Package 'abseqR'

March 31, 2025

Type Package

Title Reporting and data analysis functionalities for Rep-Seq datasets of antibody libraries

Version 1.24.0

Description AbSeq is a comprehensive bioinformatic pipeline for the analysis of sequencing datasets generated from antibody libraries and abseqR is one of its packages. abseqR empowers the users of abseqPy (https://github.com/malhamdoosh/abseqPy) with plotting and reporting capabilities and
allows them to generate interactive HTML reports for the convenience of viewing and sharing with other researchers. Additionally, abseqR extends abseqPy to compare multiple
repertoire analyses and perform further downstream analysis on its output.

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Encoding UTF-8

LazyData true

Depends R (>= 3.5.0)

Imports ggplot2, RColorBrewer, circlize, reshape2, VennDiagram, plyr, flexdashboard, BiocParallel (>= 1.1.25), png, grid, gridExtra, rmarkdown, knitr, vegan, ggcorrplot, ggdendro, plotly, BiocStyle, stringr, utils, methods, grDevices, stats, tools, graphics

VignetteBuilder knitr

RoxygenNote 6.1.0

Collate 'accessors-AbSeq.R' 'AbSeqCRep.R' 'util.R' 'distributions.R' 'upstreamAnalysis.R' 'productivityAnalysis.R' 'primerAnalysis.R' 'diversityAnalysis.R' 'annotationAnalysis.R' 'abundanceAnalysis.R' 'plotter.R' 'AbSeqRep.R' 'abseqReport.R' 'statistics.R' 'pairwise.R'

SystemRequirements pandoc (>= 1.19.2.1)

URL https://github.com/malhamdoosh/abseqR

BugReports https://github.com/malhamdoosh/abseqR/issues

biocViews Sequencing, Visualization, ReportWriting, QualityControl, MultipleComparison

Suggests testthat

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Combines 2 AbSeqCRep objects together for comparison

Description

Combines 2 AbSeqCRep objects together for comparison

Usage

```
## S4 method for signature 'AbSeqCRep,AbSeqCRep'
e1 + e2
```

Arguments

e1	AbSeqCRep.
e2	AbSeqCRep.

Value

AbSeqCRep object. Calling abseqR's functions on this object will always result in a comparison.

See Also

abseqReport returns a list of AbSeqReps

Examples

```
# Use example data from abseqR as abseqPy's output, substitute this
# with your own abseqPy output directory
abseqPyOutput <- tempdir()
file.copy(system.file("extdata", "ex", package = "abseqR"), abseqPyOutput, recursive=TRUE)
samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 0)

# The provided example data has PCR1, PCR2, and PCR3 samples contained within
# pcr12 and pcr13 are instances of AbSeqCRep
pcr12 <- samples[["PCR1"]] + samples[["PCR2"]]
pcr13 <- samples[["PCR1"]] + samples[["PCR3"]]

# all_S is also an instance of AbSeqCRep
all_S <- pcr12 + pcr13

# you can now call the report function on this object
# report(all_S)           # uncomment this line to execute report
```

`+,AbSeqCRep,AbSeqRep-method`
Combines a AbSeqCRep object with a AbSeqRep object together for comparison

Description

Combines a AbSeqCRep object with a AbSeqRep object together for comparison

Usage

```
## S4 method for signature 'AbSeqCRep,AbSeqRep'
e1 + e2
```

Arguments

e1	AbSeqCRep.
e2	AbSeqRep.

Value

AbSeqCRep object. Calling abseqR's functions on this object will always result in a comparison.

See Also

`abseqReport` returns a `list` of AbSeqReps

Examples

```
# Use example data from abseqR as abseqPy's output, substitute this
# with your own abseqPy output directory
abseqPyOutput <- tempdir()
file.copy(system.file("extdata", "ex", package = "abseqR"), abseqPyOutput, recursive=TRUE)
samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 0)

# The provided example data has PCR1, PCR2, and PCR3 samples contained within
# pcr12 is an instance of AbSeqCRep
pcr12 <- samples[["PCR1"]] + samples[["PCR2"]]
# pcr3 is instance of AbSeqRep
pcr3 <- samples[["PCR3"]]

# pcr123 is an instance of AbSeqCRep
pcr123 <- pcr12 + pcr3

# you can now call the report function on this object
# report(pcr123)          # uncomment this line to execute report
```

+,AbSeqRep,AbSeqCRep-method *Combines a AbSeqRep object with a AbSeqCRep object together for comparison*

Description

Combines a AbSeqRep object with a AbSeqCRep object together for comparison

Usage

```
## S4 method for signature 'AbSeqRep,AbSeqCRep'
e1 + e2
```

Arguments

e1	AbSeqRep.
e2	AbSeqCRep.

Value

AbSeqCRep object. Calling abseqR's functions on this object will always result in a comparison.

See Also

abseqReport returns a list of AbSeqReps

Examples

```
# Use example data from abseqR as abseqPy's output, substitute this
# with your own abseqPy output directory
abseqPyOutput <- tempdir()
file.copy(system.file("extdata", "ex", package = "abseqR"), abseqPyOutput, recursive=TRUE)
samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 0)

# The provided example data has PCR1, PCR2, and PCR3 samples contained within
# pcr1 is an instance of AbSeqRep
pcr1 <- samples[["PCR1"]]
# pcr23 is instance of AbSeqCRep
pcr23 <- samples[["PCR2"]] + samples[["PCR3"]]

# pcr123 is an instance of AbSeqCRep
pcr123 <- pcr1 + pcr23

# you can now call the report function on this object
# report(pcr123)          # uncomment this line to execute report
```

`+,AbSeqRep,AbSeqRep-method`
Combines 2 AbSeqRep objects together for comparison

Description

Combines 2 AbSeqRep objects together for comparison

Usage

```
## S4 method for signature 'AbSeqRep,AbSeqRep'
e1 + e2
```

Arguments

`e1`	AbSeqRep object.
`e2`	AbSeqRep object.

Value

AbSeqCRep object. Calling `abseqR`'s functions on this object will always result in a comparison.

See Also

`abseqReport` returns a `list` of `AbSeqReps`

Examples

```
# Use example data from abseqR as abseqPy's output, substitute this
# with your own abseqPy output directory
abseqPyOutput <- tempdir()
file.copy(system.file("extdata", "ex", package = "abseqR"), abseqPyOutput, recursive=TRUE)
samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 0)

# The provided example data has PCR1, PCR2, and PCR3 samples contained within
# pcr1 and pcr2 are instances of AbSeqRep
pcr1 <- samples[["PCR1"]]
pcr2 <- samples[["PCR2"]]

# pcr12 is an instance of AbSeqCRep
pcr12 <- pcr1 + pcr2

# you can now call the report function on this object
# report(pcr12)           # uncomment this line to execute report
```

.abundanceAnalysis *Conducts abundance analysis*

Description

Conducts abundance analysis

Usage

```
.abundanceAnalysis(abundanceDirectories, abunOut, sampleNames,
  combinedNames, mashedNames, skipDgene = FALSE, .save = TRUE)
```

Arguments

abundanceDirectories	list type. List of sample directories
abunOut	string type. Output directory
sampleNames	vector type. 1-1 correspondence with abundanceDirectories
combinedNames	string type. Title "combined" sample names
mashedNames	string type. File "mashed" names - avoid special chars
skipDgene	logical type. Skip D gene plots?
.save	logical type. Save ggplot as Rdata

Value

None

.abundancePlot *Abundance distribution*

Description

Abundance distribution

Usage

```
.abundancePlot(files, sampleNames, outputDir, skipDgene = FALSE,
  .save = TRUE)
```

