Package ‘IMGTStatClonotype’

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Type Package

Title Pairwise evaluation and visualization of IMGT clonotype (AA) diversity and expression from IMGT/HighV-QUEST output

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Imports reshape2 (>= 1.4.4), data.table (>= 1.12.8), multtest (>= 2.44.0), ggplot2 (>= 3.3.2), gridExtra (>= 2.3), DT (>= 0.14), shiny (>= 1.5.0), shinyjs(>= 1.1), colourpicker (>= 1.0), plotly(>= 4.9.2.1), d3heatmap(>= 0.6.1)

Description ‘IMGTStatClonotype’ developed by LIGM (Montpellier University, CNRS) and part of IMGT®, the international ImMunoGeneTics information system® (http://www.imgt.org) is an R package for statistical analysis of sets from IMGT/HighV-QUEST output. IMGT/HighV-QUEST is the IMGT web portal for next generation sequencing (NGS) analysis of immunoglobulins (IG) or antibodies and T cell receptor (TR) sequences. It provides a standardized and high quality output including the characterization of the IMGT clonotype (AA) diversity and expression and their comparison in up to one million sequences. ‘IMGTStatClonotype’ includes a generic and standardized procedure for evaluating the statistical significance of pairwise comparison between differences in proportions of the IMGT clonotypes (AA) diversity and expression per gene of a given IG or TR variable (V), diversity (D) or joining (J) group. The package ‘IMGTStatClonotype’ incorporates a user-friendly web interface, allowing use of the IMGT/StatClonotype tool, in users’ own browser.

URL http://www.imgt.org/StatClonotype/

License LGPL

LazyData TRUE

Encoding UTF-8

RoxygenNote 7.1.0

NeedsCompilation no

R topics documented:

clonNumDiv

2
clonNumDiv

Numbers of IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output for clonotype diversity

Description

This function allows the creation of a matrix containing the number of IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output with an IMGT gene of a given IMGT V, D or J group (IMGT clonotypes (AA) diversity).

Usage

clonNumDiv(data1, data2)

Arguments

data1 the first set from the IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function clonRem

data2 the second set from the IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function clonRem

Value

Matrix with IMGT gene names in rows and numbers of IMGT clonotypes (AA) in columns.

Examples

## Not run:
Ndiv<-clonNumDiv(MID1,MID2)

## End(Not run)
**clonNumExp**

*Numbers of IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output for clonotype expression*

**Description**

This function allows the creation of a matrix containing the number of sequences assigned to IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output with an IMGT gene of a given IMGT V, D or J group (IMGT clonotypes (AA) expression).

**Usage**

```r
clonNumExp(data1, data2)
```

**Arguments**

- `data1`: the first set from the IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function `clonRem`
- `data2`: the second set from the IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function `clonRem`

**Value**

Matrix with IMGT gene names in rows and numbers of IMGT clonotypes (AA) in columns.

**Examples**

```r
### Not run:
Nexp<-clonNumExp(MID1,MID2)
### End(Not run)
```

---

**clonRem**

*CDR3-IMGT outlier length*

**Description**

This function removes IMGT clonotypes (AA) with CDR3-IMGT outlier lengths depending on the studied species (for *Homo sapiens* by default >=45 and <=4).

**Usage**

```r
clonRem(set, min = 4, max = 45)
```

**Arguments**

- `set`: the set from the IMGT/HighV-QUEST output to be compared
- `min`: the lower level of CDR3-IMGT length
- `max`: the upper level of CDR3-IMGT length
Value

This function returns sets from the IMGT/HighV-QUEST output without IMGT clonotypes (AA) having CDR3-IMGT outlier lengths. A matrix of 25 columns:

