Package 'retrofit'

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Title RETROFIT: Reference-free deconvolution of cell mixtures in spatial transcriptomics

Version 1.11.0

Description RETROFIT is a Bayesian non-negative matrix factorization framework to decompose cell type mixtures in ST data without using external single-cell expression references. RETROFIT outperforms existing reference-based methods in estimating cell type proportions and reconstructing gene expressions in simulations with varying spot size and sample heterogeneity, irrespective of the quality or availability of the single-cell reference. RETROFIT recapitulates known cell-type localization patterns in a Slide-seq dataset of mouse cerebellum without using any single-cell data.

biocViews Transcriptomics, Visualization, RNASeq, Bayesian, Spatial, Software, GeneExpression, DimensionReduction, FeatureExtraction, SingleCell

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URL https://github.com/qunhualilab/retrofit

BugReports https://github.com/qunhualilab/retrofit/issues

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`annotateWithCorrelations`
RETROFIT matching algorithm

Description

Match cell types based on correlations with reference. decomp_w between matching algorithm description

Usage

```
annotateWithCorrelations(sc_ref, K, decomp_w, decomp_h)
```

Arguments

`sc_ref`	A Matrix or Array with two dimensions (GeneExpressions, Cell types).
`K`	integer: The number of cell types to be selected
`decomp_w`	Matrix(GeneExpressions, Components): Decomposed w matrix
`decomp_h`	Matrix(Components, Spots): Decomposed h matrix

Value

A list of selected components, cells, and correlations

- w: Filtered 2d array with GeneExpressions, Cell types
- h: Filtered2d array with Cell types, Spots
- ranked_cells: The list of cell names
- ranked_correlations: The list of correlations

See Also

papers reference

Examples

```
data("testSimulationData")
K            = 10
sc_ref       = testSimulationData$sc_ref
W            = testSimulationData$decompose$w
H            = testSimulationData$decompose$h

result       = retrofit::annotateWithCorrelations(sc_ref=sc_ref, K=K,
                                                  decomp_w=W, decomp_h=H)
H_annotated  = result$h
W_annotated  = result$w
ranked_cells = result$ranked_cells
```

---

annotateWithMarkers *RETROFIT matching algorithm*

Description

Match cell types based on correlations with reference. decomp_w between matching algorithm description

Usage

```
annotateWithMarkers(marker_ref, K, decomp_w, decomp_h)
```

Arguments

marker_ref	Key-value list: A dictionary of key: cell type, value: GeneExpression list
K	integer: The number of cell types to be selected
decomp_w	Matrix(GeneExpressions, Components): Decomposed w matrix
decomp_h	Matrix(Components, Spots): Decomposed h matrix

Value

A list of

- w
- h

See Also

papers reference

Examples

```
data("testSimulationData")
K            = 10
marker_ref   = testSimulationData$marker_ref
W            = testSimulationData$decompose$w
H            = testSimulationData$decompose$h

result       = retrofit::annotateWithMarkers(marker_ref=marker_ref, K=K,
                                             decomp_w=W, decomp_h=H)
H_annotated  = result$h
W_annotated  = result$w
ranked_cells = result$ranked_cells
```

---

decompose *RETROFIT decomposition algorithm*

Description

Receiving the input with 2d spatial transcriptomics matrix, the function returns factorized W, H, Theta. This function fulfills Structured Stochastic Variational Inference Algorithm for RETROFIT. Since exact Bayesian inference is infeasible and considering the large number of spots and genes, variational inference was adopted to approximately estimate the parameters in performant manner.

