

Package ‘sangeranalyseR’

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Type Package

Title sangeranalyseR: a suite of functions for the analysis of Sanger sequence data in R

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Description This package builds on sangerseqR to allow users to create contigs from collections of Sanger sequencing reads. It provides a wide range of options for a number of commonly-performed actions including read trimming, detecting secondary peaks, and detecting indels using a reference sequence. All parameters can be adjusted interactively either in R or in the associated Shiny applications. There is extensive online documentation, and the package can outputs detailed HTML reports, including chromatograms.

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URL <https://github.com/roblanf/sangeranalyseR>

BugReports <https://github.com/roblanf/sangeranalyseR/issues>

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'ClassObjectResults.R' 'ClassQualityReport.R'
'ClassSangerRead.R' 'ClassSangerAlignment.R'
'ClassSangerContig.R' 'Constructors.R' 'GlobalTrimApp.R'

'LoadMessage.R' 'MethodSangerAlignment.R'
 'MethodSangerContig.R' 'MethodSangerRead.R' 'MethodShared.R'
 'MethodsQualityReport.R' 'RcppExports.R'
 'ShinySangerAlignmentServer.R' 'ShinySangerAlignmentUI.R'
 'ShinySangerContigServer.R' 'ShinySangerContigUI.R'
 'ShinyServerModule.R' 'UtilitiesFunc.R'
 'UtilitiesFuncInputChecker.R' 'data.R'
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Contents

ChromatogramParam-class	3
chromatogram_overwrite	4
chromatogram_plotly	5
generateReport	6
generateReportSA	7
generateReportSC	8
generateReportSR	9
globalTrimApp	9
launchApp	10
launchAppSA	11
launchAppSC	11
MakeBaseCalls	12
ObjectResults-class	12
primaryAASeqS1	13
primaryAASeqS2	14
primaryAASeqS3	14
qualityBasePlot	15
QualityReport-class	15
QualityReport-class-qualityBasePlot	17
QualityReport-class-updateQualityParam	17
qualityReportData	18
readTable	19
SangerAlignment	19
SangerAlignment-class	23
SangerAlignment-class-generateReportSA	26
SangerAlignment-class-launchAppSA	27
SangerAlignment-class-updateQualityParam	27
SangerAlignment-class-writeFastaSA	28
sangerAlignmentData	29

sangeranalyseR	29
SangerContig	30
SangerContig-class	33
SangerContig-class-generateReportSC	36
SangerContig-class-launchAppSC	37
SangerContig-class-readTable	38
SangerContig-class-updateQualityParam	39
SangerContig-class-writeFastaSC	40
sangerContigData	41
SangerRead	41
SangerRead-class	43
SangerRead-class-generateReportSR	45
SangerRead-class-MakeBaseCalls	46
SangerRead-class-qualityBasePlot	47
SangerRead-class-readTable	48
SangerRead-class-updateQualityParam	48
SangerRead-class-writeFastaSR	49
sangerReadFData	50
updateQualityParam	51
writeFasta	52
writeFastaSA	53
writeFastaSC	54
writeFastaSR	54
Index	56

ChromatogramParam-class

ChromatogramParam

Description

An S4 class storing chromatogram related inputs in a SangerRead S4 object.

Slots

`baseNumPerRow` It defines maximum base pairs in each row. The default value is 100.

`heightPerRow` It defines the height of each row in chromatogram. The default value is 200.

`signalRatioCutoff` The ratio of the height of a secondary peak to a primary peak. Secondary peaks higher than this ratio are annotated. Those below the ratio are excluded. The default value is 0.33.

`showTrimmed` The logical value storing whether to show trimmed base pairs in chromatogram. The default value is TRUE.

Author(s)

Kuan-Hao Chao

Examples

```
Chromatogram <- new("ChromatogramParam",
                    baseNumPerRow = 100,
                    heightPerRow = 200,
                    signalRatioCutoff = 0.33,
                    showTrimmed = TRUE)
```

chromatogram_overwrite

Static base-R chromatogram renderer with a corrected color palette.

Description

Reimplementation of `sangerseqR::chromatogram` with a fix for base color rendering. Intended for static (PDF / PNG) export. For interactive embedding in Shiny see [chromatogram_plotly](#).

Usage

```
chromatogram_overwrite(
  obj,
  trim5 = 0,
  trim3 = 0,
  showcalls = c("primary", "secondary", "both", "none"),
  width = 100,
  height = 2,
  cex.mtext = 1,
  cex.base = 1,
  ylim = 3,
  filename = NULL,
  showtrim = FALSE,
  showhets = TRUE,
  colors = "default"
)
```

Arguments

<code>obj</code>	A <code>sangerseq</code> or <code>SangerRead</code> instance.
<code>trim5</code>	Integer; number of bases to mark as 5' trimmed.
<code>trim3</code>	Integer; number of bases to mark as 3' trimmed.
<code>showcalls</code>	One of "primary", "secondary", "both", or "none".
<code>width</code>	Bases per row.
<code>height</code>	Plot height per row (relative units).
<code>cex.mtext</code>	Text size for marginal annotations.
<code>cex.base</code>	Text size for base-call labels.
<code>ylim</code>	Maximum y-axis multiplier (relative to robust mean).
<code>filename</code>	Optional path to write a PDF.
<code>showtrim</code>	Logical; if TRUE, shade the trim regions.
<code>showhets</code>	Logical; if TRUE, mark heterozygous positions.
<code>colors</code>	Either "default", "cb_friendly", or a length-5 character vector of hex colours.

Value

Invisibly returns NULL; called for its side effect of plotting (or writing to filename).

Examples

```
data(sangerReadFData)

chromatogram_overwrite(sangerReadFData)
```

chromatogram_plotly *Render a Sanger chromatogram as an interactive Plotly widget*

Description

Wraps the four trace channels (A/C/G/T) of a sangerseq / SangerRead object into a single plotly htmlwidget that renders via WebGL (scattergl). Intended for embedding in Shiny dashboards where the static `chromatogram_overwrite` would be too heavy.

Usage

```
chromatogram_plotly(
  obj,
  trim5 = 0,
  trim3 = 0,
  max_points = 8000L,
  showtrim = FALSE,
  colors = "default"
)
```

Arguments

obj	A sangerseq or SangerRead instance with a populated traceMatrix.
trim5	Integer; if showtrim is TRUE, shade the first trim5 positions to indicate the 5' trim region.
trim3	Integer; if showtrim is TRUE, shade the last trim3 positions to indicate the 3' trim region.
max_points	Integer cap on the number of points rendered per channel. When the trace exceeds max_points it is downsampled by uniform stride.
showtrim	Logical; whether to overlay shaded trim regions.
colors	Either "default", "cb_friendly", or a length-5 character vector of hex colours for (A, T, C, G, other).

Value

A plotly htmlwidget. The returned object carries a `downsample_info` attribute reporting the original and rendered point counts plus the stride.

Examples

```
data(sangerReadFData)

chromatogram_plotly(sangerReadFData)
```

generateReport	<i>Method generateReport</i>
----------------	------------------------------

Description

A method which generates final reports of the SangerRead, SangerContig, and SangerAlignment instance.

Usage

```
generateReport(
  object,
  outputDir = NULL,
  includeSangerContig = TRUE,
  includeSangerRead = TRUE,
  colors = "default",
  ...
)
```

Arguments

object	A SangerRead, SangerContig, or SangerAlignment S4 instance.
outputDir	The output directory of the generated HTML report.
includeSangerContig	The parameter that decides whether to include SangerContig level report. The value is TRUE or FALSE and the default is TRUE.
includeSangerRead	The parameter that decides whether to include SangerRead level report. The value is TRUE or FALSE and the default is TRUE.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.
...	Further generateReportSR, generateReportSC, and generateReportSA related parameters.

Value

A SangerRead, SangerContig, or SangerAlignment object.