<table>
<thead>
<tr>
<th>Column</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>cdr3aa</td>
<td>CDR3-IMGT sequence (AA)</td>
</tr>
<tr>
<td>expid</td>
<td>Experimental ID</td>
</tr>
<tr>
<td>clonoIndex</td>
<td>Representative sequence index</td>
</tr>
<tr>
<td>onecopy</td>
<td>Nb of ’1 copy’</td>
</tr>
<tr>
<td>morethanone</td>
<td>Nb of ’More than one’</td>
</tr>
<tr>
<td>total</td>
<td>Total nb of ’1 copy’ and ’More than one’</td>
</tr>
<tr>
<td>indexes</td>
<td>’1 copy’ Indexes</td>
</tr>
<tr>
<td>vgene</td>
<td>V-gene</td>
</tr>
<tr>
<td>vallele</td>
<td>V-allele</td>
</tr>
<tr>
<td>dgene</td>
<td>D-gene</td>
</tr>
<tr>
<td>dallele</td>
<td>D-allele</td>
</tr>
<tr>
<td>jgene</td>
<td>J-gene</td>
</tr>
<tr>
<td>jallele</td>
<td>J-allele</td>
</tr>
<tr>
<td>cdr1</td>
<td>CDR1-IMGT</td>
</tr>
<tr>
<td>cdr2</td>
<td>CDR2-IMGT</td>
</tr>
<tr>
<td>gcdr1</td>
<td>CDR1-IMGT gapped sequence (AA)</td>
</tr>
<tr>
<td>gcdr2</td>
<td>CDR2-IMGT gapped sequence (AA)</td>
</tr>
<tr>
<td>pid</td>
<td>% identity with the closest germline IMGT V gene and allele</td>
</tr>
<tr>
<td>length</td>
<td>Sequence length</td>
</tr>
<tr>
<td>c104</td>
<td>C104 (1st-CYS)</td>
</tr>
<tr>
<td>f118</td>
<td>F118 or W118 (J-PHE or J-TRP)</td>
</tr>
<tr>
<td>anchors</td>
<td>Anchors (C104, F118 or W118)</td>
</tr>
<tr>
<td>seqid</td>
<td>Sequence ID</td>
</tr>
<tr>
<td>functionality</td>
<td>Functionality</td>
</tr>
<tr>
<td>sequenceFileName</td>
<td>Sequence file number</td>
</tr>
<tr>
<td>sequenceClonotypeFileName</td>
<td>Sequence clonotype file number</td>
</tr>
</tbody>
</table>

Examples

```r
## Not run:
data(MID1)
data(MID2)
MID1<-clonRem(MID1)
MID2<-clonRem(MID2)

## End(Not run)
```
diffpropGph

Differences in proportions graph

Description

This function draws the graph of differences in proportions of IMGT clonotypes (AA) (or sequences assigned to IMGT clonotypes (AA)) with significance and confidence interval (CI) bars.

Usage

diffpropGph(data, ...)

Arguments

data the data issued from the function `sigrepDiv` for clonotype diversity and from the function `sigrepExp` for clonotype expression
... optional parameters

Value

Graph of differences in proportions of IMGT clonotypes (AA) (or sequences assigned to IMGT clonotypes (AA)) in the two compared sets from the IMGT/HighV-QUEST output with significance and confidence interval (CI) bars.

Examples

```r
## Not run:
diffpropGph(div)$Vgenes
diffpropGph(div)$Jgenes
diffpropGph(div)$Dgenes
diffpropGph(exp)$Vgenes
diffpropGph(exp)$Jgenes
diffpropGph(exp)$Dgenes

## End(Not run)
```

Genelist

List of IMGT genes (data)

Description

The data contains the list of IMGT gene names ordered by their positions in the locus. This order is considered in the results visualization.

Usage

data("Genelist")
Format
A data frame with 4722 observations (rows) and 4 variables (columns). Rows represent the list of IMGT gene names (first column) ordered depending on species (second column), IMGT gene names with functionality (3rd column) and the locus (4th column).

Source
http://www.imgt.org/IMGTrepertoire/LocusGenes/

References

launch

Description
This function launches the application IMGT/StatClonotype pairwise comparisons through a user-friendly interface in the web browser.

Usage
launch()

Value
An interaction tool to visualize pairwise comparison between sets from IMGT/HighV-QUEST output. If no errors occurred this function returns (NULL) else it returns error(s) message(s) shown in the R console.