Usage

```
decompose(
  x,
  L = 16,
  iterations = 4000,
  init_param = NULL,
  lambda = 0.01,
  kappa = 0.5,
  verbose = FALSE
)
```

Arguments

x	matrix or array with dimension (GeneExpressions, Spots). This is the main spatial transciptomics data.
L	integer (default:16) The number of components to be decomposed
iterations	integer (default:4000) The number of maximum iterations to be executed
init_param	list Vatirational initial parameters
lambda	double (default:0.01) Background expression profile control
kappa	double (default:0.5) Learning rate factor
verbose	boolean (default:FALSE)

Details

init_param specification

- alpha_w_0 double (default:0.05)
- beta_w_0 double (default:0.0001)
- alpha_h_0 double (default:0.2)
- beta_h_0 double (default:0.2)
- alpha_th_0 double (default:1.25)
- beta_th_0 double (default:10)
- alpha_th_k array (default:array with dim c(K))
- beta_th_k array (default:array with dim c(K)),
- alpha_w_gk array (default:array with dim c(G,K)),
- beta_w_gk array (default:array with dim c(G,K)),
- alpha_h_ks array (default:array with dim c(K,S)),
- beta_h_ks array (default:array with dim c(K,S))

Value

A list of decomposed vectors that contains

- w: 2d array with GeneExpressions, Components
- h: 2d array with Components, Spots
- th: an array with Components
- durations: (verbose) durations vector (unit: second)
- relative_error:(verbose) errors with pre-defined norm vector

See Also

papers reference

Examples

```
data("testSimulationData")
x   = testSimulationData$extra5_x
res = retrofit::decompose(x, L=16, iterations=10, verbose=TRUE)
W   = res$w
H   = res$h
TH  = res$th
```

`retrofit` *RETROFIT*

Description

The main algorithm

Usage

```
retrofit(
  x,
  sc_ref = NULL,
  marker_ref = NULL,
  L = 16,
  K = 8,
  iterations = 4000,
  init_param = NULL,
  lambda = 0.01,
  kappa = 0.5,
  verbose = FALSE
)
```

Arguments

`x`	A matrix or array with dimension (GeneExpressions, Spots). This is the main spatial transciptomics data.
`sc_ref`	A matrix or array with two dimensions (GeneExpressions, Cell types).
`marker_ref`	A list with (keys, values) = (cell types, an array of genes).
`L`	integer (default:16) The number of components to be decomposed
`K`	integer: The number of cell types to be selected
`iterations`	integer (default:4000) The number of maximum iterations to be executed
`init_param`	list Vatirational initial parameters
`lambda`	double (default:0.01) Background expression profile control
`kappa`	double (default:0.5) Learning rate factor
`verbose`	boolean (default:FALSE)

Value

A list of decomposed vectors that contains

- decompose:
  - w: Decomposed 2d array with GeneExpressions, Components
  - h: Decomposed 2d array with Components, Spots
  - th: 1d array with Components
- annotateWithCorrelations:
  - w: Filtered 2d array with GeneExpressions, Cell types
  - h: Filtered2d array with Cell types, Spots
- annotateWithMarkers:
  - w: Filtered 2d array with GeneExpressions, Cell types
  - h: Filtered2d array with Cell types, Spots

See Also

papers reference

Examples

```
data("testSimulationData")
iterations  = 10
L           = 16
K           = 8
x           = testSimulationData$extra5_x
sc_ref      = testSimulationData$sc_ref

res         = retrofit::retrofit(x, sc_ref=sc_ref, L=L, K=K, iterations=iterations)
W           = res$decompose$w
W_annotated = res$annotateWithCorrelations$w
ranked_cells= res$annotateWithCorrelations$ranked_cells
```

---

testSimulationData *simulation data*

Description

A dataset with input and output of retrofit functions for reproducibility tests.

Usage

```
data(testSimulationData)
```

Format

Includes input x, references and results with large iterations

Details

- testSimulationData

`vignetteColonData` *colon vignette*

Description

A dataset supporting the colon vignette process

Usage

```
data(vignetteColonData)
```

Format

Includes colon scenario x, references, a large iterations results.

Details

- vignetteColonData

`vignetteSimulationData` *simulation vignette*

Description

A dataset supporting the simulation vignette process

Usage

```
data(vignetteSimulationData)
```

Format

Includes n10m3 scenario x, references, a large iterations results.

Details

- vignetteSimulationData

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