Arguments

files	list type. list of files in abundance directory
sampleNames	vector type. 1-1 correspondance to files
outputDir	string type.
skipDgene	logical type. Skip D germline abundance plot if TRUE.
.save	logical type. Save Rdata ggplot item

Value

None

.alignQualityHeatMaps *Plots all 5 alignment quality heatmaps*

Description

Plots alignment quality vs:

- mismatches
- gaps
- bitscore
- percent identity
- subject start

Usage

```
.alignQualityHeatMaps(abundanceDirectory, sampleName)
```

Arguments

abundanceDirectory	character type. fully qualified path to abundance directory
sampleName	character type. sample name

Value

list of ggplotly heatmaps

.allPrimerNames *Collect primer names from FASTA*

Description

Collect primer names from FASTA

Usage

```
.allPrimerNames(primerFile)
```

Arguments

primerFile	string type. Path to primer file

Value

vector of primer names as seen in primerFile

.aminoAcidBar *Plots amino acid composition logo*

Description

Plots amino acid composition logo

Usage

```
.aminoAcidBar(df, scale, region, germ = "")
```

Arguments

df	dataframe
scale	logical. scale to proportion?
region	string. which region is this
germ	string. V germline family

Value

ggplot2 object

.aminoAcidPlot *Composition logo plot*

Description

Plots 2 kinds: scaled and unscaled composition logos

Usage

```
.aminoAcidPlot(compositionDirectory, outdir, sampleName,
  regions = c("FR1", "CDR1", "FR2", "CDR2", "FR3", "CDR3", "FR4"),
  .save = TRUE)
```

Arguments

compositionDirectory	string type.
outdir	string type.
sampleName	string type.
regions	logical type. vector of FR/CDR regions to plot
.save	logical type. save ggplot object

Value

none

.analyzeUpstreamValidity *Plots the validity of upstream sequences*

Description

Plots the distribution of valid, faulty, and missing start codon in IGV germlines (repeated for gene and family levels).

Usage

```
.analyzeUpstreamValidity(upstreamDirectories, upstreamOut, expectedLength,
  upstreamLengthRange, sampleNames, combinedNames, mashedNames,
  .save = TRUE)
```

Arguments

upstreamDirectories	list type. List of sample directories
upstreamOut	string type. Output directory
expectedLength	int type. Expected length of upstream sequences. (i.e. upstream_end - upstream_start + 1). If this is infinite, no plots will be generated.
upstreamLengthRange	string type. start_end format
sampleNames	vector type. 1-1 with upstream directories
combinedNames	string type. Title friendly "combined" sample names
mashedNames	string type. File friendly "mashed-up" sample names
.save	logical type. Save Rdata?

Value

None

.annotAnalysis *Annotation analysis*

Description

Annotation analysis

Usage

```
.annotAnalysis(annotDirectories, annotOut, sampleNames, mashedNames,
  .save = TRUE)
```

Arguments

annotDirectories	list type. List of sample directories
annotOut	string type. Output directory
sampleNames	vector type. 1-1 with annotDirectories
mashedNames	string type. File output "mashed" sample names
.save	logical type. Saves ggplot object

Value

none

.asRepertoireAlignLen *Accessor for* alignlen *slot*

Description

Accessor for alignlen slot

Usage

```
.asRepertoireAlignLen(object, collapse = " - ")
```

Arguments

object	AbSeqRep object
collapse	character type, collapse the range using this string.

Value

character type. If collapse is a string, then the ranges are represented as 'start - end' in a string, if collapse is NULL, returns a character vector of length two, denoting the start and end value respectively.

.asRepertoireBitscore *Accessor for* bitscore *slot*

Description

Accessor for bitscore slot

Usage

```
.asRepertoireBitscore(object, collapse = " - ")
```

Arguments

object	AbSeqRep object
collapse	character type, collapse the range using this string.

Value

character type. If collapse is a string, then the ranges are represented as 'start - end' in a string, if collapse is NULL, returns a character vector of length two, denoting the start and end value respectively.

.asRepertoireChain *Accessor for* chain *slot*

Description

Accessor for chain slot

Usage

```
.asRepertoireChain(object)
```

Arguments

object	AbSeqRep object

Value

character type, the chain type of this sample

.asRepertoireDir *Accessor for the* outdir *slot*

Description

Accessor for the outdir slot

Usage

```
.asRepertoireDir(object)
```

Arguments

object	AbSeqRep object

Value

character type, the output directory of this object

.asRepertoireList *Accessor for AbSeqCRep's list of AbSeqRep objects*

Description

Accessor for AbSeqCRep's list of AbSeqRep objects

Usage

```
.asRepertoireList(object)
```

Arguments

object	AbSeqCRep object

Value

list type, list of AbSeqRep objects that together, compose this AbSeqCRep object.

.asRepertoireName *Accessor for the* name *slot*

Description

Accessor for the name slot

Usage

```
.asRepertoireName(object)
```

Arguments

object	AbSeqRep object

Value

character type, the sample name of this object.

.asRepertoirePrimer3 *Accessor for the* primer3end *slot*

Description

Accessor for the primer3end slot

Usage

```
.asRepertoirePrimer3(object)
```

Arguments

object	AbSeqRep object

Value

character type, the FASTA file name for primer 3' end sequences

.asRepertoirePrimer5 *Accessor for the* primer5end *slot*

Description

Accessor for the primer5end slot

Usage

```
.asRepertoirePrimer5(object)
```

Arguments

object	AbSeqRep object

Value

character type, the FASTA file name for primer 5' end sequences

---

`.asRepertoireQueryStart` *Accessor for* `qstart` *slot*

Description

Accessor for `qstart` slot

Usage

```
.asRepertoireQueryStart(object, collapse = " - ")
```

Arguments

`object`	AbSeqRep object
`collapse`	character type, collapse the range using this string.

Value

character type. If collapse is a string, then the ranges are represented as 'start - end' in a string, if collapse is NULL, returns a character vector of length two, denoting the start and end value respectively.

`.asRepertoireSubjectStart` *Accessor for* `sstart` *slot*

Description

Accessor for `sstart` slot

Usage

```
.asRepertoireSubjectStart(object, collapse = " - ")
```

Arguments

`object`	AbSeqRep object
`collapse`	character type, collapse the range using this string.

Value

character type. If collapse is a string, then the ranges are represented as 'start - end' in a string, if collapse is NULL, returns a character vector of length two, denoting the start and end value respectively.