Examples
```r
## Not run:
launch()

## End(Not run)```
meltgene

**List of IMGT V and J genes**

**Description**

This function allows the creation of a new matrix grouping the columns vgene, dgene and jgene in one column with their identifier (ID).

**Usage**

```r
meltgene(data, ..., variable.name = "Gene_Type", value.name = "Gene_Name")
```

**Arguments**

- `data`: a set from the IMGT/HighV-QUEST output
- `...`: further arguments passed to or from other methods
- `variable.name`: name of variable used to store measured variable names, by default "Gene_Type"
- `value.name`: name of variable used to store values, by default "Gene_Name"

**Details**

This function must be applied for the two sets from the IMGT/HighV-QUEST output to be compared. It is based on the function `melt` of the package `reshape2`.

**Value**

New matrix with 4 columns: "expid" (Experimental ID), "total" (Total nb of '1 copy' and 'More than one'), "Gene_Type" (V D or J genes), "Gene_Name" (Gene names).

**References**


**Examples**

```r
## Not run:
set1<-meltgene(MID1)
set2<-meltgene(MID2)

## End(Not run)
```
Description

The data of one set from IMGT/HighV-QUEST output used here as an example.

Usage

data("MID1")

Format

A data frame with 2348 observations on the following 26 variables:
cdr3aa: CDR3-IMGT sequence (AA)
expid: Experimental ID
clonoIndex: Representative sequence index
onecopy: Nb of ’1 copy’
morethanone: Nb of ’More than one’
total: Total nb of ’1 copy’ and ’More than one’
indexes: ’1 copy’ Indexes
vgene: V-gene
vallele: V-allele
dgene: D-gene
dallele: D-allele
jgene: J-gene
jallele: J-allele
cdr1: CDR1-IMGT
cdr2: CDR2-IMGT
gcdr1: CDR1-IMGT gapped sequence (AA)
gcdr2: CDR2-IMGT gapped sequence (AA)
pid: % identity with the closest germline IMGT V gene and allele
length: Sequence length
c104: C104 (1st-CYS)
f118: F118 or W118 (J-PHE or J-TRP)
anchors: Anchors (C104, F118 or W118)
seqid: Sequence ID
functionality: Functionality
sequenceFileNumber: Sequence file number
sequenceClonoFileNumber: Sequence clonotype file number
Source

Sequencing data used for this example is available in the NCBI Sequence Read Archive under the accession code SRX326382. The description of this data is available in Li S. et al. (2013).

References

Alamyar E., Giudicelli V., Li S., Duroux P., Lefranc M.-P. (2012) IMGT/High V-QUEST: The IMGT web portal for immunoglobulin (IG) or antibody and T cell receptor (TR) analysis from NGS high throughput and deep sequencing. Immunome Research. 8:1.2. doi: 10.4172/1745-7580.1000056. PMID: 22647994.


Examples

data(MID1)
str(MID1)

<table>
<thead>
<tr>
<th>MID2</th>
<th>CD4+ population at Pre-vaccination IMGT/HighV-QUEST output</th>
</tr>
</thead>
</table>

Description

The data of one set from IMGT/HighV-QUEST output used here as an example.

Usage

data("MID2")

Format

A data frame with 1882 observations on the following 26 variables:
cdr3aa: CDR3-IMGT sequence (AA)
expid: Experimental ID
clonoIndex: Representative sequence index
onecopy: Nb of '1 copy'
morethanone: Nb of 'More than one'
total: Total nb of '1 copy' and 'More than one'
indexes: '1 copy' Indexes
v gene: V-gene
vallele: V-allele
dgene: D-gene
dallele: D-allele
jgene: J-gene
jallele: J-allele
cdr1: CDR1-IMGT
cdr2: CDR2-IMGT
gcdr1: CDR1-IMGT gapped sequence (AA)
gcdr2: CDR2-IMGT gapped sequence (AA)
pid: % identity with the closest germline IMGT V gene and allele
length: Sequence length
c104: C104 (1st-CYS)
f118: F118 or W118 (J-PHE or J-TRP)
anchors: Anchors (C104, F118 or W118)
seqid: Sequence ID
functionality: Functionality
sequenceFileNumber: Sequence file number
sequenceClonoFileNumber: Sequence clonotype file number

Source

Sequencing data used for this example is available in the NCBI Sequence Read Archive under the accession code SRX326382. The description of this data is available in Li S. et al. (2013)

References


Examples

data(MID2)
str(MID2)
multprocPlot

Description

This function draws graphs from multiple testing results. It displays the number of rejected hypotheses plotted against the Type I error rate for each of the procedures and the ordered adjusted p-values plotted for each of the procedures obtained by using the functions mt.plot of the package multtest (plottype: "rvsa" and "pvst" respectively).

Usage

multprocPlot(data, ...)

Arguments

data the data issued from the function sigrepDiv or sigrepExp
...
optional parameters

Value

Graphs from multiple testing results.

Source


References


Examples

