <- rowData(sce_bead)[, c("channel_name", "is_bc")] |>
  as_tibble() |>
  filter(is_bc == TRUE) |>
  mutate(barcode = bc_key) |>
  select(marker = channel_name, barcode)
sce <- spillR::compCytobf(sce, sce_bead, marker_to_barcode, impute_value = NA)
plotDiagnostics(sce, "Yb173Di")
```

tfm

Variance stabilizing transform of counts

Description

Variance stabilizing transform of counts

Usage

```
tfm(x)
```

Arguments

x Raw count

Value

A transformed count

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