Package: SecAct (via r-universe)

May 23, 2026

Version 1.0.1

Title Secreted Signaling Activity Inference

Description Inferring secreted protein activities at bulk, single-cell, and spatial levels. SecAct uses ridge regression with permutation-based significance testing to infer the activity of over 1000 secreted proteins from gene expression profiles.

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URL https://zaoqu-liu.github.io/SecAct/, https://github.com/Zaoqu-Liu/SecAct

BugReports https://github.com/Zaoqu-Liu/SecAct/issues

Encoding UTF-8

RoxygenNote 7.3.3

Depends R (>= 3.5.0)

SystemRequirements GNU Scientific Library (GSL) - optional on Windows

Imports Matrix, ggplot2, reshape2, NMF, gganimate, metap, circlize, ggalluvial, survival, survminer, parallel, ComplexHeatmap, RANN, akima, scales, grid

Suggests testthat (>= 3.0.0), knitr, rmarkdown, RColorBrewer, patchwork

VignetteBuilder knitr

biocViews ComplexHeatmap

Config/pak/sysreqs libabsl-dev cmake libfftw3-dev libgdal-dev gdal-bin libgeos-dev make libgsl0-dev libicu-dev libjpeg-dev libpng-dev libxml2-dev libssl-dev perl libproj-dev libsqlite3-dev libudunits2-dev

Repository https://zaoqu-liu.r-universe.dev

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RemoteUrl https://github.com/Zaoqu-Liu/SecAct

RemoteRef main

RemoteSha d65240f8675448cd9f2a1ccfd02b323684279c0a

Contents

`SecAct.activity.inference`

Secreted protein activity inference

Description

Infer the signaling activity of 1248 secreted proteins from gene expression profiles.

Usage

```
SecAct.activity.inference(
  inputProfile,
  inputProfile_control = NULL,
  is.differential = FALSE,
  is.paired = FALSE,
  is.singleSampleLevel = FALSE,
  sigMatrix = "SecAct",
  is.group.sig = TRUE,
  is.group.cor = 0.9,
  lambda = 5e+05,
  nrand = 1000,
```

```
  sigFilter = FALSE
)
```

Arguments

inputProfile	Gene expression matrix with gene symbol (row) x sample (column).
inputProfile_control	Gene expression matrix with gene symbol (row) x sample (column).
is.differential	A logical indicating whether inputProfile has been differential profiles against to control.
is.paired	A logical indicating whether you want a paired operation of differential profiles between inputProfile and inputProfile_control if samples in inputProfile and inputProfile_control are paired.
is.singleSampleLevel	A logical indicating whether to calculate activity change for each single sample between inputProfile and inputProfile_control. If FALSE, calculate the overall activity change between two phenotypes.
sigMatrix	Secreted protein signature matrix.
is.group.sig	A logical indicating whether group similar signatures.
is.group.cor	Correlation cutoff of similar signatures.
lambda	Penalty factor in the ridge regression.
nrand	Number of randomization in the permutation test, with a default value 1000.
sigFilter	A logical indicating whether filter the secreted protein signatures with the genes from inputProfile.

Value

A list with four items, each is a matrix. beta: regression coefficients se: standard errors of coefficients zscore: beta/se pvalue: statistical significance

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SecAct.activity.inference.scRNAseq

Cell state activity inference from single cell data

Description

Calculate secreted protein signaling activity of cell states from single cell RNA-Sequencing data.

Usage

```
SecAct.activity.inference.scRNAseq(
  inputProfile,
  cellType_meta,
  sigMatrix = "SecAct",
  is.singleCellLevel = FALSE,
  is.group.sig = TRUE,
  is.group.cor = 0.9,
  lambda = 5e+05,
  nrand = 1000,
  sigFilter = FALSE
)
```

Arguments

inputProfile	A Seurat object.
cellType_meta	Column name in meta data that includes cell-type annotations.
sigMatrix	Secreted protein signature matrix.
is.singleCellLevel	A logical indicating whether to calculate for each single cell.
is.group.sig	A logical indicating whether to group similar signatures.
is.group.cor	Correlation cutoff of similar signatures.
lambda	Penalty factor in the ridge regression.
nrand	Number of randomization in the permutation test, with a default value 1000.
sigFilter	A logical indicating whether filter the secreted protein signatures with the genes from inputProfile.

Value

A Seurat object.

SecAct.activity.inference.ST

Spot activity inference from spatial data

Description

Calculate secreted protein signaling activity of spots from spatial transcriptomocs data.

