Package ‘SVMDO’

May 18, 2024

Title  Identification of Tumor-Discriminating mRNA Signatures via Support Vector Machines Supported by Disease Ontology

Version 1.4.0

Date  2024-02-05

Depends  R(>= 4.3), shiny (> 1.7.4)

Imports  shinyFiles (>= 0.9.3), shingtitle (> = 0.1.0), golem (> = 0.3.5), nortest (>= 1.0-4), e1071 (>= 1.7-12), BSDA (>= 1.2.1), data.table (>= 1.14.6), sjmisc (>= 2.8.9), klaR (>= 1.7-1), caTools (>= 1.18.2), caret (>= 6.0-93), survival (>= 3.4-0), DOSE (>= 3.24.2), AnnotationDbi (>= 1.60.0), org.Hs.eg.db (>= 3.16.0), dplyr (> 1.0.10), SummarizedExperiment (>= 1.28.0), grDevices, graphics, stats, utils

Description  It is an easy-to-use GUI using disease information for detecting tumor/normal sample discriminating gene sets from differentially expressed genes. Our approach is based on an iterative algorithm filtering genes with disease ontology enrichment analysis and wilk and wilk’s lambda criterion connected to SVM classification model construction. Along with gene set extraction, SVMDO also provides individual prognostic marker detection. The algorithm is designed for FPKM and RPKM normalized RNA-Seq transcriptome datasets.

biocViews  GeneSetEnrichment, DifferentialExpression, GUI, Classification, RNASeq, Transcriptomics, Survival

NeedsCompilation  no

License  GPL-3

Encoding  UTF-8

Roxygen  list(markdown = TRUE)

RoxygenNote  7.2.3

Suggests  BiocStyle, knitr, rmarkdown, testthat (>= 3.1.6)

VignetteBuilder  knitr

Config/testthat/edition  3

BugReports  https://github.com/robogeno/SVMDO/issues

git_url  https://git.bioconductor.org/packages/SVMDO
git_branch  RELEASE_3_19

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classification_server  SVMDO

description

SVMDO

Usage

innerServer_7(input, output, session)

Arguments

input server input
output server output
session server session

value

Server section of wilks lambda filtration and SVM classification of disease filtered differentially expressed gene set

classification_ui  SVMDO

description

SVMDO

Usage

innerUI_classification(id)

Arguments

id connection input
Value
UI section of wilks lambda filtration and SVM classification of disease filtered differentially expressed gene set

---

**clinic_data_input_server**  
*SVMDO*

Description
SVMDO

Usage
innerServer_clinic(input, output, session)

Arguments
- input: server input
- output: server output
- session: server session

Value
Server section of loading clinical data

---

**clinic_data_input_ui**  
*SVMDO*

Description
SVMDO

Usage
innerUI_clinic_data(id)

Arguments
- id: connection input

Value
UI section of loading clinical data
deg_server  

**Description**

SVMDO

**Usage**

innerServer_3(input, output, session, rawData, rval)

**Arguments**

- input: server input
- output: server output
- session: server session
- rawData: expression dataset provided from innerServer_exp_server
- rval: Selected radio button information provided from innerServer_rad_server

**Value**

Server section of differential gene expression analysis

deg_ui  

**Description**

SVMDO

**Usage**

innerUI_deg_analysis(id)

**Arguments**

- id: connection input

**Value**

UI section of differential gene expression analysis
**disc_gene_download_ui**  

**Description**

SVMDO

**Usage**

\[ \text{disc_gene_download_ui}(id) \]

**Arguments**

- **id**: connection input

**Value**

UI section of discriminative gene set download button

---

**disc_gene_dw_server**  

**Description**

SVMDO

**Usage**

\[ \text{disc_gene_dw_server}(\text{input}, \text{output}, \text{session}, \text{gene_list_val}) \]

**Arguments**

- **input**: server input
- **output**: server output
- **session**: server session
- **gene_list_val**: discriminative gene set list variable

