Package 'tripr'

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Type Package

Title T-cell Receptor/Immunoglobulin Profiler (TRIP)

Version 1.17.0

Description TRIP is a software framework that provides analytics services on antigen receptor (B cell receptor immunoglobulin, BcR IG | T cell receptor, TR) gene sequence data. It is a web application written in R Shiny. It takes as input the output files of the IMGT/HighV-Quest tool. Users can select to analyze the data from each of the input samples separately, or the combined data files from all samples and visualize the results accordingly.

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Encoding UTF-8

biocViews BatchEffect, MultipleComparison, GeneExpression, ImmunoOncology, TargetedResequencing

Imports shinyjs, shinyFiles, plyr, data.table, DT, stringr, stringdist, plot3D, gridExtra, RColorBrewer, plotly, dplyr, config (>= 0.3.1), golem (>= 0.3.1), methods, grDevices, graphics, stats, utils, vegan

Enhances parallel

Suggests BiocGenerics, shinycssloaders, tidyverse, BiocManager, Biostrings, xtable, rlist, motifStack, knitr, rmarkdown, testthat (>= 3.0.0), fs, BiocStyle, RefManageR, biocthis, pryr

Depends shiny (>= 1.6.0), shinyBS

Collate ``tripr-package.R'' ``global.R'' ``helpers.R'' ``run_TRIP_without_ui.R'' ``app_config.R'' ``app_server.R'' ``app_ui.R'' ``run_app.R'' ``zzz.R''

URL https://github.com/BiodataAnalysisGroup/tripr

BugReports https://github.com/BiodataAnalysisGroup/tripr/issues

BiocType Software

RoxygenNote 7.3.1

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Contents

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run_app   *Run the Shiny Application*

Description

Run the Shiny Application

Usage

```
run_app(
  onStart = NULL,
  options = list(launch.browser = TRUE),
  enableBookmarking = NULL,
```

```
    uiPattern = "/",
    ...
)
```

Arguments

onStart   A function that will be called before the app is actually run. This is only needed
      for shinyAppObj, since in the shinyAppDir case, a global.R file can be used
      for this purpose.

options   Named options that should be passed to the runApp call (these can be any of
      the following: "port", "launch.browser", "host", "quiet", "display.mode" and
      "test.mode"). You can also specify width and height parameters which pro-
      vide a hint to the embedding environment about the ideal height/width for the
      app.

enableBookmarking
      Can be one of "url", "server", or "disable". The default value, NULL, will re-
      spect the setting from any previous calls to enableBookmarking(). See enableBookmarking()
      for more information on bookmarking your app.

uiPattern   A regular expression that will be applied to each GET request to determine whether
      the ui should be used to handle the request. Note that the entire request path
      must match the regular expression in order for the match to be considered suc-
      cessful.

...   arguments to pass to golem_opts. See '?golem::get_golem_options' for more
      details.

Value

None

Examples

```
if (interactive()) {
    run_app(options = list(launch.browser = FALSE))
}
```

---

run_TRIP   *Run tripr analysis via R command line*

Description

run_TRIP() is a wrapper of {tripr} shiny analysis tool for use via R command line. Output of
analysis is saved in *tripr/extdata/output* folder, where R libraries are saved (typically *R/library*).

Usage

```
run_TRIP(
  datapath = fs::path_package("extdata", "dataset", package = "tripr"),
  output_path = fs::path_home("Documents/tripr_output"),
  filelist = c("1_Summary.txt", "2_IMGT-gapped-nt-sequences.txt",
    "4_IMGT-gapped-AA-sequences.txt", "6_Junction.txt"),
  cell = "Bcell",
  throughput = "High Throughput",
  preselection = "1,4C:W",
  selection = "5",
  identity_range = "85:100",
  vgenes = "",
  dgenes = "",
  jgenes = "",
  cdr3_length_range = "",
  aminoacid = "",
  pipeline = "1",
  select_clonotype = "V Gene + CDR3 Amino Acids",
  highly_sim_params = paste0("1-1 2-1 3-1 4-1 5-1 6-1 7-1 8-1 9-1 10-1 11-1 ",
    "12-1 13-1 14-1 15-2 16-2 17-2 18-2 19-2 20-2 21-2 23-2 24-2 25-2 ",
    "26-2 27-2 28-2 29-3 30-3 31-3 32-3 33-3 34-3 35-3 36-3 37-3 38-3 ",
    "39-3 40-3 41-3 42-3 43-3 44-3 45-3 46-3 47-3 48-3 49-3 50-3,1,Yes"),
  shared_clonotypes_params = "reads,1,Yes",
  highly_shared_clonotypes_params = "reads,1,Yes",
  repertoires_params = "1,4,6",
  identity_groups = "85:97,97:99,99:100,100:100",
  multiple_values_params = "2:7,2:3,2:5,2:11",
  alignment_params = "1,both,1,2:20",
  mutations_params = "both,0.5,0.5,2:20"
)
```