Usage

```
SecAct.activity.inference.ST(
  inputProfile,
  inputProfile_control = NULL,
  scale.factor = 1e+05,
  sigMatrix = "SecAct",
  is.group.sig = TRUE,
  is.group.cor = 0.9,
  lambda = 5e+05,
  nrand = 1000,
  sigFilter = FALSE
)
```

Arguments

inputProfile	A SpaCET object.
inputProfile_control	A SpaCET object.
scale.factor	Sets the scale factor for spot-level normalization.
sigMatrix	Secreted protein signature matrix.
is.group.sig	A logical indicating whether to group similar signatures.
is.group.cor	Correlation cutoff of similar signatures.
lambda	Penalty factor in the ridge regression.
nrand	Number of randomization in the permutation test, with a default value 1000.
sigFilter	A logical indicating whether filter the secreted protein signatures with the genes from inputProfile.

Value

A SpaCET object.

SecAct.bar.plot *Draw a bar plot*

Description

Draw a bar plot of secreted proteins.

Usage

```
SecAct.bar.plot(fg.vec, title = NULL, colors = c("#91bfdb", "#fc8d59"))
```

Arguments

fg.vec	A vector of values.
title	The title for plot.
colors	Colors.

Value

A ggplot2 object.

SecAct.CCC.circle *Cell-cell communication circle plot*

Description

Draw a circle plot of cell-cell communication mediated by secreted proteins.

Usage

```
SecAct.CCC.circle(data, colors_cellType, sender = NULL, receiver = NULL)
```

Arguments

data	A SpaCET object or a Seurat object.
colors_cellType	Colors for cell types.
sender	Sender cell types to highlight.
receiver	Receiver cell types to highlight.

Value

A circlize object.

SecAct.CCC.dot *Cell-cell communication dot plot*

Description

Draw a dot plot of cell-cell communication mediated by secreted proteins.

Usage

```
SecAct.CCC.dot(data, sender = NULL, secretedProtein = NULL, receiver = NULL)
```

Arguments

data	A SpaCET object or a Seurat object.
sender	Sender cell types.
secretedProtein	Secreted proteins.
receiver	Receiver cell types.

Value

A ggplot2 object.

SecAct.CCC.heatmap *Cell-cell communication heatmap*

Description

Draw a heatmap of cell-cell communication mediated by secreted proteins.

Usage

```
SecAct.CCC.heatmap(
  data,
  row.sorted = FALSE,
  column.sorted = FALSE,
  colors_cellType
)
```

Arguments

data	A SpaCET object or a Seurat object.
row.sorted	Whether to sort rows.
column.sorted	Whether to sort columns.
colors_cellType	Colors for cell types.

Value

A Heatmap-class object.

SecAct.CCC.sankey *Cell-cell communication sankey plot*

Description

Draw a sankey plot of cell-cell communication mediated by secreted proteins.

Usage

```
SecAct.CCC.sankey(
  data,
  colors_cellType,
  sender = NULL,
  secretedProtein = NULL,
  receiver = NULL
)
```

Arguments

data	A SpaCET object or a Seurat object.
colors_cellType	Colors for cell types.
sender	Sender cell types.
secretedProtein	Secreted proteins.
receiver	Receiver cell types.

Value

A ggplot2 object.

SecAct.CCC.scRNAseq *Cell-cell communication from single cell data*

Description

Calculate condition-specific cell-cell communication mediated by secreted proteins from scRNA-Seq data.

Usage

```
SecAct.CCC.scRNAseq(
  Seurat_obj,
  cellType_meta,
  condition_meta,
  conditionCase,
  conditionControl,
  scale.factor = 1e+05,
  act_diff_cutoff = 2,
  exp_logFC_cutoff = 0.2,
  exp_mean_all_cutoff = 2,
  exp_fraction_case_cutoff = 0.1,
  padj_cutoff = 0.01,
  sigMatrix = "SecAct",
  is.group.sig = TRUE,
  is.group.cor = 0.9,
  lambda = 5e+05,
  nrand = 1000
)
```

Arguments

`Seurat_obj`	A Seurat object.
`cellType_meta`	Column name in meta data that includes cell-type annotations.
`condition_meta`	Column name in meta data that includes condition information.
`conditionCase`	Case condition.
`conditionControl`	Control condition.
`scale.factor`	Sets the scale factor for cell-level normalization in step2.
`act_diff_cutoff`	Cut off for activity change (i.e., z score) in step 1.
`exp_logFC_cutoff`	Cut off for log fold change in step 2.
`exp_mean_all_cutoff`	Cut off for mean expression across all cells.
`exp_fraction_case_cutoff`	Cut off for the fraction of cells expressing secreted protein-coding genes in step 2.
`padj_cutoff`	Adjusted p value cut off.
`sigMatrix`	Secreted protein signature matrix.
`is.group.sig`	A logical indicating whether to group similar signatures.
`is.group.cor`	Correlation cutoff of similar signatures.
`lambda`	Penalty factor in the ridge regression.
`nrand`	Number of randomization in the permutation test, with a default value 1000.