Author(s)

Kuan-Hao Chao

Examples

```

data(sangerReadFData)
data(sangerContigData)
data(sangerAlignmentData)

generateReport(sangerReadFData)
generateReport(sangerReadFData, colors="cb_friendly")
generateReport(sangerContigData)
generateReport(sangerContigData, colors="cb_friendly")
generateReport(sangerAlignmentData)
generateReport(sangerAlignmentData, colors="cb_friendly")

```

generateReportSA	<i>Method generateReportSA</i>
------------------	--------------------------------

Description

Method generateReportSA

Usage

```

generateReportSA(
  object,
  outputDir = NULL,
  includeSangerContig = TRUE,
  includeSangerRead = TRUE,
  colors = "default",
  ...
)

```

Arguments

object	A SangerAlignment S4 instance.
outputDir	The output directory of the generated HTML report.
includeSangerContig	The parameter that decides whether to include SangerContig level report. The value is TRUE or FALSE and the default is TRUE.
includeSangerRead	The parameter that decides whether to include SangerRead level report. The value is TRUE or FALSE and the default is TRUE.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.
...	Further generateReportSA-related parameters.

Value

The output absolute path to the SangerAlignment's HTML file.

Examples

```
data(sangerAlignmentData)

generateReportSA(sangerAlignmentData)
```

generateReportSC	<i>Method generateReportSC</i>
------------------	--------------------------------

Description

Method generateReportSC

Usage

```
generateReportSC(
  object,
  outputDir = NULL,
  includeSangerRead = TRUE,
  colors = "default",
  ...
)
```

Arguments

object	A SangerContig S4 instance.
outputDir	The output directory of the generated HTML report.
includeSangerRead	The parameter that decides whether to include SangerRead level report. The value is TRUE or FALSE and the default is TRUE.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.
...	Further generateReportSC-related parameters.

Value

The output absolute path to the SangerContig's HTML file.

Examples

```
data(sangerContigData)

generateReportSC(sangerContigData)
```

generateReportSR	<i>Method generateReportSR</i>
------------------	--------------------------------

Description

Method generateReportSR

Usage

```
generateReportSR(object, outputDir = NULL, colors = "default", ...)
```

Arguments

object	A SangerRead S4 instance.
outputDir	The output directory of the generated HTML report.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.
...	Further generateReportSR-related parameters.

Value

The output absolute path to the SangerRead's HTML file.

Examples

```
data(sangerReadFData)
generateReportSR(sangerReadFData)
```

globalTrimApp	<i>Launch a global trimming controls dashboard</i>
---------------	--

Description

Opens a Shiny gadget that exposes M1/M2 trimming parameters as sliders/numeric inputs, applies any change to *every* SangerRead in the supplied SangerAlignment via 'updateQualityParam(SA, ...)', and live-previews the consensus length, contig count, and number of reads that survive the new trim.

Unlike 'launchAppSA()' (which exposes per-read trimming) this app operates globally — useful when a whole batch needs the same re-trimming policy.

Usage

```
globalTrimApp(SA)
```

Arguments

SA	A SangerAlignment instance.
----	-----------------------------

Value

The (last-applied) SangerAlignment when the user clicks "Done", or NULL if the user cancels.

Examples

```
## Not run:
data(sangerAlignmentData)
SA2 <- globalTrimApp(sangerAlignmentData)

## End(Not run)
```

launchApp

Method launchApp

Description

A method which launches Shiny application of the SangerContig and SangerAlignment instance.

Usage

```
launchApp(object, outputDir = NULL, colors = "default")
```

Arguments

object	A SangerContig or SangerAlignment S4 instance.
outputDir	The output directory of the saved new SangerContig or SangerAlignment S4 instance.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.

Value

A SangerContig or SangerAlignment object.

Author(s)

Kuan-Hao Chao

Examples

```
data(sangerContigData)
data(sangerAlignmentData)
## Not run:
launchApp(sangerContigData)
launchApp(sangerContigData, colors="cb_friendly")
launchApp(sangerAlignmentData)
launchApp(sangerAlignmentData, colors="cb_friendly")
## End(Not run)
```

launchAppSA	<i>Method launchAppSA</i>
-------------	---------------------------

Description

Method launchAppSA

Usage

```
launchAppSA(object, outputDir = NULL, colors = "default")
```

Arguments

object	A SangerAlignment S4 instance.
outputDir	The output directory of the saved new SangerAlignment S4 instance.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.

Value

A shiny.appobj object.

Examples

```
data(sangerAlignmentData)
## Not run:
launchAppSA(sangerAlignmentData)
## End(Not run)
```

launchAppSC	<i>Method launchAppSC</i>
-------------	---------------------------

Description

Method launchAppSC

Usage

```
launchAppSC(object, outputDir = NULL, colors = "default")
```

Arguments

object	A SangerContig S4 instance.
outputDir	The output directory of the saved new SangerContig S4 instance.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.

Value

A shiny.appobj object.

Examples

```
data(sangerContigData)
## Not run:
launchAppSC(sangerContigData)
## End(Not run)
```

MakeBaseCalls	<i>Method MakeBaseCalls</i>
---------------	-----------------------------

Description

Method MakeBaseCalls

Usage

```
MakeBaseCalls(object, signalRatioCutoff = 0.33)
```

Arguments

object	A SangerRead S4 instance.
signalRatioCutoff	The ratio of the height of a secondary peak to a primary peak. Secondary peaks higher than this ratio are annotated. Those below the ratio are excluded. The default value is 0.33.

Value

A SangerRead instance.

Examples

```
data(sangerReadFDData)
MakeBaseCalls(sangerReadFDData, signalRatioCutoff = 0.22)
```

ObjectResults-class	<i>ObjectResults</i>
---------------------	----------------------

Description

An S4 class storing results related inputs in a SangerRead, SangerContig, and SangerAlignment S4 object.

Slots

creationResult Single logical: TRUE if construction succeeded, FALSE if any input failed validation.
errorMessages Character vector of error messages collected during construction (one per failure).
errorTypes Character vector of machine-readable error tags (e.g. "PARAMETER_RANGE_ERROR"); same length as errorMessages.
warningMessages Character vector of warning messages emitted during construction.
warningTypes Character vector of machine-readable warning tags; same length as warningMessages.
readResultTable A data frame with one row per Sanger read processed, recording per-read creation outcome and any error tag.
printLevel Character indicating which tier ("SangerRead", "SangerContig", or "SangerAlignment") emitted these results.

Author(s)

Kuan-Hao Chao

Examples

```

objectResults <- new("ObjectResults",
  creationResult = TRUE,
  errorMessages = character(0),
  errorTypes = character(0),
  warningMessages = character(0),
  warningTypes = character(0),
  readResultTable = data.frame(),
  printLevel = "SangerRead")
  
```

primaryAASeqS1	<i>Method primaryAASeqS1</i>
----------------	------------------------------

Description

Method primaryAASeqS1

Usage

```

primaryAASeqS1(object)

## S4 method for signature 'SangerRead'
primaryAASeqS1(object)
  
```

Arguments

object A SangerRead S4 instance.

Value

The frame-1 amino-acid translation of the read's primary sequence as an AAString. Computed lazily — if the slot was populated eagerly at construction time it is returned directly; if the slot is empty (the default when refAminoAcidSeq == "" and lazyAA = TRUE) it is computed via calculateAASeq() on demand.

Examples

```
data(sangerReadFData)
primaryAASeqS1(sangerReadFData)
```

```
primaryAASeqS2      Method primaryAASeqS2
```

Description

Method primaryAASeqS2

Usage

```
primaryAASeqS2(object)

## S4 method for signature 'SangerRead'
primaryAASeqS2(object)
```

Arguments

object A SangerRead S4 instance.

Value

Frame-2 AA translation as AAString (lazy).

Examples

```
data(sangerReadFData)
primaryAASeqS2(sangerReadFData)
```

```
primaryAASeqS3      Method primaryAASeqS3
```

Description

Method primaryAASeqS3

Usage

```
primaryAASeqS3(object)

## S4 method for signature 'SangerRead'
primaryAASeqS3(object)
```

Arguments

object A SangerRead S4 instance.

Value

Frame-3 AA translation as AAStrng (lazy).

Examples

```
data(sangerReadFData)
primaryAASeqS3(sangerReadFData)
```

qualityBasePlot	<i>Method qualityBasePlot</i>
-----------------	-------------------------------

Description

Method qualityBasePlot

Usage

```
qualityBasePlot(object)
```

Arguments

object A QualityReport or SangerRead S4 instance

Value

A quality plot.