```r
## Not run:
dev.new(width=6.7, height=3.14)
multprocPlot(div)
multprocPlot(exp)
## End(Not run)
```
**normjuxBars**

*Normalized bar graph of the proportions*

**Description**

This function draws the normalized bar graph of the proportions of IMGT clonotypes (AA) (or sequences assigned to IMGT clonotypes (AA)).

**Usage**

```r
normjuxBars(data, ...)
```

**Arguments**

- `data`: the data issued from the function `sigrepDiv` or `sigrepExp`
- `...`: optional parameters

**Value**

Normalized juxtaposed bar graphs of the proportions of IMGT clonotypes (AA) (or sequences assigned to IMGT clonotypes (AA)) in two compared sets from IMGT/HighV-QUEST output.

**Examples**

```r
# Not run:
normjuxBars(div)$BarGphV
normjuxBars(div)$BarGphD
normjuxBars(div)$BarGphJ
normjuxBars(exp)$BarGphV
normjuxBars(exp)$BarGphD
normjuxBars(exp)$BarGphJ

# End(Not run)
```

**preabsDiv**

*Gene presence/absence in the IMGT clonotypes (AA) for clonotype diversity*

**Description**

This function allows the creation of a new boolean matrix indicating the presence (coded by 1) or the absence (coded by 0) of genes in the IMGT clonotypes (AA) for clonotype diversity.

**Usage**

```r
preabsDiv(datag, data)
```

**Arguments**

- `datag`: IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function `clonRem`
- `data`: issued from the function `meltgene`
**preabsExp**

**Value**

Boolean matrix with IMGT clonotypes (AA) in rows and gene names in columns.

**Examples**

```r
## Not run:
b1<-preabsDiv(MID1,set1)
b2<-preabsDiv(MID2,set2)

## End(Not run)
```

<table>
<thead>
<tr>
<th>preabsExp</th>
<th>Gene presence/absence in the IMGT clonotypes (AA) for clonotype expression</th>
</tr>
</thead>
</table>

**Description**

This function allows the creation of a new matrix indicating the presence or the absence of genes in the sequences assigned to IMGT clonotypes (AA) for clonotype expression.

**Usage**

```r
preabsExp(datag, data)
```

**Arguments**

- `datag` IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function `clonRem`
- `data` issued from the function `meltgene`

**Value**

Matrix with sequences assigned to IMGT clonotypes (AA) in rows and gene names in columns.

**Examples**

```r
## Not run:
e1<-preabsExp(MID1,set1)
e2<-preabsExp(MID2,set2)