Value

A Seurat object.

`SecAct.CCC.scST` *Cell-cell communication from spatial data*

Description

Calculate cell-cell communication mediated by secreted proteins from spatial transcriptomics data.

Usage

```
SecAct.CCC.scST(
  SpaCET_obj,
  cellType_meta,
  scale.factor = 1000,
  radius = 20,
  ratio_cutoff = 0.2,
  padj_cutoff = 0.01,
  coreNo = 6
)
```

Arguments

`SpaCET_obj`	A SpaCET object.
`cellType_meta`	Column name in meta data that includes cell-type annotations.
`scale.factor`	Sets the scale factor for spot-level normalization.
`radius`	Radius cut off (unit: um).
`ratio_cutoff`	Ratio cut off.
`padj_cutoff`	Adjusted p value cut off.
`coreNo`	Core number in parallel computation.

Value

A Seurat object.

SecAct.check.data *Check SecAct data status*

Description

Check if SecAct data is available and show its location.

Usage

```
SecAct.check.data()
```

Value

Invisible logical indicating whether data is available.

Examples

```
SecAct.check.data()
```

SecAct.coxph.regression *Survival regression*

Description

Calculate the risk score of each secreted protein.

Usage

```
SecAct.coxph.regression(mat, surv)
```

Arguments

mat	Activity matrix.
surv	Survival matrix.

Value

A matrix.

SecAct.download.data *Download SecAct signature database*

Description

Downloads the SecAct signature matrix from GitHub Release.

Usage

```
SecAct.download.data(force = FALSE, timeout = 600)
```

Arguments

force	Logical, whether to force re-download even if file exists. Default FALSE.
timeout	Download timeout in seconds. Default 600.

Value

Invisible path to the downloaded file.

Examples

```
## Not run:
SecAct.download.data()

## End(Not run)
```

SecAct.heatmap.plot *Draw a heatmap plot*

Description

Draw a heatmap plot of secreted proteins.

Usage

```
SecAct.heatmap.plot(
  fg.mat,
  title = NULL,
  colors = c("#03c383", "#aad962", "#fbbf45", "#ef6a32")
)
```

Arguments

fg.mat	A matrix of values.
title	The title for plot.
colors	Colors.

Value

A ggplot2 object.

SecAct.inference.gsl *Secreted protein activity inference*

Description

Infer the activity of over 1000 secreted proteins from tumor gene expression profiles.

Usage

```
SecAct.inference.gsl(Y, SigMat = "SecAct", lambda = 5e+05, nrand = 1000)
```

Arguments

Y	Gene expression matrix with gene symbol (row) x sample (column).
SigMat	Secreted protein signature matrix.
lambda	Penalty factor in the ridge regression.
nrand	Number of randomization in the permutation test, with a default value 1000.

Value

A list with four items, each is a matrix. beta: regression coefficients se: standard errors of coefficients zscore: beta/se pvalue: statistical significance

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SecAct.inference.r *Secreted protein activity inference*

Description

Infer the activity of over 1000 secreted proteins from tumor gene expression profiles.

Usage

```
SecAct.inference.r(Y, SigMat = "SecAct", lambda = 5e+05, nrand = 1000)
```

Arguments

Y	Gene expression matrix with gene symbol (row) x sample (column).
SigMat	Secreted protein signature matrix.
lambda	Penalty factor in the ridge regression.
nrand	Number of randomizations in the permutation test, with a default value 1000.

Value

A list with four items, each is a matrix. beta: regression coefficients se: standard errors of coefficients zscore: beta/se pvalue: statistical significance

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SecAct.lollipop.plot *Draw a lollipop plot*

Description

Draw a lollipop plot of secreted proteins.

Usage

```
SecAct.lollipop.plot(fg.vec, title = NULL)
```

Arguments

fg.vec	A vector of values.
title	The title for plot.