Examples

```
data(qualityReportData)
data(sangerReadFData)
qualityBasePlot(qualityReportData)
qualityBasePlot(sangerReadFData)
```

QualityReport-class	<i>QualityReport</i>
---------------------	----------------------

Description

An S4 class storing quality related inputs and results in a SangerRead S4 object.

Slots

TrimmingMethod The read trimming method for this SangerRead. The value must be "M1" (the default) or 'M2'.

M1TrimmingCutoff The trimming cutoff for the Method 1. If TrimmingMethod is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.

M2CutoffQualityScore The trimming cutoff quality score for the Method 2. If TrimmingMethod is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with M2SlidingWindowSize.

M2SlidingWindowSize The trimming sliding window size for the Method 2. If TrimmingMethod is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with M2CutoffQualityScore.

qualityPhredScores The Phred quality scores of each base pairs after base calling.

qualityBaseScores The probability of incorrect base call of each base pairs. They are calculated from qualityPhredScores.

rawSeqLength The number of nucleotides of raw primary DNA sequence.

trimmedSeqLength The number of nucleotides of trimmed primary DNA sequence.

trimmedStartPos The base pair index of trimming start point from 5' end of the sequence.

trimmedFinishPos The base pair index of trimming finish point from 3' end of the sequence.

rawMeanQualityScore The mean quality score of the primary sequence after base calling. In other words, it is the mean of qualityPhredScores.

trimmedMeanQualityScore The mean quality score of the trimmed primary sequence after base calling.

rawMinQualityScore The minimum quality score of the primary sequence after base calling.

trimmedMinQualityScore The minimum quality score of the trimmed primary sequence after base calling.

remainingRatio The remaining sequence length ratio after trimming.

Author(s)

Kuan-Hao Chao

Examples

```
inputFilePath <- system.file("extdata/", package = "sangeranalyseR")
A_chloroticaFFN <- file.path(inputFilePath,
                             "Allolobophora_chlorotica",
                             "ACHLO",
                             "Ach1_ACHLO006-09_1_F.ab1")
sangerReadF <- new("SangerRead",
                   inputSource      = "ABIF",
                   readFeature      = "Forward Read",
                   readFileName     = A_chloroticaFFN,
                   geneticCode      = GENETIC_CODE,
                   TrimmingMethod   = "M1",
                   M1TrimmingCutoff = 0.0001,
                   M2CutoffQualityScore = NULL,
                   M2SlidingWindowSize = NULL,
                   baseNumPerRow    = 100,
                   heightPerRow     = 200,
```

```

                                signalRatioCutoff = 0.33,
                                showTrimmed       = TRUE)
"@"(sangerReadF, QualityReport)

```

QualityReport-class-qualityBasePlot
qualityBasePlot

Description

A QualityReport method which creates quality base interactive plot.

Usage

```
## S4 method for signature 'QualityReport'
qualityBasePlot(object)
```

Arguments

object A QualityReport S4 instance.

Value

A quality plot.

Examples

```
data("qualityReportData")

qualityBasePlot(qualityReportData)
```

QualityReport-class-updateQualityParam
updateQualityParam

Description

A QualityReport method which updates quality base interactive plot.

Usage

```
## S4 method for signature 'QualityReport'
updateQualityParam(
  object,
  TrimmingMethod = "M1",
  M1TrimmingCutoff = 1e-04,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL
)
```

Arguments

object	A QualityReport S4 instance.
TrimmingMethod	The read trimming method for this SangerRead. The value must be "M1" (the default) or 'M2'.
M1TrimmingCutoff	The trimming cutoff for the Method 1. If TrimmingMethod is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
M2CutoffQualityScore	The trimming cutoff quality score for the Method 2. If TrimmingMethod is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with M2SlidingWindowSize.
M2SlidingWindowSize	The trimming sliding window size for the Method 2. If TrimmingMethod is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with M2CutoffQualityScore.

Value

A QualityReport instance.

Examples

```
data("qualityReportData")
updateQualityParam(qualityReportData,
  TrimmingMethod      = "M2",
  M1TrimmingCutoff    = NULL,
  M2CutoffQualityScore = 30,
  M2SlidingWindowSize = 15)
```

qualityReportData *QualityReport instance*

Description

A pre-built QualityReport S4 object derived from the bundled ACHLO ABIF fixture, suitable for vignette and example use without re-running the trimming pipeline.

Usage

```
data(qualityReportData)
```

Format

A [QualityReport-class](#) S4 object containing per-base Phred scores, the trimmed start/finish positions, and the raw / trimmed mean / minimum quality scores.

Author(s)

Kuan-Hao Chao

readTable	<i>Method readTable</i>
-----------	-------------------------

Description

Method readTable

Usage

```
readTable(object, indentation = 0, ...)
```

Arguments

object	A SangerRead, SangerContig, or SangerAlignment S4 instance.
indentation	The indentation for different level printing
...	Further generateReportSR-related parameters.

Value

None.

Examples

```
data(sangerReadFData)
data(sangerContigData)

readTable(sangerReadFData)
readTable(sangerContigData)
```

SangerAlignment	<i>SangerAlignment</i>
-----------------	------------------------

Description

the wrapper function for SangerAlignment

Usage

```
SangerAlignment(
  printLevel = "SangerAlignment",
  inputSource = "ABIF",
  processMethod = "REGEX",
  ABIF_Directory = NULL,
  FASTA_File = NULL,
  REGEX_SuffixForward = NULL,
  REGEX_SuffixReverse = NULL,
  CSV_NamesConversion = NULL,
  geneticCode = GENETIC_CODE,
  TrimmingMethod = "M1",
```

```

M1TrimmingCutoff = 1e-04,
M2CutoffQualityScore = NULL,
M2SlidingWindowSize = NULL,
baseNumPerRow = 100,
heightPerRow = 200,
signalRatioCutoff = 0.33,
showTrimmed = TRUE,
refAminoAcidSeq = "",
minReadsNum = 2,
minReadLength = 20,
minFractionCall = 0.5,
maxFractionLost = 0.5,
acceptStopCodons = TRUE,
readingFrame = 1,
processorsNum = 1,
BPPARAM = NULL,
lazyAA = TRUE,
minOverlapFraction = 0,
minOverlapBases = 0L,
alignSeqsParams = list(),
consensusMethod = "strict",
qualityAware = FALSE
)

```

Arguments

<code>printLevel</code>	Internal — controls log verbosity when this constructor is called recursively from a parent class. Defaults to "SangerAlignment"; do not set manually.
<code>inputSource</code>	The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".
<code>processMethod</code>	The method used to group reads into contigs. Either "REGEX" (use <code>REGEX_SuffixForward</code> / <code>REGEX_SuffixReverse</code>) or "CSV" (use <code>CSV_NamesConversion</code>). The default is "REGEX".
<code>ABIF_Directory</code>	The parent directory of all of the reads contained in ABIF format you wish to analyse. In <code>SangerAlignment</code> , all reads in subdirectories will be scanned recursively.
<code>FASTA_File</code>	If <code>inputSource</code> is "FASTA", then this value has to be the name of the FASTA file; if <code>inputSource</code> is "ABIF", then this value is "" by default.
<code>REGEX_SuffixForward</code>	The suffix of the filenames for forward reads in regular expression, i.e. reads that do not need to be reverse-complemented. For forward reads, it should be "_F.ab1".
<code>REGEX_SuffixReverse</code>	The suffix of the filenames for reverse reads in regular expression, i.e. reads that need to be reverse-complemented. For reverse reads, it should be "_R.ab1".
<code>CSV_NamesConversion</code>	The file path to the CSV file that provides read names that follow the naming regulation. If <code>inputSource</code> is "FASTA", then users need to prepare the csv file or make sure the original names inside FASTA file are valid; if <code>inputSource</code> is "ABIF", then this value is NULL by default.