Arguments

datapath	(character) The directory where the folders of the data is located. Note that every sample of the dataset must have **its own individual folder** and every sample folder must be in **one root folder**. Note that **every** file in the root folder will be used in the analysis. Supposedly the dataset is in user's *Documents/* folder, one could use: fs::path_home("Documents", "dataset"), with the help of [path_home](#) function. See the package vignette for more.
output_path	(character) The directory where the output data will be stored. Please provide a valid path, ideally the same way as datapath by using the [path_home](#) function. The default value points to *Documents/tripr_output* directory.
filelist	(character vector) The character vector of files of the IMGT output that will be used through the analysis from each sample.
cell	(character) 'Bcell' (default) or 'Tcell'.
throughput	(character) 'High Throughput' (default) or 'Low Throughput'.

preselection   (character) Preselection options:
                 1 == Only take into account Functional V-Gene,
                 2 == Only take into account CDR3 with no Special Characters (X,*,#,.),
                 3 == Only take into account Productive Sequences,
                 4 == Only take into account CDR3 with valid start/end landmarks.,
                 For Preselection option 4, select start/end landmarks.,
                 Use the vertical line 'l' to add more than one start or end landmarks,
                 Use comma ',' to seperate the list of options, use semicolon ':' to seperate start
                 and end landmarks.

selection   (character) Selection options:
                 5 == V-REGION identity 6 == Select Specific V Gene ,
                 7 == Select Specific J Gene ,
                 8 == Select Specific D Gene ,
                 9 == Select CDR3 length range ,
                 10 == Only select CDR3 containing specific amino-acid sequence.
                 Use comma ',' to seperate the list of options.

identity_range   (character) V-REGION identity Use colon ':' to seperate identity low and high

vgenes   (character) Filter in specific V Genes,
                 Separate the different V-Gene names with 'l' e.g. TRBV11-2|TRBV29-1*03 (F)

dgenes   (character) Filter in specific D Genes,
                 Separate the different D-Gene names with | e.g. TRBD2|TRBD1

jgenes   (character) Filter in specific J Genes,
                 Separate the different J-Gene names with | e.g. TRBJ2-6|TRBJ2-2

cdr3_length_range
                 (character) Filter in rows with CDR3 lengths within a range,
                 Use colon ':' to seperate identity low and high

aminoacid   (character) Filter in rows with CDR3 containing specific amino-acid sequence

pipeline   (character) Pipeline options:
                 1 == Clonotypes Computation,
                 2 == Highly Similar Clonotypes computation,
                 3 == Shared Clonotypes Computation,
                 4 == Highly Similar Shared Clonotypes Computation,
                 5 == Repertoires Extraction,
                 6 == Repertoires Comparison,
                 7 == Highly Similar Repertoires Extraction,
                 8 == Insert Identity groups,
                 9 == Somatic hypermutation status,
                 10 == CDR3 Distribution,
                 11 == Pi Distribution,
                 12 == Multiple value comparison,
                 13 == CDR3 with 1 length difference,
                 14 == Alignment,
                 15 == Somatic hypermutations,
                 16 == Logo,
                 17 == SHM normal,
                 18 == SHM High similarity,