.asRepertoireUpstream *Accessor for the* upstream *slot*

Description

Accessor for the upstream slot

Usage

```
.asRepertoireUpstream(object)
```

Arguments

object	AbSeqRep object

Value

character type

.boxPlot *Creates a box plot*

Description

Creates a box plot

Usage

```
.boxPlot(dataframes, sampleNames, plotTitle, xlabel = "", ylabel = "",
  subs = "")
```

Arguments

dataframes	list type. List of sample dataframes
sampleNames	vector type. 1-1 with dataframes
plotTitle	string type
xlabel	string type
ylabel	string type
subs	string type

Value

ggplot2 object

.calculateDInd *Calculates the "standard" diversity indices*

Description

Calculates the "standard" diversity indices

Usage

```
.calculateDInd(df)
```

Arguments

df	clonotype dataframe. Vegan format: +————————————+ | S.1| S.2| S.3 | S.4 | ... | (each species should have its own column) +————————————+ | v1 |v2 | v3 | .... | (each species' count values are placed in the corresponding column) +————————————+

Value

dataframe with the column headers: shannon , simpson.con , simpson.inv , simpson.gini , renyi.0 , renyi.1 , renyi.2 , renyi.Inf , hill.0 , hill.1 , hill.2 , hill.Inf

renyi.0 => species richness renyi.1 => shannon entropy renyi.2 => inv.gini renyi.Inf => min.entropy

finally: hill_a = exp(renyi_a)

.calculateDiversityEstimates *Calculates Lower Bound Estimates for unseen species and Common Diversity Indices from clonotype tables*

Description

Employ common techniques to calculate LBE for unseen species and commonly used diversity indices

Usage

```
.calculateDiversityEstimates(diversityDirectories, diversityOut,
  sampleNames)
```

Arguments

diversityDirectories	list type. List of directories to diversity dir
diversityOut	string type. Output directory
sampleNames	vector type. 1-1 with diversityDirectories sample names

Value

None

.canonicalizeTitle *Convert file names to human friendly text*

Description

Convert file names to human friendly text

Usage

```
.canonicalizeTitle(str)
```

Arguments

str	string type

Value

string

.capitalize *Helper function to capitalize the first letter of* str

Description

Helper function to capitalize the first letter of str

Usage

```
.capitalize(str)
```

Arguments

str	string type

Value

string, str capitalized

.checkVert — *Checks if abseqPy has a metadata line that suggests the orientation*

Description

Checks if abseqPy has a metadata line that suggests the orientation

Usage

```
.checkVert(filename)
```

Arguments

filename	csv filename

Value

True if CSV metadata says "plot vertically"

.cloneDistHist — *Marginal histogram of clonotypes (blue for shared, grey for total). The y axis is scaled by sqrt (but it doesn't really matter anyway, since we're stripping away the y-ticks)*

Description

Marginal histogram of clonotypes (blue for shared, grey for total). The y axis is scaled by sqrt (but it doesn't really matter anyway, since we're stripping away the y-ticks)

Usage

```
.cloneDistHist(df.original, otherClones, lim.min, flip)
```

Arguments

df.original	dataframe with all clones
otherClones	clones from the other dataframe
lim.min	x-axis minimum limit
flip	logical type

Value

ggplot2 object

.cloneDistMarginal *Marginal density graph of clonotypes (blue for shared, grey for total, purple for exclusive clones)*

Description

Marginal density graph of clonotypes (blue for shared, grey for total, purple for exclusive clones)

Usage

```
.cloneDistMarginal(df.original, otherClones, lim.min, flip)
```

Arguments

df.original	dataframe with all clones
otherClones	clones from the other dataframe
lim.min	x-axis minimum limit
flip	logical type

Value

ggplot2 object

.clonotypeAnalysis *Comprehensive clonotype analyses*

Description

Comprehensive clonotype analyses

Usage

```
.clonotypeAnalysis(diversityDirectories, clonotypeOut, sampleNames,
  mashedNames, .save = TRUE)
```

Arguments

diversityDirectories	list type. List of directories to diversity dir
clonotypeOut	string type. Output directory
sampleNames	vector type. 1-1 with diversityDirectories
mashedNames	string type. Prefix for ooutput files using "mashed-up"
.save	logical type. Save ggplot object?

Value

Nothing

`.collateReports` *Collate all HTML reports into a single directory and cretate an entry* `index.html` *file that redirects to all collated HTML files*

Description

Collate all HTML reports into a single directory and cretate an entry `index.html` file that redirects to all collated HTML files

Usage

```
.collateReports(reports, individualSamples, outputDirectory)
```

Arguments

`reports`	list/vector type. Collection of strings that are path(s) to <sample>_report.html
`individualSamples`	list type. list of AbSeqRep objects. Used to extract filtering information and % read counts.
`outputDirectory`	string type. Where should the report be placed.

Value

Nothing

`.commonPrimerNames` *Collect the intersection of all primer names within a collection of primer files*

Description

Collect the intersection of all primer names within a collection of primer files

Usage

```
.commonPrimerNames(primerFiles)
```

Arguments

`primerFiles`	list / vector type. Collection of primer files

Value

vector type. Vector of primerNames that are present in ALL primerFiles. NULL if there's no intersection at all

.correlationTest *Conducts pearson and spearman correlation analysis on dataframe*

Description

Conducts pearson and spearman correlation analysis on dataframe

Usage

```
.correlationTest(df)
```

Arguments

df	dataframe with at least the following 2 columns: +————————+ ⁞ prop.x ⁞ prop.y ⁞ +————————+ ⁞..... ⁞ .... ⁞ +————————+ where prop.x and prop.y are normalized counts (i.e. frequencies) of the clones They may contain 0 in a column to denote it being missing from sample x or y.

Value

named list of pearson, pearson.p, spearman, spearman.p

.distanceMeasure *Computes the distance between pariwise samples*

Description

Computes the distance between pariwise samples

Usage

```
.distanceMeasure(df)
```

Arguments

df	dataframe with at least the following 2 columns: +————————+ ⁞ prop.x ⁞ prop.y ⁞ +————————+ ⁞..... ⁞ .... ⁞ +————————+ where prop.x and prop.y are normalized counts (i.e. frequencies) of the clones They may contain 0 in a column to denote it being missing from sample x or y.

Value

named list of bray.curtis, jaccard, and morisita.horn

.diversityAnalysis *Title Diversity analysis*

Description

Title Diversity analysis

Usage

```
.diversityAnalysis(diversityDirectories, diversityOut, sampleNames,
  mashedNames, .save = TRUE)
```

Arguments

diversityDirectories	list type. List of directories to diversity dir
diversityOut	string type. Output directory
sampleNames	vector type. 1-1 with diversityDirectories
mashedNames	string type. Prefix for output files using "mashed-up" sample names
.save	logical type. Save ggplot object?

Value

None

.emptyPlot *Creates and returns an empty plot*

Description

Creates and returns an empty plot

Usage

```
.emptyPlot()
```

Value

empty ggplot2 object

`.findRepertoires` *Given a directory = <abseqPy_outputdir>/RESULT_DIR/, returns the directories (repositories) in 'directory'. That is, will not return any sample_vs_sample directories. This is done by asserting that a 'repository' must have an (analysis.params) file, and a summary.txt file.*

Description

A sample_vs_sample directory will not have these files.

Usage

```
.findRepertoires(directory)
```

Arguments

`directory`	string. Path up until <abseqPy_outputdir>/RESULT_DIR/

Value

vector of strings that are samples in 'directory', note, this is NOT a full path, but just the sample/repertoire name itself

`.generateAllSpectratypes` *Generates all FR/CDR spectratypes*

Description

Generates all FR/CDR spectratypes

Usage

```
.generateAllSpectratypes(diversityDirectories, diversityOut, sampleNames,
  mashedNames, .save = TRUE)
```

Arguments

`diversityDirectories`	list type. List of directories to diversity dir
`diversityOut`	string type. Output directory
`sampleNames`	vector type. 1-1 with diversityDirectories
`mashedNames`	string type. Prefix for output files using "mashed-up" sample names
`.save`	logical type. Save ggplot object?

Value

Nothing

.generateDelayedReport *Generates report for all samples in 'compare'*

Description

This function is needed because we are delaying the generation of reports until after all threads/processes have joined. There's currently an issue with rmarkdown::render() in parallel execution, see: https://github.com/rstudio/rm

Usage

```
.generateDelayedReport(root, compare, interactivePlot)
```

Arguments

root	string, project root directory.
compare	vector of strings, each string is a comparison defined by the user (assumes that this value has been checked).
interactivePlot	logical, whether or not to plot interactive plotly plots.