geneticCode	Named character vector in the same format as GENETIC_CODE (the default), which represents the standard genetic code. This is the code with which the function will attempt to translate your DNA sequences. You can get an appropriate vector with the getGeneticCode() function. The default is the standard code.
TrimmingMethod	TrimmingMethod The read trimming method for this SangerRead. The value must be "M1" (the default) or 'M2'.
M1TrimmingCutoff	The trimming cutoff for the Method 1. If TrimmingMethod is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
M2CutoffQualityScore	The trimming cutoff quality score for the Method 2. If TrimmingMethod is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with M2SlidingWindowSize.
M2SlidingWindowSize	The trimming sliding window size for the Method 2. If TrimmingMethod is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with M2CutoffQualityScore.
baseNumPerRow	It defines maximum base pairs in each row. The default value is 100.
heightPerRow	It defines the height of each row in chromatogram. The default value is 200.
signalRatioCutoff	The ratio of the height of a secondary peak to a primary peak. Secondary peaks higher than this ratio are annotated. Those below the ratio are excluded. The default value is 0.33.
showTrimmed	The logical value storing whether to show trimmed base pairs in chromatogram. The default value is TRUE.
refAminoAcidSeq	An amino acid reference sequence supplied as a string or an AAString object. If your sequences are protein-coding DNA sequences, and you want to have frameshifts automatically detected and corrected, supply a reference amino acid sequence via this argument. If this argument is supplied, the sequences are then kept in frame for the alignment step. Fwd sequences are assumed to come from the sense (i.e. coding, or "+") strand. The default value is "".
minReadsNum	The minimum number of reads required to make a consensus sequence, must be 2 or more. The default value is 2.
minReadLength	Reads shorter than this will not be included in the readset. The default 20 means that all reads with length of 20 or more will be included. Note that this is the length of a read after it has been trimmed.
minFractionCall	Minimum fraction of the sequences required to call a consensus sequence for SangerContig at any given position (see the ConsensusSequence() function from DECIPHER for more information). Defaults to 0.75 implying that 3/4 of all reads must be present in order to call a consensus.
maxFractionLost	Numeric giving the maximum fraction of sequence information that can be lost in the consensus sequence for SangerContig (see the ConsensusSequence() function from DECIPHER for more information). Defaults to 0.5, implying that each consensus base can ignore at most 50 percent of the information at a given position.

acceptStopCodons	The logical value TRUE or FALSE. TRUE (the default): keep all reads, regardless of whether they have stop codons; FALSE: reject reads with stop codons. If FALSE is selected, then the number of stop codons is calculated after attempting to correct frameshift mutations (if applicable).
readingFrame	1, 2, or 3. Only used if <code>accept.stop.codons == FALSE</code> . This specifies the reading frame that is used to determine stop codons. If you use a <code>refAminoAcidSeq</code> , then the frame should always be 1, since all reads will be shifted to frame 1 during frameshift correction. Otherwise, you should select the appropriate reading frame.
processorsNum	The number of processors to use, or NULL (the default) for all available processors.
BPPARAM	A <code>BiocParallelParam</code> instance that controls how the per-SangerRead construction loop is parallelised. Defaults to NULL, in which case it is derived from <code>processorsNum</code> .
lazyAA	Logical (default TRUE). When TRUE and <code>refAminoAcidSeq == ""</code> , the per-read 3-frame amino-acid translation is skipped at construction time and computed on demand via <code>primaryAASeqS1/S2/S3()</code> .
minOverlapFraction	Numeric in [0, 1] (default 0.0). When > 0, after read alignment the smallest pairwise non-gap overlap is computed; if it falls below <code>minOverlapFraction * shorter_read_length</code> , a <code>LOW_OVERLAP_WARN</code> is logged. Use this to detect spurious merges of poorly-overlapping forward/reverse reads (issues #94, #66).
minOverlapBases	Integer (default 0L). Like <code>minOverlapFraction</code> but expressed in absolute base pairs; the warning fires if the smallest pairwise overlap is below this value. Whichever of the two thresholds is larger applies.
alignSeqsParams	A named list (default <code>list()</code>) of additional arguments forwarded to <code>DECIPHER::AlignSeqs</code> (or <code>AlignTranslation</code> when <code>refAminoAcidSeq != ""</code>). Useful for tuning alignment behaviour on minimal-overlap 16S reads (e.g. <code>list(iterations = 1L, refinements = 1L)</code>).
consensusMethod	One of "strict" (default; uses DECIPHER's <code>ConsensusSequence</code> with IU-PAC ambiguity codes), "majority" (per-column plurality vote, no ambiguity codes), or "quality_weighted" (per-column vote weighted by source-read Phred scores). Issues #87, #48.
qualityAware	Logical shorthand (default FALSE); when TRUE, equivalent to <code>consensusMethod = "quality_weighted"</code> . Issue #48.

Value

A `SangerAlignment` instance.

Author(s)

Kuan-Hao Chao

Examples

```
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
```

```

parentDir <- file.path(rawDataDir, "Allolobophora_chlorotica", "RBNII")
REGEX_SuffixForward <- "_[0-9]*_F.ab1$"
REGEX_SuffixReverse <- "_[0-9]*_R.ab1$"
sangerAlignment <- SangerAlignment(
  inputSource          = "ABIF",
  ABIF_Directory      = parentDir,
  REGEX_SuffixForward = REGEX_SuffixForward,
  REGEX_SuffixReverse = REGEX_SuffixReverse,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHA FIMIFFMVMPIIM
  TrimmingMethod      = "M1",
  M1TrimmingCutoff    = 0.0001,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  baseNumPerRow       = 100,
  heightPerRow        = 200,
  signalRatioCutoff   = 0.33,
  showTrimmed         = TRUE,
  processorsNum        = 2)

```

SangerAlignment-class *SangerAlignment*

Description

An S4 class containing SangerContigs lists and contigs alignment results which corresponds to a final alignment in Sanger sequencing.

Slots

objectResults This is the object that stores all information of the creation result.

inputSource The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".

processMethod The method to create a contig from reads. The value is "REGEX" or "CSV". The default value is "REGEX".

ABIF_Directory If inputSource is "ABIF", then this value is the path of a parent directory storing all reads in ABIF format you want to analyse. If inputSource is "FASTA", then this value has to be NULL by default.

FASTA_File If inputSource is "FASTA", then this value has to be the path to a valid FASTA file ; if inputSource is "ABIF", then this value has to be NULL by default.

REGEX_SuffixForward The suffix of the filenames for forward reads in regular expression, i.e. reads that do not need to be reverse-complemented. For forward reads, it should be "_F.ab1".

REGEX_SuffixReverse The suffix of the filenames for reverse reads in regular expression, i.e. reads that need to be reverse-complemented. For reverse reads, it should be "_R.ab1".

CSV_NamesConversion The file path to the CSV file that provides read names, directions, and their contig groups. If processMethod is "CSV", then this value has to be the path to a valid CSV file; if processMethod is "REGEX", then this value has to be NULL by default.

geneticCode Named character vector in the same format as GENETIC_CODE (the default), which represents the standard genetic code. This is the code with which the function will attempt to translate your DNA sequences. You can get an appropriate vector with the getGeneticCode() function. The default is the standard code.

`refAminoAcidSeq` An amino acid reference sequence supplied as a string or an `AAString` object. If your sequences are protein-coding DNA sequences, and you want to have frameshifts automatically detected and corrected, supply a reference amino acid sequence via this argument. If this argument is supplied, the sequences are then kept in frame for the alignment step. Fwd sequences are assumed to come from the sense (i.e. coding, or "+") strand. The default value is "".

`contigList` A list storing all `SangerContigs S4` instances.

`contigsConsensus` The consensus read of all `SangerContig S4` instances in `DNAString` object.

`contigsAlignment` The alignment of all `SangerContig S4` instances with the called consensus sequence in `DNAStringSet` object. Users can use `BrowseSeqs()` to view the alignment.

`contigsTree` A phylo instance returned by `bionj` function in `ape` package. It can be used to draw the tree.