19 == Diagnosis,
Use comma ',' to seperate the list of options

select_clonotype

(character) Compute clonotypes.
Select one the following options:
"V Gene + CDR3 Amino Acids",
"V Gene and Allele + CDR3 Amino Acids",
"V Gene + CDR3 Nucleotide",
"V Gene and Allele + CDR3 Nucleotide",
"J Gene + CDR3 Amino Acids",
"J Gene and Allele + CDR3 Amino Acids",
"J Gene + CDR3 Nucleotide",
"J Gene and Allele + CDR3 Nucleotide",
"CDR3 Amino Acids",
"CDR3 Nucleotide",
"Sequence

highly_sim_params

(character) Select number of missmatches, the threshold of the clonotype fre-
quency and whether you want to take gene into account. Use dashes '-' to show
the length of the CDR3 sequences and the number of allowed missmatches and
spaces ' ' to separate. For the CDR3 lengths with not specified number of miss-
matches the default value is 1. Use comma ',' to separate the three options.

shared_clonotypes_params

(character) Shared clonotypes computation.
Select 'reads' of 'threshold' for clonotypes, the number of reads or the threshold
percentage accordingly, and whether you want to take gene into account. Use
comma ',' to seperate the 3 options

highly_shared_clonotypes_params

(character) Highly Similar Shared Clonotypes Computation
Select 'reads' of 'threshold' for clonotypes, the number of reads or the threshold
percentage accordingly, and whether you want to take gene into account. Use
comma ',' to seperate the 3 options

repertoires_params

(character) Repertoires Extraction
Options:
1 == V Gene
2 == V Gene and allele
3 == J Gene
4 == J Gene and allele
5 == D Gene
6 == D Gene and allele
Use comma ',' to seperate the selected options

identity_groups

(character) Insert identity groups
Insert low and high values as follows:
low_values:high_values
Seperate low_values and high_values using comma ','.

multiple_values_params

> (character) Multiple value comparison
> Options:
> 1 == V GENE
> 2 == V GENE and allele
> 3 == J GENE
> 4 == J GENE and allele
> 5 == D GENE
> 6 == D GENE and allele
> 7 == CDR3-IMGT length
> 8 == D-REGION reading frame
> 9 == Molecular mass
> 10 == pI
> 11 == V-REGION identity Use colon ':' to indicate combinations of 2 values,
> use comma "," to seperate the selected options

alignment_params

> (character) Alignment parameters:
> Region for Alignment: 1 == V.D.J.REGION or 2 == V.J.REGION
> AA or Nt: Select 'aa' or 'nt' or 'both'
> Germline: 1 == Use Allele's germline or 2 == Use Gene's germline
> Use: 1 == All clonotypes or 2 == Select top N clonotypes or 3 == Select threshold for clonotypes
> Use comma ',' to seperate the 4 parameters. If you select option 2 or 3 at the 4th
> parameter you have to set the N or the threshold as well using colon ':'.

mutations_params

> (character) Somatic hypermutations parameters:
> AA or Nt: Select 'aa' or 'nt' or 'both'
> Set threshold for AA
> Set threshold for Nt
> Use: 1 == All clonotypes or 2 == Select top N clonotypes or 3 == Select threshold for clonotypes
> Use comma ',' to seperate the 3 parameters. If you select option 2 or 3 at the 3rd
> parameter you have to set the N or the threshold as well using colon ':'.

Value

None

Examples

```
## Do not run

run_TRIP(
    output_path=tools::R_user_dir("tripr", which="cache"),
    filelist=c("1_Summary.txt", "2_IMGT-gapped-nt-sequences.txt",
        "4_IMGT-gapped-AA-sequences.txt", "6_Junction.txt"),
    cell="Bcell",
    throughput="High Throughput",
    preselection="1,2,3,4C:W",
```

```
selection="5",
identity_range="88:100",
cdr3_length_range="",
pipeline="1",
select_clonotype="V Gene + CDR3 Amino Acids")
```

---

tripr	*tripr*

Description

T-cell Receptor/Immunoglobulin Profiler (TRIP)

Details

The only function you're likely to need from tripr is [run_app()]. Otherwise refer to the vignettes for using tripr.

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See Also

Useful links:

- https://github.com/BiodataAnalysisGroup/tripr
- Report bugs at https://github.com/BiodataAnalysisGroup/tripr/issues

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