## End(Not run)
```
Description

The data of one set from IMGT/HighV-QUEST output used here as an example.

Usage

data("S1")

Format

A data frame with 27731 observations on the following 26 variables:
cdr3aa: CDR3-IMGT sequence (AA)
expid: Experimental ID
clonoIndex: Representative sequence index
onecopy: Nb of ‘1 copy’
morethanone: Nb of ’More than one’
total: Total nb of ’1 copy’ and ’More than one’
indexes: ’1 copy’ Indexes
vgene: V-gene
vallele: V-allele
dgene: D-gene
dallele: D-allele
jgene: J-gene
jallele: J-allele
cdr1: CDR1-IMGT
cdr2: CDR2-IMGT
gcdr1: CDR1-IMGT gapped sequence (AA)
gcdr2: CDR2-IMGT gapped sequence (AA)
pid: % identity with the closest germline IMGT V gene and allele
length: Sequence length
c104: C104 (1st-CYS)
f118: F118 or W118 (J-PHE or J-TRP)
anchors: Anchors (C104, F118 or W118)
seqid: Sequence ID
functionality: Functionality
sequenceFileNumber: Sequence file number
sequenceClonoFileNumber: Sequence clonotype file number
Source

Sequencing data used for this example is available in the NCBI Sequence Read Archive under the accession code SRX470417. The description of this data is available in Mroczek E.S. et al. (2014).

References


Examples

data(S1)
str(S1)

---

**Memory IgD- B cell IMGT/HighV-QUEST output**

Description

The data of one set from IMGT/HighV-QUEST output used here as an example.

Usage

data("S2")

Format

A data frame with 17308 observations on the following 26 variables:
cdr3aa: CDR3-IMGT sequence (AA)
expid: Experimental ID
clonoIndex: Representative sequence index
onecopy: Nb of ‘1 copy’
morethanone: Nb of ‘More than one’
total: Total nb of ‘1 copy’ and ‘More than one’
indexes: ‘1 copy’ Indexes
vgene: V-gene
vallele: V-allele
dgene: D-gene
dallele: D-allele
jgene: J-gene
jallele: J-allele
cdr1: CDR1-IMGT
cdr2: CDR2-IMGT
Source

Sequencing data used for this example is available in the NCBI Sequence Read Archive under the accession code SRX470416. The description of this data is available in Mroczek E.S. et al. (2014).

References


Examples

data(52)
str(52)

def sigrepDiv(Data, data1, data2)

Description

This function tests the significance of the difference in proportions with 95% confidence interval (CI) for IMGT clonotype (AA) diversity between two sets from IMGT/HighV-QUEST output.

Usage

sigrepDiv(Data, data1, data2)
Arguments

Data the matrix issued from the function `clonNumDiv` containing the number of IMGT clonotypes (AA)
data1 the first set from IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function `clonRem`
data2 the second set from IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function `clonRem`

Value

A matrix of 21 columns:

<table>
<thead>
<tr>
<th>Gene_Name</th>
<th>The list of IMGT gene names found in the two compared sets from the IMGT/HighV-QUEST output</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gene_Type</td>
<td>The type of genes (V, D or J)</td>
</tr>
<tr>
<td>Nb_IMGT_clonotype_AA.set1</td>
<td>The nb of IMGT clonotypes (AA) in the first IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”</td>
</tr>
<tr>
<td>Proportion.set1</td>
<td>The proportion of IMGT clonotypes (AA) in the first IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”</td>
</tr>
<tr>
<td>Normalized_proportion.set1</td>
<td>The normalized proportion for 10000 IMGT clonotypes (AA) in the first IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”</td>
</tr>
<tr>
<td>Nb_IMGT_clonotype_AA.set2</td>
<td>The nb of IMGT clonotypes (AA) in the second IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”</td>
</tr>
<tr>
<td>Proportion.set2</td>
<td>The proportion of IMGT clonotypes (AA) in the second IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”</td>
</tr>
<tr>
<td>Normalized_proportion.set2</td>
<td>The normalized proportion for 10000 IMGT clonotypes (AA) in the second IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”</td>
</tr>
<tr>
<td>Difference_proportion</td>
<td>The difference in proportions of IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output with the corresponding gene indicated in the first column “Gene_Name”</td>
</tr>
<tr>
<td>z</td>
<td>The z-score values to determine the significance of the difference between two proportions</td>
</tr>
<tr>
<td>Lower_bound_IC_diff_prop</td>
<td>The lower bound of the 95% confidence interval (CI) for the difference in proportions of IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output</td>
</tr>
<tr>
<td>Upper_bound_IC_diff_prop</td>
<td>The upper bound of the 95% confidence interval (CI) for the difference in proportions of IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output</td>
</tr>
</tbody>
</table>
The p-values obtained from z-scores to evaluate the significance of difference in proportions of IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output.

The adjusted p-values issued from the Bonferroni multiple testing procedure.

The adjusted p-values issued from the Holm multiple testing procedure.

The adjusted p-values issued from the Hochberg multiple testing procedure.

The adjusted p-values issued from the Sidak single-step (SS) multiple testing procedure.

The adjusted p-values issued from the Sidak single-down (SD) multiple testing procedure.

The adjusted p-values issued from the Benjamini & Hochberg (BH) multiple testing procedure.

The adjusted p-values issued from the Benjamini & Yekutieli (BY) multiple testing procedure.

The test interpretation: before adjustment of p-values (rawp) non-significant and after adjustment by the multiple testing procedure: significant differences in proportions validated by the seven procedures (All_p), by two or more procedures (Min_2p) and only by BH (Only_BH).

Source


References


Examples