Author(s)

Kuan-Hao Chao

Examples

```
## Simple example
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, 'Allolobophora_chlorotica', 'ACHLO')
my_aligned_contigs <- new("SangerAlignment",
  ABIF_Directory = parentDir,
  REGEX_SuffixForward = "_[0-9]*_F.ab1$",
  REGEX_SuffixReverse = "_[0-9]*_R.ab1$")

rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, 'Allolobophora_chlorotica', 'ACHLO')
CSV_NamesConversion <- file.path(rawDataDir, "ab1", "SangerAlignment", "names_conversion.csv")
sangerAlignment <- new("SangerAlignment",
  processMethod = "CSV",
  ABIF_Directory = parentDir,
  CSV_NamesConversion = CSV_NamesConversion)

## Input From ABIF file format (Regex)
REGEX_SuffixForward <- "_[0-9]*_F.ab1$"
REGEX_SuffixReverse <- "_[0-9]*_R.ab1$"
sangerAlignment <- new("SangerAlignment",
  printLevel = "SangerAlignment",
  inputSource = "ABIF",
  processMethod = "REGEX",
  FASTA_File = NULL,
  CSV_NamesConversion = NULL,
  ABIF_Directory = parentDir,
  REGEX_SuffixForward = REGEX_SuffixForward,
  REGEX_SuffixReverse = REGEX_SuffixReverse,
  TrimmingMethod = "M1",
  M1TrimmingCutoff = 0.0001,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  baseNumPerRow = 100,
  heightPerRow = 200,
  signalRatioCutoff = 0.33,
  showTrimmed = TRUE,
```

```

refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPIMI
  minReadsNum      = 2,
  minReadLength    = 20,
  minFractionCall  = 0.5,
  maxFractionLost  = 0.5,
  geneticCode      = GENETIC_CODE,
  acceptStopCodons = TRUE,
  readingFrame     = 1,
  processorsNum    = 2)

## Input From ABIF file format (Csv three column)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, 'Allolobophora_chlorotica', 'ACHLO')
CSV_NamesConversion <- file.path(rawDataDir, "ab1", "SangerAlignment",
  "names_conversion_all.csv")
sangerAlignment <- new("SangerAlignment",
  inputSource      = "ABIF",
  processMethod    = "CSV",
  ABIF_Directory  = parentDir,
  CSV_NamesConversion = CSV_NamesConversion,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPIMI
  TrimmingMethod  = "M1",
  M1TrimmingCutoff = 0.0001,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  baseNumPerRow   = 100,
  heightPerRow    = 200,
  signalRatioCutoff = 0.33,
  showTrimmed     = TRUE,
  processorsNum   = 2)

## Input From FASTA file format (No Csv - Regex)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
fastaFN <- file.path(rawDataDir, "fasta",
  "SangerAlignment", "Sanger_all_reads.fa")
REGEX_SuffixForwardFa <- "_[0-9]*_F$"
REGEX_SuffixReverseFa <- "_[0-9]*_R$"
sangerAlignmentFa <- new("SangerAlignment",
  inputSource      = "FASTA",
  processMethod    = "REGEX",
  FASTA_File       = fastaFN,
  REGEX_SuffixForward = REGEX_SuffixForwardFa,
  REGEX_SuffixReverse = REGEX_SuffixReverseFa,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPIMI
  processorsNum    = 2)

## Input From FASTA file format (Csv three column method)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
fastaFN <- file.path(rawDataDir, "fasta",
  "SangerAlignment", "Sanger_all_reads.fa")
CSV_NamesConversion <- file.path(rawDataDir, "fasta",
  "SangerAlignment", "names_conversion.csv")
sangerAlignmentFa <- new("SangerAlignment",
  inputSource      = "FASTA",
  processMethod    = "CSV",
  FASTA_File       = fastaFN,
  CSV_NamesConversion = CSV_NamesConversion,

```

```
refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPIN
processorsNum = 2)
```

```
SangerAlignment-class-generateReportSA
    generateReportSA
```

Description

A SangerAlignment method which generates final reports of the SangerContig instance.

Usage

```
## S4 method for signature 'SangerAlignment'
generateReportSA(
  object,
  outputDir,
  includeSangerContig = TRUE,
  includeSangerRead = TRUE,
  colors
)
```

Arguments

object	A SangerAlignment S4 instance.
outputDir	The output directory of the generated HTML report.
includeSangerContig	The parameter that decides whether to include SangerContig level report. The value is TRUE or FALSE and the default is TRUE.
includeSangerRead	The parameter that decides whether to include SangerRead level report. The value is TRUE or FALSE and the default is TRUE.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.

Value

The output absolute path to the SangerAlignment's HTML file.

Examples

```
data("sangerAlignmentData")

generateReportSA(sangerAlignmentData)
generateReportSA(sangerAlignmentData, colors="cb_friendly")
```

SangerAlignment-class-launchAppSA
launchAppSA

Description

A SangerAlignment method which launches Shiny app for SangerAlignment instance.

Usage

```
## S4 method for signature 'SangerAlignment'
launchAppSA(object, outputDir = NULL, colors = "default")
```

Arguments

object	A SangerAlignment S4 instance.
outputDir	The output directory of the saved new SangerContig S4 instance.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.

Value

A shiny.appobj object.

Examples

```
data("sangerAlignmentData")
RShinySA <- launchAppSA(sangerAlignmentData)
RShinySA <- launchAppSA(sangerAlignmentData, colors="cb_friendly")
```

SangerAlignment-class-updateQualityParam
updateQualityParam

Description

A SangerAlignment method which updates QualityReport parameter for each the SangerRead instance inside SangerAlignment.

Usage

```
## S4 method for signature 'SangerAlignment'
updateQualityParam(
  object,
  TrimmingMethod = "M1",
  M1TrimmingCutoff = 1e-04,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  processorsNum = NULL
)
```

Arguments

object	A SangerAlignment S4 instance.
TrimmingMethod	The read trimming method for this SangerRead. The value must be "M1" (the default) or 'M2'.
M1TrimmingCutoff	The trimming cutoff for the Method 1. If TrimmingMethod is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
M2CutoffQualityScore	The trimming cutoff quality score for the Method 2. If TrimmingMethod is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with M2SlidingWindowSize.
M2SlidingWindowSize	The trimming sliding window size for the Method 2. If TrimmingMethod is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with M2CutoffQualityScore.
processorsNum	The number of processors to use, or NULL (the default) for all available processors.

Value

A SangerAlignment instance.

Examples

```
data("sangerAlignmentData")

updateQualityParam(sangerAlignmentData,
  TrimmingMethod      = "M2",
  M1TrimmingCutoff    = NULL,
  M2CutoffQualityScore = 40,
  M2SlidingWindowSize = 15)
```

SangerAlignment-class-writeFastaSA
writeFastaSA

Description

A SangerAlignment method which writes sequences into Fasta files.

Usage

```
## S4 method for signature 'SangerAlignment'
writeFastaSA(
  object,
  outputDir = NULL,
  compress = FALSE,
  compression_level = NA,
  selection = "all"
)
```

Arguments

object	A SangerAlignment S4 instance.
outputDir	The output directory of generated FASTA files.
compress	Like for the save function in base R, must be TRUE or FALSE (the default), or a single string specifying whether writing to the file is to use compression. The only type of compression supported at the moment is "gzip". This parameter will be passed to writeXStringSet function in Biostrings package.
compression_level	This parameter will be passed to writeXStringSet function in Biostrings package.
selection	This value can be all, contigs_alignment, contigs_unalignment or all_reads. It generates reads and contigs FASTA files.

Value

The output directory of FASTA files.

Examples

```
data("sangerAlignmentData")
writeFastaSA(sangerAlignmentData)
```

sangerAlignmentData *SangerAlignment instance*

Description

A pre-built SangerAlignment S4 object aggregating four contigs from the ACHLO fixture.

Usage

```
data(sangerAlignmentData)
```

Format

A *SangerAlignment-class* S4 object containing contigList, contigsAlignment, contigsConsensus, and a contigsTree phylo instance.