**Value**

Server section of discriminative gene set download button
do_based_gene_filtration_server

SVMDO

Description
SVMDO

Usage
innerServer_6(input, output, session)

Arguments
- input: server input
- output: server output
- session: server session

Value
Server section of disease ontology based filtration of differentially expressed genes

---

do_based_gene_filtration_ui

SVMDO

Description
SVMDO

Usage
innerUI_disease_ont_class(id)

Arguments
- id: connection input

Value
UI section of disease ontology based filtration of differentially expressed genes
expression_dataset_input_server

Description
SVMD0

Usage
innerServer_exp(input, output, session)

Arguments
input server input
output server output
session server session

Value
Server section of providing expression dataset

gene_directory_selection_server

Description
SVMD0

Usage
innerServer(input, output, session)

Arguments
input server input
output server output
session server session

Value
Server section of entering output/working for gene list directory
<table>
<thead>
<tr>
<th>Method</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>gene_directory_selection_ui</code></td>
<td>SVMDO</td>
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<td><code>innerUI_path(id)</code></td>
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</tr>
<tr>
<td><code>id</code></td>
<td>connection input</td>
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<tr>
<td><strong>Value</strong></td>
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</tr>
<tr>
<td></td>
<td>UI section of entering output/working for gene list directory</td>
</tr>
</tbody>
</table>

<table>
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<th>Description</th>
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</thead>
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<td>SVMDO</td>
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<td>server input</td>
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<tr>
<td><code>output</code></td>
<td>server output</td>
</tr>
<tr>
<td><code>session</code></td>
<td>server session</td>
</tr>
<tr>
<td><strong>Value</strong></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Server section of entering final gene list name</td>
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</tbody>
</table>
gene_list_table_visualization_ui

<table>
<thead>
<tr>
<th>gene_list_name_ui</th>
<th>SVMDO</th>
</tr>
</thead>
</table>

**Description**

SVMDO

**Usage**

innerUI_gene_names(id)

**Arguments**

id | connection input

**Value**

UI section of entering top gene value

---

gene_list_table_visualization_ui

<table>
<thead>
<tr>
<th>gene_list_table_visualization_ui</th>
<th>SVMDO</th>
</tr>
</thead>
</table>

**Description**

SVMDO

**Usage**

deg_data_table_ui(id)

**Arguments**

id | connection input

**Value**

Providing table form of discriminative gene sets in GUI
**globals**

<table>
<thead>
<tr>
<th><strong>Description</strong></th>
<th><strong>SVMDO</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td>Including script files and global variables of GUI required to be initiated at the runApp file execution</td>
<td></td>
</tr>
</tbody>
</table>

**gui_obj_removal_server**

<table>
<thead>
<tr>
<th><strong>Description</strong></th>
<th><strong>SVMDO</strong></th>
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</thead>
<tbody>
<tr>
<td>SVMDO</td>
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<table>
<thead>
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**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
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<tbody>
<tr>
<td>input</td>
<td>server input</td>
</tr>
<tr>
<td>output</td>
<td>server output</td>
</tr>
<tr>
<td>session</td>
<td>server session</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th><strong>Value</strong></th>
<th></th>
</tr>
</thead>
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<td>Server section of workspace clearance</td>
<td></td>
</tr>
</tbody>
</table>
gui_obj_removal_ui SVMDO

Description

SVMDO

Usage

innerUI_clear_env(id)

Arguments

id connection input

Value

UI section of workspace clearance

innerServer_exp_ui SVMDO

Description

SVMDO

Usage

innerUI_exp_data(id)

Arguments

id connection input

Value

UI section of providing expression dataset into GUI
package_req_list

Description

SVMDO

Value

List of packages involved in SVMDO

plot_list_server

Description

SVMDO

Usage

plot_list_server(input, output, session)

Arguments

input server input
output server output
session server session

Value

Server section of preparing plot list to be visualized in GUI page
plot_list_ui  SVMDO