```r
## Not run:
div<-sigrepDiv(Ndiv,MID1,MID2)
## End(Not run)
```

Description

This function tests the significance of the difference in proportions with 95% confidence interval (CI) for IMGT clonotype (AA) expression between two sets from IMGT/HighV-QUEST output.
Usage

sigrepExp(Data, data1, data2)

Arguments

Data: the matrix issued from the function clonNumExp containing the number of IMGT clonotypes (AA)
data1: the first set from the IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function clonRem
data2: the second set from the IMGT/HighV-QUEST output without CDR3-IMGT outlier lengths issued from the function clonRem

Value

A matrix of 21 columns:

Gene_Name: The list of IMGT gene names found in the two compared sets from the IMGT/HighV-QUEST output
Gene_Type: The type of genes (V, D or J)
Nb_IMGT_clonotype_AA.set1: The nb of sequences assigned to IMGT clonotypes (AA) in the first IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”
Proportion.set1: The proportion of sequences assigned to IMGT clonotypes (AA) in the first IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”
Normalized_proportion.set1: The normalized proportion for 10000 sequences assigned to IMGT clonotypes (AA) in the first IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”
Nb_IMGT_clonotype_AA.set2: The nb of sequences assigned to IMGT clonotypes (AA) in the second IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”
Proportion.set2: The proportion of sequences assigned to IMGT clonotypes (AA) in the second IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”
Normalized_proportion.set2: The normalized proportion for 10000 sequences assigned to IMGT clonotypes (AA) in the second IMGT/HighV-QUEST output (set) with the corresponding gene indicated in the first column “Gene_Name”
Difference_proportion: The difference in proportions of sequences assigned to IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output with the corresponding gene indicated in the first column “Gene_Name”
z: The z-score values to determine the significance of the difference between two proportions
**Lower_bound_IC_diff_prop**
The lower bound of the 95% confidence interval (CI) for the difference in proportions of sequences assigned to IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output.

**Upper_bound_IC_diff_prop**
The upper bound of the 95% confidence interval (CI) for the difference in proportions of sequences assigned to IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output.

**rawp**
The \( p \)-values obtained from \( z \)-scores to evaluate the significance of difference in proportions of sequences assigned to IMGT clonotypes (AA) in the two compared sets from the IMGT/HighV-QUEST output.

**Bonferroni**
The adjusted \( p \)-values issued from the Bonferroni multiple testing procedure.

**Holm**
The adjusted \( p \)-values issued from the Holm multiple testing procedure.

**Hochberg**
The adjusted \( p \)-values issued from the Hochberg multiple testing procedure.

**SidakSS**
The adjusted \( p \)-values issued from the Sidak single-step (SS) multiple testing procedure.

**SidakSD**
The adjusted \( p \)-values issued from the Sidak single-down (SD) multiple testing procedure.

**BH**
The adjusted \( p \)-values issued from the Benjamini & Hochberg (BH) multiple testing procedure.

**BY**
The adjusted \( p \)-values issued from the Benjamini & Yekutiel (BY) multiple testing procedure.

**Test_interpretation**
The test interpretation: before adjustment of \( p \)-values (rawp) non-significant and after adjustment by the multiple testing procedure: significant differences in proportions validated by the seven procedures (All_p), by two or more procedures (Min_2p) and only by BH (Only_BH).

**Source**

**References**

**Examples**

```r
## Not run:
exp<-sigrepExp(Nexp,MID1,MID2)

## End(Not run)
```
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