

# Package ‘abseqR’

May 6, 2026

**Type** Package

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

**Version** 1.31.0

**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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## Contents

+ ,AbSeqCRep,AbSeqCRep-method	4
+ ,AbSeqCRep,AbSeqRep-method	5
+ ,AbSeqRep,AbSeqCRep-method	6
+ ,AbSeqRep,AbSeqRep-method	7
.abundanceAnalysis	8
.abundancePlot	8
.alignQualityHeatMaps	9
.allPrimerNames	9
.aminoAcidBar	10
.aminoAcidPlot	10
.analyzeUpstreamValidity	11
.annotAnalysis	11
.asRepertoireAlignLen	12
.asRepertoireBitscore	12
.asRepertoireChain	13
.asRepertoireDir	13
.asRepertoireList	14
.asRepertoireName	14
.asRepertoirePrimer3	15
.asRepertoirePrimer5	15
.asRepertoireQueryStart	16
.asRepertoireSubjectStart	16
.asRepertoireUpstream	17
.boxPlot	17
.calculateDInd	18
.calculateDiversityEstimates	18
.canonicalizeTitle	19
.capitalize	19
.checkVert	20
.cloneDistHist	20
.cloneDistMarginal	21
.clonotypeAnalysis	21
.collateReports	22
.commonPrimerNames	22
.correlationTest	23
.distanceMeasure	23
.diversityAnalysis	24
.emptyPlot	24
.findRepertoires	25

.generateAllSpectratypes . . . . .	25
.generateDelayedReport . . . . .	26
.generateReport . . . . .	26
.getLineTypes . . . . .	27
.getTotal . . . . .	27
.hmFromMatrix . . . . .	28
.inferAnalyzed . . . . .	28
.loadMatrixFromDF . . . . .	29
.loadSamplesFromString . . . . .	29
.pairwiseComparison . . . . .	30
.plotCirclize . . . . .	30
.plotDist . . . . .	31
.plotDiversityCurves . . . . .	32
.plotDuplication . . . . .	32
.plotErrorDist . . . . .	33
.plotIGVErrors . . . . .	33
.plotIGVUpstreamLenDist . . . . .	34
.plotIGVUpstreamLenDistDetailed . . . . .	35
.plotPrimerIGVStatus . . . . .	35
.plotPrimerIntegrity . . . . .	36
.plotRarefaction . . . . .	37
.plotRecapture . . . . .	37
.plotSamples . . . . .	38
.plotSpectratype . . . . .	38
.plotUpstreamLength . . . . .	39
.plotUpstreamLengthDist . . . . .	40
.primerAnalysis . . . . .	40
.prodDistPlot . . . . .	41
.productivityAnalysis . . . . .	42
.productivityPlot . . . . .	42
.readSummary . . . . .	43
.regionAnalysis . . . . .	43
.reportLBE . . . . .	44
.saveAs . . . . .	44
.scatterPlot . . . . .	45
.scatterPlotComplex . . . . .	45
.secretionSignalAnalysis . . . . .	46
.substituteStringInFile . . . . .	47
.summarySE . . . . .	47
.topNDist . . . . .	48
.UTR5Analysis . . . . .	48
.vennIntersection . . . . .	49
AbSeqCRep-class . . . . .	49
AbSeqRep-class . . . . .	50
abseqReport . . . . .	52
report . . . . .	54

---

+,AbSeqCRep,AbSeqCRep-method

*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**

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

**Value**

None

---

*.abundancePlot*      *Abundance distribution*

---

**Description**

Abundance distribution

**Usage**

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

**Arguments**

<i>files</i>	list type. list of files in abundance directory
<i>sampleNames</i>	vector type. 1-1 correspondance to files
<i>outputDir</i>	string type.
<i>skipDgene</i>	logical type. Skip D germline abundance plot if TRUE.
<i>.save</i>	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**

<code>df</code>	dataframe
<code>scale</code>	logical. scale to proportion?
<code>region</code>	string. which region is this
<code>germ</code>	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**

<code>compositionDirectory</code>	string type.
<code>outdir</code>	string type.
<code>sampleName</code>	string type.
<code>regions</code>	logical type. vector of FR/CDR regions to plot
<code>.save</code>	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**

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

**Value**

none

---

`.asRepertoireAlignLen` *Accessor for alignlen slot*

---

**Description**

Accessor for alignlen slot

**Usage**

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

**Arguments**

<code>object</code>	AbSeqRep object
<code>collapse</code>	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**

<code>object</code>	AbSeqRep object
<code>collapse</code>	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

---

<code>.asRepertoireList</code>	<i>Accessor for <a href="#">AbSeqCRep</a>'s list of <a href="#">AbSeqRep</a> objects</i>
--------------------------------	--

---

**Description**

Accessor for [AbSeqCRep](#)'s list of [AbSeqRep](#) objects

**Usage**

```
.asRepertoireList(object)
```

**Arguments**

object	<a href="#">AbSeqCRep</a> object
--------	----------------------------------

**Value**

list type, list of [AbSeqRep](#) objects that together, compose this [AbSeqCRep](#) object.