Author(s)

Kuan-Hao Chao

sangeranalyseR *sangeranalyseR-package*

Description

sangeranalyseR-package

SangerContig	<i>SangerContig</i>
--------------	---------------------

Description

the wrapper function for SangerContig

Usage

```
SangerContig(
  printLevel = "SangerContig",
  inputSource = "ABIF",
  processMethod = "REGEX",
  ABIF_Directory = NULL,
  FASTA_File = NULL,
  REGEX_SuffixForward = NULL,
  REGEX_SuffixReverse = NULL,
  CSV_NamesConversion = NULL,
  contigName = NULL,
  geneticCode = GENETIC_CODE,
  TrimmingMethod = "M1",
  M1TrimmingCutoff = 1e-04,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  baseNumPerRow = 100,
  heightPerRow = 200,
  signalRatioCutoff = 0.33,
  showTrimmed = TRUE,
  refAminoAcidSeq = "",
  minReadsNum = 2,
  minReadLength = 20,
  minFractionCall = 0.5,
  maxFractionLost = 0.5,
  acceptStopCodons = TRUE,
  readingFrame = 1,
  processorsNum = 1,
  BPPARAM = NULL,
  lazyAA = TRUE,
  minOverlapFraction = 0,
  minOverlapBases = 0L,
  alignSeqsParams = list(),
  consensusMethod = "strict",
  qualityAware = FALSE
)
```

Arguments

printLevel	Internal — controls log verbosity when this constructor is called recursively from a parent class. Defaults to "SangerContig"; do not set manually.
inputSource	The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".

processMethod	Either "REGEX" or "CSV". Default "REGEX".
ABIF_Directory	The parent directory of all of the reads contained in ABIF format you wish to analyse. In SangerContig, all reads must be in the first layer in this directory.
FASTA_File	If inputSource is "FASTA", then this value has to be the name of the FASTA file; if inputSource is "ABIF", then this value is "" by default.
REGEX_SuffixForward	The suffix of the filenames for forward reads in regular expression, i.e. reads that do not need to be reverse-complemented. For forward reads, it should be "_F.ab1".
REGEX_SuffixReverse	The suffix of the filenames for reverse reads in regular expression, i.e. reads that need to be reverse-complemented. For reverse reads, it should be "_R.ab1".
CSV_NamesConversion	The file path to the CSV file that provides read names that follow the naming regulation. If inputSource is "FASTA", then users need to prepare the csv file or make sure the original names inside FASTA file are valid; if inputSource is "ABIF", then this value is NULL by default.
contigName	The contig name of all the reads in ABIF_Directory.
geneticCode	Named character vector in the same format as GENETIC_CODE (the default), which represents the standard genetic code. This is the code with which the function will attempt to translate your DNA sequences. You can get an appropriate vector with the getGeneticCode() function. The default is the standard code.
TrimmingMethod	TrimmingMethod The read trimming method for this SangerRead. The value must be "M1" (the default) or 'M2'.
M1TrimmingCutoff	The trimming cutoff for the Method 1. If TrimmingMethod is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
M2CutoffQualityScore	The trimming cutoff quality score for the Method 2. If TrimmingMethod is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with M2SlidingWindowSize.
M2SlidingWindowSize	The trimming sliding window size for the Method 2. If TrimmingMethod is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with M2CutoffQualityScore.
baseNumPerRow	It defines maximum base pairs in each row. The default value is 100.
heightPerRow	It defines the height of each row in chromatogram. The default value is 200.
signalRatioCutoff	The ratio of the height of a secondary peak to a primary peak. Secondary peaks higher than this ratio are annotated. Those below the ratio are excluded. The default value is 0.33.
showTrimmed	The logical value storing whether to show trimmed base pairs in chromatogram. The default value is TRUE.
refAminoAcidSeq	An amino acid reference sequence supplied as a string or an AAString object. If your sequences are protein-coding DNA sequences, and you want to have frameshifts automatically detected and corrected, supply a reference amino acid sequence via this argument. If this argument is supplied, the sequences are then

	kept in frame for the alignment step. Fwd sequences are assumed to come from the sense (i.e. coding, or "+") strand. The default value is "".
minReadsNum	The minimum number of reads required to make a consensus sequence, must be 2 or more. The default value is 2.
minReadLength	Reads shorter than this will not be included in the readset. The default 20 means that all reads with length of 20 or more will be included. Note that this is the length of a read after it has been trimmed.
minFractionCall	Minimum fraction of the sequences required to call a consensus sequence for SangerContig at any given position (see the ConsensusSequence() function from DECIPHER for more information). Defaults to 0.75 implying that 3/4 of all reads must be present in order to call a consensus.
maxFractionLost	Numeric giving the maximum fraction of sequence information that can be lost in the consensus sequence for SangerContig (see the ConsensusSequence() function from DECIPHER for more information). Defaults to 0.5, implying that each consensus base can ignore at most 50 percent of the information at a given position.
acceptStopCodons	The logical value TRUE or FALSE. TRUE (the default): keep all reads, regardless of whether they have stop codons; FALSE: reject reads with stop codons. If FALSE is selected, then the number of stop codons is calculated after attempting to correct frameshift mutations (if applicable).
readingFrame	1, 2, or 3. Only used if accept.stop.codons == FALSE. This specifies the reading frame that is used to determine stop codons. If you use a refAminoAcidSeq, then the frame should always be 1, since all reads will be shifted to frame 1 during frameshift correction. Otherwise, you should select the appropriate reading frame.
processorsNum	The number of processors to use, or NULL (the default) for all available processors.
BPPARAM	A BiocParallelParam instance for the per-read parallel loop. Default NULL (derived from processorsNum).
lazyAA	Logical (default TRUE). Skip eager 3-frame AA translation when no refAminoAcidSeq is supplied; use the primaryAASeqS1/S2/S3() accessors on demand instead.
minOverlapFraction	Numeric in [0, 1] (default 0.0). Triggers a LOW_OVERLAP_WARN when the smallest pairwise non-gap overlap is below minOverlapFraction * shorter_read_length. See SangerAlignment for full discussion.
minOverlapBases	Integer (default 0L). Absolute-base-pair threshold variant of minOverlapFraction.
alignSeqsParams	A named list (default list()) of additional arguments forwarded to DECIPHER::AlignSeqs.
consensusMethod	One of "strict" (default), "majority", or "quality_weighted". See SangerAlignment for full discussion.
qualityAware	Logical shorthand for consensusMethod = "quality_weighted". Issue #48.

Value

A SangerContig instance.

Author(s)

Kuan-Hao Chao

Examples

```

rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, "Allolobophora_chlorotica", "ACHLO")
contigName <- "Ach1_ACHL0006-09"
REGEX_SuffixForward <- "_F.ab1"
REGEX_SuffixReverse <- "_R.ab1"
sangerContig <- SangerContig(
  inputSource          = "ABIF",
  ABIF_Directory       = parentDir,
  contigName           = contigName,
  REGEX_SuffixForward  = REGEX_SuffixForward,
  REGEX_SuffixReverse  = REGEX_SuffixReverse,
  refAminoAcidSeq     = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIIVTAHAFAIMIFFMVPIMIG
  TrimmingMethod      = "M2",
  M1TrimmingCutoff    = NULL,
  M2CutoffQualityScore = 20,
  M2SlidingWindowSize = 10,
  baseNumPerRow        = 100,
  heightPerRow         = 200,
  signalRatioCutoff    = 0.33,
  showTrimmed          = TRUE,
  processorsNum        = 2)

```

SangerContig-class *SangerContig*

Description

An S4 class containing forward and reverse SangerRead lists and alignment, consensus read results which corresponds to a contig in Sanger sequencing.

Slots

objectResults This is the object that stores all information of the creation result.

inputSource The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".

processMethod The method to create a contig from reads. The value is "REGEX" or "CSV". The default value is "REGEX".

ABIF_Directory If inputSource is "ABIF", then this value is the path of a parent directory storing all reads in ABIF format you want to analyse. If inputSource is "FASTA", then this value has to be NULL by default.

FASTA_File If inputSource is "FASTA", then this value has to be the path to a valid FASTA file ; if inputSource is "ABIF", then this value has to be NULL by default.

REGEX_SuffixForward The suffix of the filenames for forward reads in regular expression, i.e. reads that do not need to be reverse-complemented.

REGEX_SuffixReverse The suffix of the filenames for reverse reads in regular expression, i.e. reads that need to be reverse-complemented.

