

# Package: tripr (via r-universe)

June 22, 2024

**Type** Package

**Title** T-cell Receptor/Immunoglobulin Profiler (TRIP)

**Version** 1.11.0

**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.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** false

**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

**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** 7.2.0**VignetteBuilder** knitr**Config/testthat/edition** 3**Repository** https://bioc.r-universe.dev**RemoteUrl** https://github.com/bioc/tripr**RemoteRef** HEAD**RemoteSha** 32a5a993cac0f677826033decfc256873f8445af

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run_app	<i>Run the Shiny Application</i>
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## 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 provide 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 respect the setting from any previous calls to <code>enableBookmarking()</code> . See <code>enableBookmarking()</code> 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 successful.
...	arguments to pass to <code>golem_opts</code> . See <code>'?golem::get_golem_options'</code> 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 <b>its own individual folder</b> and every sample folder must be in <b>one root folder</b> . Note that <b>every</b> file in the root folder will be used in the analysis. Supposedly the dataset is in user's <i>Documents/</i> folder, one could use: <code>fs::path_home("Documents", "dataset")</code> , with the help of <a href="#">path_home</a> 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 <a href="#">path_home</a> function. The default value points to <i>Documents/tripr_output</i> 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 ' ' to add more than one start or end landmarks, Use comma ',' to separate the list of options, use semicolon ':' to separate 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 separate the list of options.
identity_range	(character) V-REGION identity Use colon ':' to separate identity low and high

vgenes (character) Filter in specific V Genes,  
Separate the different V-Gene names with '|' 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 separate 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 separate 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 mismatches and spaces ' ' to separate. For the CDR3 lengths with not specified number of mismatches 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 separate 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 separate 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 separate the selected options

#### identity\_groups

(character) Insert identity groups

Insert low and high values as follows:

low\_values:high\_values

Separate 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 separate 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 separate 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

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 separate 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

## 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")
```

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tripr

*tripr*

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## 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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