Value

a named list of samples, each an AbSeqRep object found in "root"

.generateReport *Generates HTML report from AbSeqRep and AbSeqCRep ojects*

Description

Generates HTML report from AbSeqRep and AbSeqCRep ojects

Usage

```
.generateReport(object, root, outputDir, interactivePlot = TRUE,
  .indexHTML = "#")
```

Arguments

object	AbSeqCRep type.
root	string type. Root directory of the sample(s)
outputDir	string type. The path where the HTML will be generated
interactivePlot	logical type. Interactive or not
.indexHTML	character type. The back button will redirect to this link. This is typically used to redirect users back to index.html page

Value

path (including HTML name) where the report (HTML file) was saved to

.getLineTypes *Helper function to return line types by importance based on provided CD/Fs regions*

Description

In the aesthetics of diversity plots (rarefaction, recapture, and duplication), the line types should emphasise the most important antibody region, they're ranked in ascending order of: "FR4", "FR1", "FR2", "FR3", "CDR1", "CDR2", "CDR3", "V".

Usage

```
.getLineTypes(regions)
```

Arguments

regions	a list/vector of strings (regions)

Value

vector of strings, each corresponding to the appropriate line type for `regions`.

.getTotal *Get total number of samples (n)*

Description

Often enough, the CSV values supplied do not contain raw counts but percentages (so this value will let us know exactly the sample size).

Usage

```
.getTotal(filename)
```

Arguments

filename	csv filename

Value

string, sample size.

.hmFromMatrix *Plots a plotly heatmap from provided matrix*

Description

Plots a plotly heatmap from provided matrix

Usage

```
.hmFromMatrix(m, title, xlabel = "", ylabel = "")
```

Arguments

m	matrix type
title	character type
xlabel	character type
ylabel	character type

Value

list with keys: static and interactive (ggplot2 object and plotly object respectivelyb)

.inferAnalyzed *Returns all samples found under* sampleDirectory

Description

Returns all samples found under sampleDirectory

Usage

```
.inferAnalyzed(sampleDirectory)
```

Arguments

sampleDirectory	string, path to sample directory.

Value

un-normalized path to all samples under sampleDirectory

`.loadMatrixFromDF` *Given a dataframe with the columns "from", "to", and value.var, return a symmetric matrix (with diagonal values = diag). I.e. a call to isSymmetric(return_value_of_this_function) will always be TRUE.*

Description

Given a dataframe with the columns "from", "to", and value.var, return a symmetric matrix (with diagonal values = diag). I.e. a call to isSymmetric(return_value_of_this_function) will always be TRUE.

Usage

```
.loadMatrixFromDF(dataframe, value.var, diag, unidirectional = TRUE)
```

Arguments

`dataframe`	dataframe with 3 required columns, namely: +————————————————+ | from | to | value.var | ... | +————————————————+ | | | | | +————————————————+ where value.var is the string provided in the function parameter
`value.var`	the column to use as the matrix value
`diag`	what should the diagonal values be if the dataframe doesn't provide them
`unidirectional`	logical type. If the dataframe provided has the reverse pairs (i.e. a from-to pair AND a to-from pair with the save values in the value.var column), then this should be FALSE. Otherwise, this function will flip the from-to columns to generate a symmetric dataframe (and hence, a symmetric matrix).

Value

a symmetric matrix with rownames(mat) == colnames(mat) The diagonal values are filled with diag if the dataframe itself doesn't have diagonal data

`.loadSamplesFromString` *Loads AbSeqCRep or AbSeqRep objects from a list of sampleNames*

Description

Loads AbSeqCRep or AbSeqRep objects from a list of sampleNames

Usage

```
.loadSamplesFromString(sampleNames, root, warnMove = TRUE)
```

Arguments

sampleNames	vector, singleton or otherwise
root	string type. root directory
warnMove	logical type. Warning message ("message" level, not "warning" level) if the directory has been moved?

Value

AbSeqRep or AbSeqCRep object depending on sampleNames

.pairwiseComparison *Conduct all vs all pairwise comparison analyses*

Description

Conduct all vs all pairwise comparison analyses

Usage

```
.pairwiseComparison(dataframes, sampleNames, outputPath, .save = TRUE)
```

Arguments

dataframes	list of dataframes
sampleNames	1-1 vector corresponding to dataframes
outputPath	string
.save	logical

Value

nothing

.plotCirclize *V-J association plot*

Description

V-J association plot

Usage

```
.plotCirclize(sampleName, path, outputdir)
```

Arguments

sampleName	string type
path	string type. Path to _vjassoc.csv
outputdir	string type

Value

None

`.plotDist` *Bar plotter*

Description

Plots barplot for all sample in dataframes. If length(sampleNames) == 1, then the bars will also have y-values (or x if horizontal plot) labels on them. Use 'perc' to control if the values are percentages.

Usage

```
.plotDist(dataframes, sampleNames, plotTitle, vert = TRUE, xlabel = "",
  ylabel = "", perc = TRUE, subs = "", sorted = TRUE,
  cutoff = 15, legendPos = "right")
```

Arguments

`dataframes`	list type. List of dataframes
`sampleNames`	vector type. 1-1 correspondence to dataframes.
`plotTitle`	string type.
`vert`	boolean type. True if the plot should be vertical
`xlabel`	string type
`ylabel`	string type
`perc`	boolean type. True if data's axis is a percentage proportion (instead of 0-1) only used if length(sampleNames) == 1
`subs`	string type
`sorted`	boolean type. True if bar plot should be sorted in descending order
`cutoff`	int type. Number of maximum ticks to show (x on vert plots, y on hori plots).
`legendPos`	string type. Where to position legend (see ggplot's theme())

Value

ggplot2 object

.plotDiversityCurves *Plots rarefaction, recapture, and de-dup plots for specified* region

Description

Plots rarefaction, recapture, and de-dup plots for specified region

Usage

```
.plotDiversityCurves(region, diversityDirectories, sampleNames,
  mashedNames, diversityOut, .save = TRUE)
```

Arguments

region	string type. One of: "cdr", "cdr_v", and "fr". "cdr" means CDR1-3, "cdr_v" means CDR3 and V only, and finally "fr" means FR1-4.
diversityDirectories	list type. List of directories to diversity dir
sampleNames	vector type. 1-1 with diversityDirectories
mashedNames	string type. Prefix for output files using "mashed-up"
diversityOut	string type. Output directory sample names
.save	logical type. Save ggplot object?

Value

Nothing

.plotDuplication *Duplication level plot*

Description

bins singletons, doubletons, and higher order clonotypes into a line plot

Usage

```
.plotDuplication(files, sampleNames, regions = c("CDR3", "V"))
```

Arguments

files	list type. List of strings to _cdr_v_duplication.csv pathname
sampleNames	vector type. Vector of strings each representing sample names
regions	vector type. Which regions to include in the plot. Default = c("CDR3", "V")

Value

ggplot2 object

.plotErrorDist — *Plots the error distribution for each region: CDRs, FRs, IGV, IGD, and IGJ*

Description

Plots the distribution of indels (gaps), indels in out-of-frame sequences, and the distribution of mismatches for CDRs, FRs, IGV, IGD, and IGJ.

Usage

```
.plotErrorDist(productivityDirectories, prodOut, sampleNames,
  combinedNames, mashedNames, .save = TRUE)
```

Arguments

productivityDirectories	list type. List of directories
prodOut	string type. Output directory
sampleNames	vector type. 1-1 with productivity directories
combinedNames	string type. Title friendly "combined" sample names
mashedNames	string type. File friendly "mashed-up" sample names
.save	logical type. Save Rdata?