- CSV_NamesConversion** The file path to the CSV file that provides read names, directions, and their contig groups. If `processMethod` is "CSV", then this value has to be the path to a valid CSV file; if `processMethod` is "REGEX", then this value has to be NULL by default.
- contigName** The contig name of all the reads in `ABIF_Directory`.
- geneticCode** Named character vector in the same format as `GENETIC_CODE` (the default), which represents the standard genetic code. This is the code with which the function will attempt to translate your DNA sequences. You can get an appropriate vector with the `getGeneticCode()` function. The default is the standard code.
- forwardReadList** The list of `SangerRead S4` instances which are all forward reads.
- reverseReadList** The list of `SangerRead S4` instances which are all reverse reads.
- minReadsNum** The minimum number of reads required to make a consensus sequence, must be 2 or more. The default value is 2.
- minReadLength** Reads shorter than this will not be included in the readset. The default 20 means that all reads with length of 20 or more will be included. Note that this is the length of a read after it has been trimmed.
- refAminoAcidSeq** An amino acid reference sequence supplied as a string or an `AAString` object. If your sequences are protein-coding DNA sequences, and you want to have frameshifts automatically detected and corrected, supply a reference amino acid sequence via this argument. If this argument is supplied, the sequences are then kept in frame for the alignment step. Fwd sequences are assumed to come from the sense (i.e. coding, or "+") strand. The default value is "".
- minFractionCall** Minimum fraction of the sequences required to call a consensus sequence for `SangerContig` at any given position (see the `ConsensusSequence()` function from `DECIPHER` for more information). Defaults to 0.75 implying that 3/4 of all reads must be present in order to call a consensus.
- maxFractionLost** Numeric giving the maximum fraction of sequence information that can be lost in the consensus sequence for `SangerContig` (see the `ConsensusSequence()` function from `DECIPHER` for more information). Defaults to 0.5, implying that each consensus base can ignore at most 50 percent of the information at a given position.
- acceptStopCodons** The logical value `TRUE` or `FALSE`. `TRUE` (the default): keep all reads, regardless of whether they have stop codons; `FALSE`: reject reads with stop codons. If `FALSE` is selected, then the number of stop codons is calculated after attempting to correct frameshift mutations (if applicable).
- readingFrame** 1, 2, or 3. Only used if `accept.stop.codons == FALSE`. This specifies the reading frame that is used to determine stop codons. If you use a `refAminoAcidSeq`, then the frame should always be 1, since all reads will be shifted to frame 1 during frameshift correction. Otherwise, you should select the appropriate reading frame.
- contigSeq** The consensus read of all `SangerRead S4` instances in `DNAString` object.
- alignment** The alignment of all `SangerRead S4` instances with the called consensus sequence in `DNAStringSet` object. Users can use `BrowseSeqs()` to view the alignment.
- differencesDF** A data frame of the number of pairwise differences between each read and the consensus sequence, as well as the number of bases in each input read that did not contribute to the consensus sequence. It can assist in detecting incorrect reads, or reads with a lot of errors.
- distanceMatrix** A distance matrix of genetic distances (corrected with the JC model) between all of the input reads.
- dendrogram** A list storing cluster groups in a data frame and a dendrogram object depicting the `distance.matrix`. Users can use `plot()` to see the dendrogram.

`indelsDF` If users specified a reference sequence via `refAminoAcidSeq`, then this will be a data frame describing the number of indels and deletions that were made to each of the input reads in order to correct frameshift mutations.

`stopCodonsDF` If users specified a reference sequence via `refAminoAcidSeq`, then this will be a data frame describing the number of stop codons in each read.

`secondaryPeakDF` A data frame with one row for each column in the alignment that contained more than one secondary peak. The data frame has three columns: the column number of the alignment; the number of secondary peaks in that column; and the bases (with IUPAC ambiguity codes representing secondary peak calls) in that column represented as a string.

Author(s)

Kuan-Hao Chao

Examples

```
## Simple example
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, "Allolobophora_chlorotica", "RBNII")
contigName <- "Ach1_RBNII384-13"
REGEX_SuffixForward <- "_[0-9]*_F.ab1$"
REGEX_SuffixReverse <- "_[0-9]*_R.ab1$"
sangerContig <- new("SangerContig",
                    ABIF_Directory      = parentDir,
                    contigName          = contigName,
                    REGEX_SuffixForward = REGEX_SuffixForward,
                    REGEX_SuffixReverse = REGEX_SuffixReverse)

## forward / reverse reads match error
## Input From ABIF file format (Regex)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, "Allolobophora_chlorotica", "ACHLO")
contigName <- "Ach1_ACHLO006-09"
REGEX_SuffixForward <- "_[0-9]*_F.ab1$"
REGEX_SuffixReverse <- "_[0-9]*_R.ab1$"
sangerContig <- new("SangerContig",
                    inputSource          = "ABIF",
                    processMethod        = "REGEX",
                    ABIF_Directory      = parentDir,
                    contigName          = contigName,
                    REGEX_SuffixForward = REGEX_SuffixForward,
                    REGEX_SuffixReverse = REGEX_SuffixReverse,
                    refAminoAcidSeq     = "SRQWLFSTNHKDIGTLYIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIIVTAHAFIMIFFMVMPIMIG",
                    TrimmingMethod       = "M1",
                    M1TrimmingCutoff     = 0.0001,
                    baseNumPerRow       = 100,
                    heightPerRow        = 200,
                    signalRatioCutoff   = 0.33,
                    showTrimmed          = TRUE,
                    minReadsNum         = 2,
                    processorsNum       = 2)

## Input From ABIF file format (Csv three column method)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, "Allolobophora_chlorotica", "RBNII")
CSV_NamesConversion <- file.path(rawDataDir, "ab1", "SangerContig", "names_conversion_2.csv")
```

```

sangerContig <- new("SangerContig",
  inputSource      = "ABIF",
  processMethod    = "CSV",
  ABIF_Directory   = parentDir,
  CSV_NamesConversion = CSV_NamesConversion,
  contigName       = "Ach1_RBNII384-13",
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFIMIFFMVPIMIG
  TrimmingMethod   = "M1",
  M1TrimmingCutoff = 0.000001,
  baseNumPerRow    = 100,
  heightPerRow     = 200,
  signalRatioCutoff = 0.33,
  showTrimmed      = TRUE,
  processorsNum     = 2)

## Input From FASTA file format (Regex)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
fastaFN <- file.path(rawDataDir, "fasta",
  "SangerContig", "Ach1_ACHL0006-09.fa")
contigName <- "Ach1_ACHL0006-09"
REGEX_SuffixForwardFa <- "_[0-9]*_F$"
REGEX_SuffixReverseFa <- "_[0-9]*_R$"
sangerContigFa <- new("SangerContig",
  inputSource      = "FASTA",
  processMethod    = "REGEX",
  FASTA_File       = fastaFN,
  contigName       = contigName,
  REGEX_SuffixForward = REGEX_SuffixForwardFa,
  REGEX_SuffixReverse = REGEX_SuffixReverseFa,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFIMIFFMVPIMIG
  processorsNum     = 2)

## Input From FASTA file format (Csv - Csv three column method)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
fastaFN <- file.path(rawDataDir, "fasta",
  "SangerContig", "Ach1_ACHL0006-09.fa")
CSV_NamesConversion <- file.path(rawDataDir, "fasta", "SangerContig", "names_conversion_1.csv")
sangerContigFa <- new("SangerContig",
  inputSource      = "FASTA",
  processMethod    = "CSV",
  FASTA_File       = fastaFN,
  CSV_NamesConversion = CSV_NamesConversion,
  contigName       = "Ach1_ACHL0006-09",
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFIMIFFMVPIMIG
  processorsNum     = 2)

```

SangerContig-class-generateReportSC
generateReportSC

Description

A SangerContig method which generates final reports of the SangerContig instance.

Usage

```
## S4 method for signature 'SangerContig'
generateReportSC(
  object,
  outputDir,
  includeSangerRead = TRUE,
  colors,
  navigationAlignmentFN = NULL
)
```

Arguments

object	A SangerContig S4 instance.
outputDir	The output directory of the generated HTML report.
includeSangerRead	The parameter that decides whether to include SangerRead level report. The value is TRUE or FALSE and the default is TRUE.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.
navigationAlignmentFN	The internal parameter passed to HTML report. Users should not modify this parameter on their own.

Value

The output absolute path to the SangerContig's HTML file.