Value

A ggplot2 object.

SecAct.signaling.pattern *Secreted protein signaling pattern*

Description

Calculate the signaling pattern of secreted proteins based on their activities.

Usage

```
SecAct.signaling.pattern(SpaCET_obj, scale.factor = 1e+05, radius = 200, k)
```

Arguments

SpaCET_obj	A SpaCET object.
scale.factor	Sets the scale factor for spot-level normalization.
radius	Radius cut off.
k	Number of patterns for NMF.

Value

A SpaCET object with pattern results.

Examples

```
## Not run:
SpaCET_obj <- SecAct.signaling.pattern(SpaCET_obj, k=3)

## End(Not run)
```

`SecAct.signaling.pattern.gene`
Pattern-associated secreted proteins

Description

Enumerate secreted proteins associated with each signaling pattern.

Usage

```
SecAct.signaling.pattern.gene(SpaCET_obj, n)
```

Arguments

`SpaCET_obj`	A SpaCET object.
`n`	Pattern order.

Value

A matrix.

Examples

```
## Not run:
res <- SecAct.signaling.pattern.gene(SpaCET_obj, n=3)

## End(Not run)
```

`SecAct.signaling.velocity.scST` *Secreted protein signaling velocity for single-cell ST*

Description

Calculate the signaling velocity of secreted proteins based on their activities.

Usage

```
SecAct.signaling.velocity.scST(
  SpaCET_obj,
  sender,
  secretedProtein,
  receiver,
  cellType_meta,
  scale.factor = 1e+05,
  CustomizedAreaCoordinates = NULL,
  radius = 20,
  colors_cellType = NULL
)
```

Arguments

`SpaCET_obj`	A SpaCET object.
`sender`	Sender cell types.
`secretedProtein`	Secreted proteins.
`receiver`	Receiver cell types.
`cellType_meta`	Column name in meta data that includes cell-type annotations.
`scale.factor`	Sets the scale factor for spot-level normalization.
`CustomizedAreaCoordinates`	Optional coordinates for customized area c(x.left, x.right, y.bottom, y.top).
`radius`	Radius cut off (unit: um).
`colors_cellType`	Named vector of colors for cell types.

Details

The velocity direction starts from the source cell producing a secreted protein and moves to sink cells receiving the secreted protein signal. The velocity magnitude represents the product between the secreted protein-coding gene expression at source cells and signaling activities at sink cells.

Value

A ggplot2 object.

Examples

```
## Not run:
SecAct.signaling.velocity.scST(SpaCET_obj, sender="Fibroblast",
  secretedProtein="THBS2", receiver="Tumor_boundary", cellType_meta="cellType")

## End(Not run)
```

`SecAct.signaling.velocity.spotST`

Secreted protein signaling velocity

Description

Calculate the signaling velocity of secreted proteins based on their activities.

Usage

```
SecAct.signaling.velocity.spotST(
  SpaCET_obj,
  scale.factor = 1e+05,
  gene,
  signalMode = "receiving",
  radius = 200,
  contourMap = FALSE,
  coutourBins = 11,
  animated = FALSE
)
```

Arguments

`SpaCET_obj`	A SpaCET object.
`scale.factor`	Sets the scale factor for spot-level normalization.
`gene`	Gene symbol coding a secreted protein.
`signalMode`	Mode of signaling velocity, i.e., "receiving", "sending", and "both".
`radius`	Radius cut off.
`contourMap`	A logical indicating whether transform as contour map.
`coutourBins`	Number of bins for contour map.
`animated`	A logical indicating whether generate animated figure.

Details

The velocity direction starts from the source cell producing a secreted protein and moves to sink cells receiving the secreted protein signal. The velocity magnitude represents the product between the secreted protein-coding gene expression at source cells and signaling activities at sink cells.

Value

A ggplot2 object.

Examples

```
## Not run:
SecAct.signaling.velocity.spotST(SpaCET_obj, gene="TGFB1", signalMode="receiving")
SecAct.signaling.velocity.spotST(SpaCET_obj, gene="TGFB1", signalMode="sending")

## End(Not run)
```

SecAct.survival.plot *Draw a survival plot*

Description

Draw a survival plot of secreted proteins.

Usage

```
SecAct.survival.plot(mat, surv, gene, x.title = "Time")
```

Arguments

mat	Activity matrix.
surv	Survival matrix.
gene	Gene symbol.
x.title	Title for x axis.

Value

A ggplot2 object.

Index