Value

None

.plotIGVErrors — *Plots the error distribution for IGV germlines*

Description

Plots the distribution of in-frame unproductive, out-of-frame unproductive, and productive IGV germlines.

Usage

```
.plotIGVErrors(productivityDirectories, prodOut, sampleNames,
  combinedNames, mashedNames, .save = TRUE)
```

Arguments

productivityDirectories	list type. List of directories
prodOut	string type. Output directory
sampleNames	vector type. 1-1 with productivity directories
combinedNames	string type. Title friendly "combined" sample names
mashedNames	string type. File friendly "mashed-up" sample names
.save	logical type, save Rdata?

Value

None

`.plotIGVUpstreamLenDist` *Plot IGV family distribution for a given* `upstreamLengthRange`

Description

Given an upstream length range, plot the distributions of IGV family without showing their actual lengths. If their actual lengths matter, refer to `.plotIGVUpstreamLenDistDetailed`.

Usage

```
.plotIGVUpstreamLenDist(upstreamDirectories, upstreamOut,
  upstreamLengthRange, lengthType, sampleNames, combinedNames, mashedNames,
  .save = TRUE)
```

Arguments

`upstreamDirectories`	list type. List of sample directories
`upstreamOut`	string type. Output directory
`upstreamLengthRange`	The range of upstream sequences to be included in this plot. This is usually determined by abseqPy and the format should be as follows: "min_max", e.g.: 1_15 means range(1, 15) inclusive.string type.
`lengthType`	string type. "" (the empty string) denotes everything and "_short" denotes a short sequence. abseqPy dictates this because it's used for locating the files.
`sampleNames`	vector type. 1-1 with upstream directories
`combinedNames`	string type. Title friendly "combined" sample names
`mashedNames`	string type. File friendly "mashed-up" sample names
`.save`	logical type. Save Rdata?

Value

None

.plotIGVUpstreamLenDistDetailed

Plots the detailed length distribution for IGV families

Description

A boxplot for each IGV families showing the IQR of upstream lengths. In contrast to `.plotIGVUpstreamLenDist`, which only shows the distribution of IGV families over `upstreamLengthRange`.

Usage

```
.plotIGVUpstreamLenDistDetailed(upstreamDirectories, upstreamOut,
  upstreamLengthRange, lengthType, sampleNames, combinedNames, mashedNames,
  .save = TRUE)
```

Arguments

`upstreamDirectories`	list type. List of sample directories
`upstreamOut`	string type. Output directory
`upstreamLengthRange`	The range of upstream sequences to be included in this plot. This is usually determined by abseqPy and the format should be as follows: "min_max", e.g.: 1_15 means range(1, 15) inclusive.string type.
`lengthType`	string type. "" (the empty string) denotes everything and "_short" denotes a short sequence. abseqPy dictates this because it's used for locating the files.
`sampleNames`	vector type. 1-1 with upstream directories
`combinedNames`	string type. Title friendly "combined" sample names
`mashedNames`	string type. File friendly "mashed-up" sample names
`.save`	logical type. Save Rdata?

Value

None

.plotPrimerIGVStatus *Plots, for a given* `category` *and* `pend`*, the* `primer` *IGV indelled distribution in a bar plot*

Description

Plots the abundace of indelled primers relative to IGV germlines

Usage

```
.plotPrimerIGVStatus(primer, pend, category, primerDirectories,
  sampleNames, primerOut, combinedNames, mashedNames, .save = TRUE)
```

Arguments

primer	string, primer name
pend	string, either 3 or 5 (primer end)
category	string, either "all", "productive", or "outframe"
primerDirectories	string type. Path to primer analysis directory
sampleNames	vector type. 1-1 with primerDirectories
primerOut	string type. output directory
combinedNames	string type. Title friendly "combined" sample names
mashedNames	string type. File friendly "mashed-up" sample names
.save	logical type. Save Rdata?

Value

None

.plotPrimerIntegrity *Plots the distribution of primer integrity for a given* category *and 5' or 3'* pend

---

Description

Plots the distribution of primer integrity for a given category and 5' or 3' pend

Usage

```
.plotPrimerIntegrity(primerIntegrity, pend, category, primerDirectories,
  sampleNames, primerOut, combinedNames, mashedNames, .save = TRUE)
```

Arguments

primerIntegrity	string. One of "stopcodon", "integrity", "indelled", "indel_pos"
pend	string, either 3 or 5 (primer end)
category	string, either "all", "productive", or "outframe"
primerDirectories	string type. Path to primer analysis directory
sampleNames	vector type. 1-1 with primerDirectories
primerOut	string type. output directory
combinedNames	string type. Title friendly "combined" sample names
mashedNames	string type. File friendly "mashed-up" sample names
.save	logical type. Save Rdata?

Value

None

.plotRarefaction *Rarefaction plot*

Description

Plots the number of unique clonotypes (on the y-axis) drawn from a sample size on the x axis. The number of unique clonotypes is averaged over 5 repeated rounds.

Usage

```
.plotRarefaction(files, sampleNames, regions = c("CDR3", "V"))
```

Arguments

files	list type. A list of files consisting of path to samples
sampleNames	vector type. A vector of strings, each being the name of samples in files
regions	vector type. A vector of strings, regions to be included. Defaults to c("CDR3", "V")

Value

ggplot2 object

.plotRecapture *Plots capture-recapture*

Description

Plots the percent of recapture clonotypes (on the y-axis) drawn from a repeated (with replacement) sample size on the x axis. The percentage of recaptured clonotypes is averaged over 5 recapture rounds.

Usage

```
.plotRecapture(files, sampleNames, regions = c("CDR3", "V"))
```

Arguments

files	list type. List of _cdr_v_recapture.csv.gz files.
sampleNames	vector type. A vector of strings each representing the name of samples in files.
regions	vector type. A vector of strings, regions to be included in the plot. defaults to c("CDR3", "V")

Value

ggplot2 object

.plotSamples *Monolith AbSeq Plot function - the "driver" program*

Description

Monolith AbSeq Plot function - the "driver" program

Usage

```
.plotSamples(sampleNames, directories, analysis, outputDir, primer5Files,
  primer3Files, upstreamRanges, skipDgene = FALSE)
```

Arguments

sampleNames	vector type. Vector of sample names in strings
directories	vector type. Vector of directories in strings, must be 1-1 with sampleNames
analysis	vector / list type. What analysis to plot for. If sampleNames or directories is > 1 (i.e. AbSeqCRep), then make sure that it's an intersection of all analysis conducted by the repertoires, otherwise, it wouldn't make sense
outputDir	string type. Where to dump the output
primer5Files	vector / list type. Collection of strings that the sample used for primer5 analysis. If sample N doesn't have a primer 5 file, leave it as anthing but a valid file path.
primer3Files	vector / list type. Collection of strings that the sample used for primer 3 analysis. If sample N doesn't have a primer 3 file, leave it as anthing but a valid file path.
upstreamRanges	list type. Collection of "None"s or vector denoting upstreamStart and upstreamEnd for each sample.
skipDgene	logical type. Whether or not to skip D gene distribution plot

Value

none

.plotSpectratype *Spectratype plotter*

Description

Plots length distribution

Usage

```
.plotSpectratype(dataframes, sampleNames, region, title = "Spectratype",
  subtitle = "", xlabel = "Length(AA)", ylabel = "Distribution",
  showLabel = FALSE)
```

Arguments

dataframes	list type. List of dataframes.
sampleNames	vector type. 1-1 correspondance with dataframes
region	string type. Region that will be displayed in the plot title. This specifies which region this spectratype belongs to. If not supplied, a default (start, end) range will be displayed instead
title	string type. Ignored if region is specified.
subtitle	string type
xlabel	string type
ylabel	string type
showLabel	bool type. Show geom_text? - Ignored if samples > 1

Value

ggplot2 object

.plotUpstreamLength *Plot upstream distribution*

Description

Plot upstream distribution

Usage

```
.plotUpstreamLength(upstreamDirectories, upstreamOut, expectedLength,
  upstreamLengthRange, sampleNames, combinedNames, mashedNames,
  .save = TRUE)
```

Arguments

upstreamDirectories	list type. List of sample directories
upstreamOut	string type. Output directory
expectedLength	int type. Expected length of upstream sequences. (i.e. upstream_end - upstream_start + 1).
upstreamLengthRange	string type. start_end format
sampleNames	vector type. 1-1 with upstream directories
combinedNames	string type. Title friendly "combined" sample names
mashedNames	string type. File friendly "mashed-up" sample names
.save	logical type. Save Rdata?