---

<code>.asRepertoireName</code>	<i>Accessor for the name slot</i>
--------------------------------	-----------------------------------

---

**Description**

Accessor for the name slot

**Usage**

```
.asRepertoireName(object)
```

**Arguments**

object	<a href="#">AbSeqRep</a> 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(qualityDirectories, diversityOut, sampleNames)
```

**Arguments**

qualityDirectories list type. List of directories to diversity dir

diversityOut string type. Output directory

sampleNames vector type. 1-1 with qualityDirectories 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

---

<code>.checkVert</code>	<i>Checks if abseqPy has a metadata line that suggests the orientation</i>
-------------------------	--

---

**Description**

Checks if abseqPy has a metadata line that suggests the orientation

**Usage**

```
.checkVert(filename)
```

**Arguments**

<code>filename</code>	csv filename
-----------------------	--------------

**Value**

True if CSV metadata says "plot vertically"

---

<code>.cloneDistHist</code>	<i>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)</i>
-----------------------------	---

---

**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**

<code>df.original</code>	dataframe with all clones
<code>otherClones</code>	clones from the other dataframe
<code>lim.min</code>	x-axis minimum limit
<code>flip</code>	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

---

<code>.collateReports</code>	<i>Collate all HTML reports into a single directory and create an entry index.html file that redirects to all collated HTML files</i>
------------------------------	---

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

Nothing

---

<code>.commonPrimerNames</code>	<i>Collect the intersection of all primer names within a collection of primer files</i>
---------------------------------	---

---

**Description**

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

**Usage**

```
.commonPrimerNames(primerFiles)
```

**Arguments**

<code>primerFiles</code>	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**

<code>diversityDirectories</code>	list type. List of directories to diversity dir
<code>diversityOut</code>	string type. Output directory
<code>sampleNames</code>	vector type. 1-1 with <code>diversityDirectories</code>
<code>mashedNames</code>	string type. Prefix for output files using "mashed-up" sample names
<code>.save</code>	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/rmarkdown>

### Usage

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

### Arguments

<code>root</code>	string, project root directory.
<code>compare</code>	vector of strings, each string is a comparison defined by the user (assumes that this value has been checked).
<code>interactivePlot</code>	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` objects*

---

### Description

Generates HTML report from `AbSeqRep` and `AbSeqCRep` objects

### Usage

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

### Arguments

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

### Value

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

---

.getLineTypes	<i>Helper function to return line types by importance based on provided CD/Fs regions</i>
---------------	---

---

**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	<i>Get total number of samples (n)</i>
-----------	--

---

**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.

---

<code>.hmFromMatrix</code>	<i>Plots a plotly heatmap from provided matrix</i>
----------------------------	--

---

**Description**

Plots a plotly heatmap from provided matrix

**Usage**

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

**Arguments**

<code>m</code>	matrix type
<code>title</code>	character type
<code>xlabel</code>	character type
<code>ylabel</code>	character type

**Value**

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

---

<code>.inferAnalyzed</code>	<i>Returns all samples found under sampleDirectory</i>
-----------------------------	--

---

**Description**

Returns all samples found under sampleDirectory

**Usage**

```
.inferAnalyzed(sampleDirectory)
```

**Arguments**

<code>sampleDirectory</code>	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	<i>Bar plotter</i>
-----------	--------------------

---

**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**

<code>region</code>	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.
<code>diversityDirectories</code>	list type. List of directories to diversity dir
<code>sampleNames</code>	vector type. 1-1 with diversityDirectories
<code>mashedNames</code>	string type. Prefix for output files using "mashed-up"
<code>diversityOut</code>	string type. Output directory sample names
<code>.save</code>	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**

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

**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**

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

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

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

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

**Value**

None

---

<code>.prodDistPlot</code>	<i>Plots a distribution plot for different productivity analysis files</i>
----------------------------	--

---

**Description**A wrapper for `plotDist`**Usage**

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

**Arguments**

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

**Value**

None

---

*.productivityAnalysis* *Conducts productivty analysis*

---

**Description**

Conducts productivty analysis

**Usage**

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

**Arguments**

<i>productivityDirectories</i>	list type. List of directories
<i>prodOut</i>	string type. Output directory
<i>sampleNames</i>	vector type. 1-1 with productivity directories
<i>combinedNames</i>	string type. Title friendly "combined" sample names
<i>mashedNames</i>	string type. File friendly "mashed-up" sample names
<i>.save</i>	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**

<i>dataframes</i>	list type. List of sample dataframes
<i>sampleNames</i>	vector type. 1-1 with dataframes

**Value**

ggplot2 object

---

.readSummary	<i>Return value specified by key from AbSeq's summary file</i>
--------------	--

---

### Description

Return value specified 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) <ul style="list-style-type: none"><li>• RawReads</li><li>• AnnotatedReads</li><li>• FilteredReads</li><li>• ProductiveReads</li></ul>

### 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	<i>Title Shows varying regions for a given clonotype defined by its CDR3</i>
-----------------	--

---

### 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

---

<code>.reportLBE</code>	<i>Reports abundance-based (Lower bound) diversity estimates using the Vegan package</i>
-------------------------	--

---

### 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 .... | +-----+

---

<code>.saveAs</code>	<i>Saves ggplot object as a Rdata file.</i>
----------------------	---

---

### Description

It's a convenient 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 technique was shamelessly plagiarised from <https://github.com/mikessh/vdjtools/blob/master> (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 occurrence of 'key' with 'value' in 'filename'*

---

### Description

Substitutes the first occurrence 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](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 summarized
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	<i>Title Clonotype table</i>
-----------	------------------------------

---

**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	<i>5' UTR analysis</i>
---------------	------------------------

---

**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`, 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 specified 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: <ul style="list-style-type: none"> <li>• 0 - does nothing (returns named list of <a href="#">AbSeqRep</a> objects)</li> <li>• 1 - generates plots for csv files</li> <li>• 2 - generates a report that collates all plots</li> <li>• 3 - generates interactive plots in report (default)</li> </ul>

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](#). Analogous function, but takes input from a string that signifies the output directory of abseqPy as the first argument 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
```

