Package 'abseqR'

January 29, 2026

Type Package

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

Version 1.28.0

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 capabili-
ties 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

.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

.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

.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 distri-
butions 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 sam-
                 ples. (i.e. the intersection)

.save   logical type, save Rdata?

Value

`.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

.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 com-
                 pare "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 option-
ally 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 AbSe-
qRep 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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