Value

None

.plotUpstreamLengthDist

Plot upstream sequence length distribution for upstream sequences (5'UTR or secretion signal) for a given `upstreamLengthRange`

Description

Given an upstream length range, plot the distribution of upstream sequence lengths.

Usage

```
.plotUpstreamLengthDist(upstreamDirectories, upstreamOut,
  upstreamLengthRange, lengthType, sampleNames, combinedNames, mashedNames,
  .save)
```

Arguments

`upstreamDirectories`	list type. List of sample directories
`upstreamOut`	string type. Output directory
`upstreamLengthRange`	The range of upstream sequences to be included in this plot. This is usually determined by abseqPy and the format should be as follows: "min_max", e.g.: 1_15 means range(1, 15) inclusive.string type.
`lengthType`	string type. "" (the empty string) denotes everything and "_short" denotes a short sequence. abseqPy dictates this because it's used for locating the files.
`sampleNames`	vector type. 1-1 with upstream directories
`combinedNames`	string type. Title friendly "combined" sample names
`mashedNames`	string type. File friendly "mashed-up" sample names
`.save`	logical type. Save Rdata?

Value

None

.primerAnalysis *Conducts primer specificity analysis*

Description

Conducts primer specificity analysis

Usage

```
.primerAnalysis(primerDirectories, primer5Files, primer3Files, primerOut,
  sampleNames, combinedNames, mashedNames, .save = TRUE)
```

Arguments

primerDirectories	string type. Path to primer analysis directory
primer5Files	vector / list type. 5' end primer files
primer3Files	vector / list type. 3' end primer files
primerOut	string type. output directory
sampleNames	vector type. 1-1 with primerDirectories
combinedNames	string type. Title friendly "combined" sample names
mashedNames	string type. File friendly "mashed-up" sample names
.save	logical type. Save Rdata?

Value

None

.prodDistPlot *Plots a distribution plot for different productivity analysis files*

Description

A wrapper for plotDist

Usage

```
.prodDistPlot(productivityDirectories, sampleNames, title, reg,
  outputFileName, region, .save = TRUE)
```

Arguments

productivityDirectories	vector type. directories where all productivity csv files lives (usually <sample-name>/productivity/)
sampleNames	vector type.
title	string type.
reg	string type. Regular expression to find the right files for this particular distribution plot
outputFileName	string type. Vector of file names to save in the order of regions
region	string type. Most of the dist plots are regional based. use "" if no regions are involved
.save	logical type. Save Rdata?

Value

None

.productivityAnalysis *Conducts productivty analysis*

Description

Conducts productivty analysis

Usage

```
.productivityAnalysis(productivityDirectories, prodOut, sampleNames,
  combinedNames, mashedNames, .save = TRUE)
```

Arguments

productivityDirectories	list type. List of directories
prodOut	string type. Output directory
sampleNames	vector type. 1-1 with productivity directories
combinedNames	string type. Title friendly "combined" sample names
mashedNames	string type. File friendly "mashed-up" sample names
.save	logical type. Save Rdata

Value

None

.productivityPlot *Summary of productivity*

Description

Shows the percentage of 1. productivity, 2. non-functional + reason for being unproductive, i.e. "Stop Codon" or "Out of frame" or "Stop & Out"

Usage

```
.productivityPlot(dataframes, sampleNames)
```

Arguments

dataframes	list type. List of sample dataframes
sampleNames	vector type. 1-1 with dataframes

Value

ggplot2 object

.readSummary *Return value specifed by key from AbSeq's summary file*

Description

Return value specifed by key from AbSeq's summary file

Usage

```
.readSummary(sampleRoot, key)
```

Arguments

sampleRoot	sample's root directory. For example, /path/to/<outputdir>/reports/<sample_name>.
key	character type. Possible values are (though they might change) • RawReads • AnnotatedReads • FilteredReads • ProductiveReads

Value

value associated with key from summary file. "NA" (in string) if the field is not available refer to util.R for the key values

.regionAnalysis *Title Shows varying regions for a given clonotype defined by its CDR3*

Description

Title Shows varying regions for a given clonotype defined by its CDR3

Usage

```
.regionAnalysis(path, sampleName, top = 15)
```

Arguments

path	string type. Path to diversity folder where <sampleName>_clonotype_diversity_region_analysis.csv.g is located
sampleName	string type
top	int type. Top N number of clones to analyze

Value

ggplot2 object

.reportLBE — *Reports abundance-based (Lower bound) diversity estimates using the Vegan package*

Description

Reports abundance-based (Lower bound) diversity estimates using the Vegan package

Usage

```
.reportLBE(df)
```

Arguments

df	clonotype dataframe. Vegan format: +————————————+ | S.1| S.2| S.3 | S.4 | ... | (each species should have its own column) +————————————+ | v1 |v2 | v3 | .... | (each species' count values are placed in the corresponding column) +————————————+

Value

dataframe with the format: +———————————————————————————-+ \| S.obs \| S.chao1 \| se.chao1 \| S.ACE \| se.ACE \| s.jack1 \| s.jack2\| +———————————————————————————————————-+ \| v1 \| v2 .... \| +———————————————————————————-+

.saveAs — *Saves ggplot object as a Rdata file.*

Description

It's a convinient function that does the check and saves at the same time, for brevity within other areas of the code (to eliminate repeated if checks).

Usage

```
.saveAs(.save, filename, plot)
```

Arguments

.save	logical type. Whether or not we should save.
filename	string.
plot	ggplot object.

Value

nothing

.scatterPlot *Title Creates a scatter plot*

Description

Title Creates a scatter plot

Usage

```
.scatterPlot(df1, df2, name1, name2, cloneClass)
```

Arguments

df1	dataframe for sample 1
df2	dataframe for sample 2
name1	string type, Sample 1 name
name2	string type. Sample 2 name
cloneClass	string type. What region was used to classify clonotypes - appears in title. For example, CDR3 or V region

Value

ggplot2 object

.scatterPlotComplex *Creates a complex scatter plot*

Description

Creates a complex scatter plot

Usage

```
.scatterPlotComplex(df.union, df1, df2, name1, name2, cloneClass)
```

Arguments

df.union	a 'lossless' dataframe created by intersecting sample1 and sample2's dataframes. It should contain NAs where clones that appear in one sample doesn't appear in the other. For example: +————————————————-+ | Clonotype | prop.x | prop.y | Count.x | Count.y | +————————————————-+ | ABCDEF NA 0.01 NA 210 | | ..... | +————————————————-+
df1	dataframe for sample 1
df2	dataframe for sample 2
name1	string type, Sample 1 name
name2	string type. Sample 2 name

cloneClass	string type. What region was used to classify clonotypes - appears in title. For example, CDR3 or V region this plotting techique was shamelessly plagarised from https://github.com/mikessh/vdjtools/blob/mast (VDJTools) with minor modifications

Value

ggplot2 object

`.secretionSignalAnalysis` *Secretion signal analysis*

Description

Generates all the required plots for Secretion signal analysis. This includes upstream length distributions and upstream sequence validity.