# Index

- + , AbSeqCRep, AbSeqCRep-method, 4
- + , AbSeqCRep, AbSeqRep-method, 5
- + , AbSeqRep, AbSeqCRep-method, 6
- + , AbSeqRep, AbSeqRep-method, 7
- .UTR5Analysis, 48
- .abundanceAnalysis, 8
- .abundancePlot, 8
- .alignQualityHeatMaps, 9
- .allPrimerNames, 9
- .aminoAcidBar, 10
- .aminoAcidPlot, 10
- .analyzeUpstreamValidity, 11
- .annotAnalysis, 11
- .asRepertoireAlignLen, 12
- .asRepertoireBitscore, 12
- .asRepertoireChain, 13
- .asRepertoireDir, 13
- .asRepertoireList, 14
- .asRepertoireName, 14
- .asRepertoirePrimer3, 15
- .asRepertoirePrimer5, 15
- .asRepertoireQueryStart, 16
- .asRepertoireSubjectStart, 16
- .asRepertoireUpstream, 17
- .boxPlot, 17
- .calculateDInd, 18
- .calculateDiversityEstimates, 18
- .canonicalizeTitle, 19
- .capitalize, 19
- .checkVert, 20
- .cloneDistHist, 20
- .cloneDistMarginal, 21
- .clonotypeAnalysis, 21
- .collateReports, 22
- .commonPrimerNames, 22
- .correlationTest, 23
- .distanceMeasure, 23
- .diversityAnalysis, 24
- .emptyPlot, 24
- .findRepertoires, 25
- .generateAllSpectratypes, 25
- .generateDelayedReport, 26
- .generateReport, 26
- .getLineTypes, 27
- .getTotal, 27
- .hmFromMatrix, 28
- .inferAnalyzed, 28
- .loadMatrixFromDF, 29
- .loadSamplesFromString, 29
- .pairwiseComparison, 30
- .plotCirclize, 30
- .plotDist, 31
- .plotDiversityCurves, 32
- .plotDuplication, 32
- .plotErrorDist, 33
- .plotIGVErrors, 33
- .plotIGVUpstreamLenDist, 34, 35
- .plotIGVUpstreamLenDistDetailed, 34, 35
- .plotPrimerIGVStatus, 35
- .plotPrimerIntegrity, 36
- .plotRarefaction, 37
- .plotRecapture, 37
- .plotSamples, 38
- .plotSpectratype, 38
- .plotUpstreamLength, 39
- .plotUpstreamLengthDist, 40
- .primerAnalysis, 40
- .prodDistPlot, 41
- .productivityAnalysis, 42
- .productivityPlot, 42
- .readSummary, 43
- .regionAnalysis, 43
- .reportLBE, 44
- .saveAs, 44
- .scatterPlot, 45
- .scatterPlotComplex, 45
- .secretionSignalAnalysis, 46
- .substituteStringInFile, 47
- .summarySE, 47
- .topNDist, 48
- .vennIntersection, 49
- AbSeqCRep, 4–7, 14, 26, 49, 50, 53–55
- AbSeqCRep (AbSeqCRep-class), 49
- AbSeqCRep-class, 49
- AbSeqRep, 5–7, 14, 26, 49, 52–55
- AbSeqRep (AbSeqRep-class), 50

AbSeqRep-class, [50](#)  
abseqReport, [4–7](#), [49–51](#), [52](#), [54](#), [55](#)  
report, [49](#), [50](#), [52](#), [53](#), [54](#)  
report, AbSeqCRep-method (report), [54](#)  
report, AbSeqRep-method (report), [54](#)