Description
SVMDO

Usage
innerUI_collect_plot_data(id)

Arguments
id  connection output

Value
UI section of preparing plot list to be visualized in GUI page

plot_push_server  SVMDO

Description
SVMDO

Usage
plot_push_server(input, output, session)

Arguments
input  server input
output  server output
session  server session

Value
Server section of providing information about total number of survival plots for visualization
plot_push_ui

Description
SVMDO

Usage
innerUI_plot_inject(id)

Arguments
id connection input

Value
UI section of providing information about total number of survival plots for visualization

plot_show_server

Description
SVMDO

Usage
plot_show_server(input, output, session, max_data)

Arguments
input server input
output server output
session server session
max_data Information of total number of survival plots prepared with discriminative gene set

Value
Server section of providing information about total number of survival plots for visualization
**Description**

SVMDO

**Usage**

innerUI_plot_show(id)

**Arguments**

- id: connection input

**Value**

UI section of providing information about total number of survival plots for visualization

---

**Description**

SVMDO

**Usage**

linebreaks(n)

**Arguments**

- n: linebreak function variable

**Value**

Returning GUI window screen

**Examples**

```r
#SVMDO::runGUI() Calling GUI without activating library
#runGUI() Calling GUI after activating library
# Disease Ontology Enrichment of a differentially expressed gene (entrez id): a_1c<-DOSE::enrichDO(2981,ont="DO")
```
survival_analysis_server

SVMDO

Description
SVMDO

Usage
innerServer_8(input, output, session, rawData_2, rval)

Arguments
- input: server input
- output: server output
- session: server session
- rawData_2: Clinical data provided from clinic_data_input_server
- rval: Selected radio button information provided from innerServer_rad_server

Value
Server section of survival analysis of final discriminative gene set

survival_analysis_ui

SVMDO

Description
SVMDO

Usage
innerUI_surv(id)

Arguments
- id: connection input

Value
UI section of survival analysis of final discriminative gene set
surv_plot_dw_server  SVMDO

Description

SVMDO

Usage

surv_plot_dw_server(input, output, session)

Arguments

  input     server input
  output    server output
  session   server session

Value

Server section of downloading survival plots of discriminative gene set

surv_plot_dw_ui  SVMDO

Description

SVMDO

Usage

surv_plots_download_ui(id)

Arguments

  id         connection input

Value

UI section of downloading survival plots of discriminative gene set
Description

Package Description: It is an easy-to-use GUI using disease information for detecting tumor/normal sample discriminating gene sets from differentially expressed genes. Our approach is based on an iterative algorithm filtering genes with disease ontology enrichment analysis and wilk’s lambda criterion connected to SVM classification model construction. Along with gene set extraction, SVMDO also provides individual prognostic marker detection among the discriminative genes. The algorithm is designed for FPKM and RPKM normalized RNA-Seq transcriptome datasets. To provide experience about the GUI usage, a test section involving dummy example using SummarizedExperiment objects of transcriptome (small form) and clinical datasets is also included.

Value

Providing package-level manual page

Package Sections

1. Analysis: Acquiring discriminative gene sets and further detecting the gene subset with prognostic characteristics
2. Result: Visualization and Download of discriminative gene sets and survival plot list of prognostic genes