Usage

```
.secretionSignalAnalysis(secDirectories, secOut, sampleNames,
  combinedNames, mashedNames, upstreamRanges, .save = TRUE)
```

Arguments

secDirectories	list type. Secretion signal directories where files are located
secOut	string type. Where to dump output
sampleNames	vector type. 1-1 with secDirectories
combinedNames	string type. Title friendly string
mashedNames	string type. File name friendly string
upstreamRanges	list type. Upstream ranges for each sample. If length(secDirectories) > 1, the plots will only be generated for upstream ranges that are present in ALL samples. (i.e. the intersection)
.save	logical type, save Rdata?

Value

none

.substituteStringInFile *Substitutes the first occurance of ‘key‘ with ‘value‘ in ‘filename‘*

Description

Substitutes the first occurance of ‘key‘ with ‘value‘ in ‘filename‘

Usage

```
.substituteStringInFile(filename, key, value, fixed = FALSE)
```

Arguments

filename	character type
key	character type
value	character type
fixed	logical type

Value

None

.summarySE *Summary of dataframe*

Description

Gives count, mean, standard deviation, standard error of the mean, and confidence interval (default 95%).

adapted from http://www.cookbook-r.com/Graphs/Plotting_means_and_error_bars_(ggplot2)/#Helper functions

Usage

```
.summarySE(data = NULL, measurevar, groupvars = NULL, na.rm = FALSE,
  conf.interval = 0.95, .drop = TRUE)
```

Arguments

data	a data frame.
measurevar	the name of a column that contains the variable to be summariezed
groupvars	a vector containing names of columns that contain grouping variables
na.rm	a boolean that indicates whether to ignore NA's
conf.interval	the percent range of the confidence interval (default is 95%)
.drop	logical.

Value

dataframe

.topNDist *Title Clonotype table*

Description

Title Clonotype table

Usage

```
.topNDist(dataframes, sampleNames, top = 10)
```

Arguments

dataframes	list type. List of dataframes.
sampleNames	vector type. vector of strings representing sample names should have one-to-one correspondence with dataframes
top	int type. Top N clonotypes to plot

Value

None

.UTR5Analysis *5' UTR analysis*

Description

Generates all the required plots for 5' UTR analysis. This includes upstream length distributions and upstream sequence validity.

Usage

```
.UTR5Analysis(utr5Directories, utr5Out, sampleNames, combinedNames,
  mashedNames, upstreamRanges, .save = TRUE)
```

Arguments

utr5Directories	list type. 5UTR directories where files are located
utr5Out	string type. Where to dump output
sampleNames	vector type. 1-1 with utr5Directories
combinedNames	string type. Title friendly string
mashedNames	string type. File name friendly string
upstreamRanges	list type. Upstream ranges for each sample. If length(utr5Directories) > 1, the plots will only be generated for upstream ranges that are present in ALL samples. (i.e the intersection)
.save	logical type, save Rdata?

Value

none

.vennIntersection *Title Creates Venndiagram for clonotype intersection*

Description

Title Creates Venndiagram for clonotype intersection

Usage

```
.vennIntersection(dataframes, sampleNames, outFile, top = Inf)
```

Arguments

dataframes	list type. List of sample dataframes. Only accepts 2 - 5 samples. Warning message will be generated for anything outside of the range
sampleNames	vector type. 1-1 with dataframes
outFile	string type. Filename to be saved as
top	int type. Top N cutoff, defaults to ALL clones if not specified

Value

Nothing

AbSeqCRep-class *S4 class - AbSeqCompositeRepertoire analysis object*

Description

AbSeqCRep is a collection of AbSeqRep S4 objects. This S4 class contains multiple samples(repertoires) and it can be "combined" with other samples by using the + operator to create an extended AbSeqCRep object. This value, in turn, can be used as the first argument to report which generates a comparison between all samples included in the + operation.

Users do not manually construct this class, but rather indirectly obtain this class object as a return value from the + operation between two AbSeqRep objects, which are in turn, obtained indirectly from abseqReport and report functions. It is also possible to obtain this class object by + (adding) AbSeqCRep objects.

Value

AbSeqCRep

Slots

repertoires list of AbSeqRep objects.

See Also

AbSeqRep

Examples

```
# Use example data from abseqR as abseqPy's output, substitute this
# with your own abseqPy output directory
abseqPyOutput <- tempdir()
file.copy(system.file("extdata", "ex", package = "abseqR"), abseqPyOutput, recursive=TRUE)
samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 0)

# The provided example data has PCR1, PCR2, and PCR3 samples contained within
# pcr12 and pcr13 are instances of AbSeqCRep
pcr12 <- samples[["PCR1"]] + samples[["PCR2"]]
pcr13 <- samples[["PCR1"]] + samples[["PCR3"]]

# all_S is also an instance of AbSeqCRep
all_S <- pcr12 + pcr13
```

AbSeqRep-class *S4 class - AbSeqRepertoire analysis object*

Description

The AbSeqRep object contains all metadata associated with the AbSeq (python backend) run conducted on it. This S4 class represents a single sample(repertoire) and it can be "combined" with other samples by using the + operator to create an AbSeqCRep object. This value, in turn, can be used as the first argument to report which generates a comparison between all samples included in the + operation.

Users do not manually construct this class, but rather indirectly obtain this class object as a return value from the abseqReport and report functions.

Value

AbSeqRep

Slots

`f1` character. Path to FASTA/FASTQ file 1.

`f2` character. Path to FASTA/FASTQ file 2.

`chain` character. Type of chain, possible values:

- hv
- lv
- kv
- klv

each representing **H**eavy, **L**ambda and **K**appa respectively.

`task` character. Type of analysis conducted, possible values:

- all
- annotate
- abundance
- diversity
- productivity

- fastqc
- primer
- 5utr
- rsasimple
- seqlen
- secretion
- seqlenclass

`name` character. Name of analysis.

`bitscore` numeric. Part of filtering criteria: V gene bitscore filter value.

`qstart` numeric. Part of filtering criteria: V gene query start filter value.

`sstart` numeric. Part of filtering criteria: V gene subject start filter value.

`alignlen` numeric. Part of filtering criteria: V gene alignment length filter value.

`clonelimit` numeric. Number of clones to export into csv file. This is only relevant in `-t all` or `-t diversity` where clonotypes are exported into `<outdir>/<name>/diversity/clonotypes`

`detailedComposition` logical. Plots composition logo by IGHV families if set to true, otherwise, plots logos by FR/CDRs.

`log` character. Path to log file.

`merger` character. Merger used to merge paired-end reads.

`fmt` character. File format of `file1` and (if present) `file2`. Possible values are FASTA or FASTQ.

`sites` character. Path to restriction sites `txt` file. This option is only used if `-t rsasimple`

`primer5end` ANY. Path to 5' end primer FASTA file.

`primer3end` ANY. Path to 3' end primer FASTA file.

`trim5` numeric. Number of nucleotides to trimd at the 5' end;

`trim3` numeric. Number of nucleotides to trimd at the 3' end;

`outdir` character. Path to output directory

`primer5endoffset` numeric. Number of nucleotides to offset before aligning 5' end primers in `primer5end` FASTA file.

`threads` numeric. Number of threads to run.