Steps of Analysis Screen

1. To search your transcriptome dataset, use the file detection in Choose Your Expression Dataset section. The file will be automatically uploaded into the GUI.
2. To prevent clashing with test datasets, "None" option has to be selected from the radio button section.
3. By clicking on DEG Analysis button you further apply differential expression analysis. Labels of tissue_type column in dataset must contain “Nor” and “Tum” for determining normal/tumour (or tumor) samples. A message window saying Process Completed will appear if there is not any problem.
4. When the differential expression process is completed, a user-defined input size (n) is selected to filter the initial gene list (i.e., n number of upregulated and downregulated genes) by entering a number in Input Size section. It is predetermined as 50 in GUI which can be changed based on the user. If there is problem with the value of input size, you will get a warning about inappropriate input size selection. If the input size remains, algorithm selects all of the differentially expressed genes to be used in the next process.
5. To apply disease ontology-based gene filtration, click on DO Analysis button. A message window saying process completed will appear if there is not any problem.
6. To further apply the following feature selection and classification processes, click on the Classification button. A message window saying process completed will appear if there is not any problem.
7. Acquired discriminative gene set can be further used for survival analysis to detect individual prognostic genes. To apply this process, use the file detection in Choose Clinical Data section for searching clinical data about patient survival followed by clicking on Survival Analysis button.

Steps of Result Screen

1. To visualize discriminative gene sets inside GUI screen, click on Show Gene Results button. When you click this button, a table of gene set will appear. If there is a problem in the analysis, an error message will appear.

2. To visualize survival plots of individual genes, two steps have to be applied. First of all, click on Prepare Plot Lists button to feed plot information to the visualization system. After that, click on Show Plots button to visualize survival plots.

3. Before downloading files, you can adjust the output directory with Choose Directory button. It can be used for separating files by selecting a destination before clicking download buttons. If it is desired, files can be downloaded to the same folder by selecting an output directory just one time before the download steps. If you do not select any output directory, files will be downloaded to your working directory.

4. To download the resulting discriminative gene set, it is obligatory to define a filename in the Enter Final Gene Set Filename section. After that, you can click on Download Gene List button to complete the process.

5. To download survival plots, you have to click on Download Plot List button. Names of plot files are automatically done by assigning gene names.

Application of Test Datasets

SVMDO includes test datasets providing dummy examples for gaining experience on the GUI usage. Test datasets consist of simplified forms of TCGA-COAD (COAD) and TCGA-LUSC (LUSC) with 400 genes along with clinical datasets loaded into summarized experiment objects. When test datasets are used, predetermined expression and clinical datasets are automatically uploaded into the GUI. A test-based analysis is done with predefined input size (n=50). Therefore, users have to continue with DO Analysis after DEG Analysis.

Workspace Clearance

When the user task is completed, click on the Clear Environment button to remove the global variables created during the algorithm sections. To prevent error in the next usages of GUI, it is a necessary process. It can be applied at any moment without the necessity of completing all of the steps of algorithm.
**table_ui**

**Usage**

   table_server(input, output, session)

**Arguments**

   input server input  
   output server output  
   session server session  

**Value**

Server section of providing discriminative gene set for preparing table

---

**Description**

SVMDO

**Usage**

   innerUI_table_show(id)

**Arguments**

   id connection input  

**Value**

UI section of providing discriminative gene set for preparing table

---

**test_data_selection_server**

**SVMDO**

---

**Description**

SVMDO

**Usage**

   innerServer_rad(input, output, session)
Arguments

input  server input
output  server output
session  server session

Value

Server section of providing information about selected radio button

test_data_selection_ui

Description

SVMDO

Usage

innerUI_test_data(id)

Arguments

id  connection input

Value

UI section of providing information about selected radio button

top_val_based_deg_filtration

Description

SVMDO

Usage

innerServer_5(input, output, session, top_val)
Arguments

input  server input
output  server output
session  server session
top_val  top gene number value provided from top_val_server

Value

Server section of selecting differentially expressed genes based on top gene value

top_val_based_deg_filtration_ui

Description
SVMDO

Usage
innerUI_top_gene_selection(id)

Arguments
id  connection input

Value
UI section of selecting differentially expressed genes based on top gene value

top_val_server

Description
SVMDO

Usage
innerServer_4(input, output, session)

Arguments
input  server input
output  server output
session  server session
**Value**

Server section of entering top gene value

**Description**

SVMDO

**Usage**

`innerUI_top_gene_val(id)`

**Arguments**

`id` connection input

**Value**

UI section of entering top gene value
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