`upstream` character. Index (range) of upstream nucleotides to analyze. This option is only used if `-t 5utr` or `-t secretion`.

`seqtype` character. Sequence type, possible values are either `dna` or `protein`.

`database` character. Path to IgBLAST database.

`actualqstart` numeric. Query sequence's starting index (indexing starts from 1). This value overrides the inferred query start position by AbSeq.

`fr4cut` logical. The end of FR4 is marked as the end of the sequence if set to TRUE, otherwise the end of the sequence is either the end of the read itself, or trimmed to `--trim3 <num>`.

`domainSystem` character. Domain system to use in IgBLAST, possible values are either `imgt` or `kabat`.

See Also

`abseqReport` returns a `list` of `AbSeqRep` objects.

Examples

```
# this class is not directly constructed by users, but as a return
# value from the abseqReport method.

# Use example data from abseqR as abseqPy's output, substitute this
# with your own abseqPy output directory
abseqPyOutput <- tempdir()
file.copy(system.file("extdata", "ex", package = "abseqR"), abseqPyOutput, recursive=TRUE)
samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 0)
```

`abseqReport` *Visualize all analysis conducted by abseqPy*

Description

Plots all samples in the output directory supplied to abseqPy's `--outdir` or `-o` argument. Users can optionally specify which samples in `directory` should be compared. Doing so generates additional plots for clonotype comparison and the usual plots will also conveniently include these samples using additional `aesthetics`.

Calling this function with a valid `directory` will always return a named `list` of objects; these individual objects can be combined using the `+` operator to form a new comparison, in which the report function accepts as its first parameter.

Usage

```
abseqReport(directory, report, compare, BPPARAM)
```

Arguments

`directory`	string type. directory as specified in `-o` or `--outdir` in abseqPy. This tells AbSeq where to look for abseqPy's output.
`report`	(optional) integer type. The possible values are: • 0 - does nothing (returns named list of AbSeqRep objects) • 1 - generates plots for csv files • 2 - generates a report that collates all plots • 3 - generates interactive plots in report (default) each higher value also does what the previous values do. For example, `report = 2` will return a named list of AbSeqRep objects, plot csv files, and generate a (non-interactive)HTML report that collates all the plots together.
`compare`	(optional) vector of strings. From the samples in found in `directory` directory, they can be selected and compared against each other. For example, to compare "sample1" with "sample2" and "sample3" with "sample4", `compare` should be c("sample1,sample2", "sample3,sample4"). An error will be thrown if the samples specified in this parameter are not found in `directory`.
`BPPARAM`	(optional) BiocParallel backend. Configures the parallel implementation. Refer to BiocParallel for more information. By default, use all available cores.

Value

named list. List of AbSeqRep objects. The names of the list elements are taken directly from the repertoire object itself. This return value is consistent with the return value of `report`.

See Also

AbSeqRep

`report`. Analogous function, but takes input from an AbSeqRep or AbSeqCRep object instead.

Examples

```
# Use example data from abseqR as abseqPy's output, substitute this
# with your own abseqPy output directory
abseqPyOutput <- tempdir()
file.copy(system.file("extdata", "ex", package = "abseqR"), abseqPyOutput, recursive=TRUE)

### 1. The `report` parameter usage example:

# report = 0; don't plot, don't collate a HTML report, don't show anything interactive
samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 0)
# samples is now a named list of AbSeqRep objects

# report = 1; just plot pngs; don't collate a HTML report; nothing interactive
# samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 1)
# samples is now a named list of AbSeqRep objects

# report = 2; plot pngs; collate a HTML report; HTML report will NOT be interactive
# samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 2)
# samples is now a named list of AbSeqRep objects

# report = 3 (default); plot pngs; collate a HTML report; HTML report will be interactive
# samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 3)
# samples is now a named list of AbSeqRep objects

### 2. Using the return value of abseqReport:

# NOTE, often, this is used to load multiple samples from different directories
# using abseqReport (with report = 0), then the samples are added together
# before calling the report function. This is most useful when the samples
# live in different abseqPy output directory.

# Note that the provided example data has PCR1, PCR2, and PCR3
# samples contained within the directory
stopifnot(names(samples) == c("PCR1", "PCR2", "PCR3"))

# as a hypothetical example, say we found something
# interesting in PCR1 and PCR3, and we want to isolate them:
# we want to explicitly compare PCR1 with PCR3
pcr13 <- samples[["PCR1"]] + samples[["PCR3"]]

# see abseqR::report for more information.
# abseqR::report(pcr13)      # uncomment this line to run

### BPPARAM usage:

# 4 core machine, use all cores -  use whatever value that suits you
```

```
nproc <- 4
# samples <- abseqReport(file.path(abseqPyOutput, "ex"),
#                        BPPARAM = BiocParallel::MulticoreParam(nproc))


# run sequentially - no multiprocessing
# samples <- abseqReport(file.path(abseqPyOutput, "ex"),
#                        BPPARAM = BiocParallel::SerialParam())

# see https://bioconductor.org/packages/release/bioc/html/BiocParallel.html
# for more information about how to use BPPARAM and BiocParallel in general.
```

`report` *Plots AbSeqRep or AbSeqCRep object to the specfied directory*

Description

Plots all samples in the `object` argument and saves the analysis in `outputDir`. Users can optionally specify which samples in `object` should be compared. Doing so generates additional plots for clonotype comparison and the usual plots will also conveniently include these samples using additional `aesthetics`.

This method is analogous to `abseqReport`. The only difference is that this method accepts AbSeqRep or AbSeqCRep objects as its first parameter, and the `outputDir` specifies where to store the result.

Usage

```
report(object, outputDir, report = 3)

## S4 method for signature 'AbSeqRep'
report(object, outputDir, report = 3)

## S4 method for signature 'AbSeqCRep'
report(object, outputDir, report = 3)
```

Arguments

`object`	AbSeqRep or AbSeqCRep object to plot.
`outputDir`	string type. Directory where analysis will be saved to.
`report`	(optional) integer type. The possible values are: • 0 - does nothing (returns named list of AbSeqRep objects) • 1 - generates plots for csv files • 2 - generates a report that collates all plots • 3 - generates interactive plots in report (default) each value also does what the previous values do. For example, `report = 2` will return a named list of AbSeqRep objects, plot csv files, and generate a (non-interactive)HTML report that collates all the plots together.

Value

named list. List of AbSeqRep objects. The names of the list elements are taken directly from the repertoire object itself. This return value is consistent with the return value of `abseqReport`.

See Also

`abseqReport`. Analogus function, but takes input from a string that signifies the output directory of abseqPy as the first arugment instead.

AbSeqRep

AbSeqCRep

Examples

```
# Use example data from abseqR as abseqPy's output, substitute this
# with your own abseqPy output directory
abseqPyOutput <- tempdir()
file.copy(system.file("extdata", "ex", package = "abseqR"), abseqPyOutput, recursive=TRUE)
samples <- abseqReport(file.path(abseqPyOutput, "ex"), report = 0)


# The provided example data has PCR1, PCR2, and PCR3 samples contained within
# We can use the + operator to combine samples, thus requesting the
# report function to compare them:
pcr12 <- samples[["PCR1"]] + samples[["PCR2"]]

# generate plots and report for this new comparison
# report(pcr12, "PCR1_vs_PCR2")

# generate plots only
# report(pcr12, "PCR1_vs_PCR2", report = 1)

# generate plots, and a non-interactive report
# report(pcr12, "PCR1_vs_PCR2", report = 2)

# generate plots, and an interactive report
# report(pcr12, "PCR1_vs_PCR2", report = 3)   # this is the default
```

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