Examples

```
data("sangerContigData")

generateReportSC(sangerContigData)
generateReportSC(sangerContigData, colors="cb_friendly")
```

SangerContig-class-launchAppSC
launchAppSC

Description

A SangerContig method which launches Shiny app for SangerContig instance.

Usage

```
## S4 method for signature 'SangerContig'
launchAppSC(object, outputDir = NULL, colors = "default")
```

Arguments

object	A SangerContig S4 instance.
outputDir	The output directory of the saved new SangerContig S4 instance.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.

Value

A shiny.appobj object.

Examples

```
data("sangerContigData")
RShinySC <- launchAppSC(sangerContigData)
RShinySC <- launchAppSC(sangerContigData, colors="cb_friendly")
```

SangerContig-class-readTable
readTable

Description

A SangerContig method which generates summary table for SangerContig instance

Usage

```
## S4 method for signature 'SangerContig'
readTable(object, indentation = 0)
```

Arguments

object	A SangerContig S4 instance.
indentation	The indentation for different level printing.

Value

None

Examples

```
data(sangerReadFData)
data(sangerContigData)

readTable(sangerReadFData)
readTable(sangerContigData)
```

SangerContig-class-updateQualityParam
updateQualityParam

Description

A SangerContig method which updates QualityReport parameter for each the SangerRead instance inside SangerContig.

Usage

```
## S4 method for signature 'SangerContig'
updateQualityParam(
  object,
  TrimmingMethod = "M1",
  M1TrimmingCutoff = 1e-04,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  processorsNum = NULL
)
```

Arguments

object	A SangerContig S4 instance.
TrimmingMethod	The read trimming method for this SangerRead. The value must be "M1" (the default) or 'M2'.
M1TrimmingCutoff	The trimming cutoff for the Method 1. If TrimmingMethod is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
M2CutoffQualityScore	The trimming cutoff quality score for the Method 2. If TrimmingMethod is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with M2SlidingWindowSize.
M2SlidingWindowSize	The trimming sliding window size for the Method 2. If TrimmingMethod is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with M2CutoffQualityScore.
processorsNum	The number of processors to use, or NULL (the default) for all available processors.

Value

A SangerContig instance.

Examples

```
data("sangerContigData")

updateQualityParam(sangerContigData,
  TrimmingMethod = "M2",
```

```

M1TrimmingCutoff      = NULL,
M2CutoffQualityScore  = 40,
M2SlidingWindowSize   = 15)

```

SangerContig-class-writeFastaSC
writeFastaSC

Description

A SangerContig method which writes sequences into Fasta files.

Usage

```

## S4 method for signature 'SangerContig'
writeFastaSC(
  object,
  outputDir = NULL,
  compress = FALSE,
  compression_level = NA,
  selection = "all"
)

```

Arguments

object	A SangerContig S4 instance.
outputDir	The output directory of generated FASTA files.
compress	Like for the save function in base R, must be TRUE or FALSE (the default), or a single string specifying whether writing to the file is to use compression. The only type of compression supported at the moment is "gzip". This parameter will be passed to writeXStringSet function in Biostrings package.
compression_level	This parameter will be passed to writeXStringSet function in Biostrings package.
selection	This value can be all, reads_alignment, reads_unalignment or contig. It generates reads and the contig FASTA files.

Value

The output directory of FASTA files.

Examples

```

data("sangerContigData")
writeFastaSC(sangerContigData)

```

sangerContigData	<i>SangerContig instance</i>
------------------	------------------------------

Description

A pre-built SangerContig S4 object containing one forward + one reverse SangerRead from the ACHLO fixture, plus the assembled contig consensus.

Usage

```
data(sangerContigData)
```

Format

A [SangerContig-class](#) S4 object.

Author(s)

Kuan-Hao Chao

SangerRead	<i>SangerRead</i>
------------	-------------------

Description

the wrapper function for SangerRead

Usage

```
SangerRead(  
  printLevel = "SangerRead",  
  inputSource = "ABIF",  
  readFeature = "",  
  readFileName = "",  
  fastaReadName = NULL,  
  geneticCode = GENETIC_CODE,  
  TrimmingMethod = "M1",  
  M1TrimmingCutoff = 1e-04,  
  M2CutoffQualityScore = NULL,  
  M2SlidingWindowSize = NULL,  
  baseNumPerRow = 100,  
  heightPerRow = 200,  
  signalRatioCutoff = 0.33,  
  showTrimmed = TRUE,  
  lazyAA = TRUE  
)
```

Arguments

printLevel	Internal — controls log verbosity when this constructor is called recursively from a parent class. Defaults to "SangerRead"; do not set manually.
inputSource	The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".
readFeature	The direction of the Sanger read. The value must be "Forward Read" or "Reverse Read".
readFileName	The filename of the target ABIF file.
fastaReadName	If inputSource is "FASTA", then this value has to be the name of the read inside the FASTA file; if inputSource is "ABIF", then this value is "" by default.
geneticCode	Named character vector in the same format as GENETIC_CODE (the default), which represents the standard genetic code. This is the code with which the function will attempt to translate your DNA sequences. You can get an appropriate vector with the getGeneticCode() function. The default is the standard code.
TrimmingMethod	TrimmingMethod The read trimming method for this SangerRead. The value must be "M1" (the default) or "M2". M1 is the modified Mott's trimming algorithm that can also be found in Phred/Phrap and Biopython. M2 is like trimomatic's sliding window method.
M1TrimmingCutoff	The trimming cutoff for the Method 1. If TrimmingMethod is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
M2CutoffQualityScore	The trimming cutoff quality score for the Method 2. If TrimmingMethod is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with M2SlidingWindowSize.
M2SlidingWindowSize	The trimming sliding window size for the Method 2. If TrimmingMethod is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with M2CutoffQualityScore.
baseNumPerRow	It defines maximum base pairs in each row. The default value is 100.
heightPerRow	It defines the height of each row in chromatogram. The default value is 200.
signalRatioCutoff	The ratio of the height of a secondary peak to a primary peak. Secondary peaks higher than this ratio are annotated. Those below the ratio are excluded. The default value is 0.33.
showTrimmed	The logical value storing whether to show trimmed base pairs in chromatogram. The default value is TRUE.
lazyAA	Logical (default TRUE). Skip eager 3-frame AA translation; use primaryAASeqS1/S2/S3() accessors instead.

Value

A SangerRead instance.

Author(s)

Kuan-Hao Chao

Examples

```

inputFilePath <- system.file("extdata/", package = "sangeranalyseR")
A_chloroticaFdFN <- file.path(inputFilePath,
                             "Allolobophora_chlorotica",
                             "ACHLO",
                             "Ach1_ACHLO0006-09_1_F.ab1")

sangerRead <- SangerRead(
  printLevel           = "SangerRead",
  inputSource          = "ABIF",
  readFeature          = "Forward Read",
  readFileName         = A_chloroticaFdFN,
  geneticCode          = GENETIC_CODE,
  TrimmingMethod       = "M1",
  M1TrimmingCutoff     = 0.0001,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  baseNumPerRow        = 100,
  heightPerRow         = 200,
  signalRatioCutoff    = 0.33,
  showTrimmed          = TRUE)

```

SangerRead-class	<i>SangerRead</i>
------------------	-------------------

Description

An S4 class extending sangerseq S4 class which corresponds to a single ABIF file in Sanger sequencing.

Slots

objectResults This is the object that stores all information of the creation result.

inputSource The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".

readFeature The direction of the Sanger read. The value must be "Forward Read" or "Reverse Read".

readFileName The filename of the target input file.

fastaReadName If inputSource is "FASTA", then this value has to be the name of the read inside the FASTA file; if inputSource is "ABIF", then this value is NULL by default.

geneticCode Named character vector in the same format as GENETIC_CODE (the default), which represents the standard genetic code. This is the code with which the function will attempt to translate your DNA sequences. You can get an appropriate vector with the getGeneticCode() function. The default is the standard code.

abifRawData An S4 class containing all fields in the ABIF file. It is the abif class defined in sangerseqR package.

QualityReport A S4 class containing quality trimming related inputs and trimming results.

ChromatogramParam A S4 class containing chromatogram inputs.

primaryAASeqS1 A polypeptide translated from primary DNA sequence starting from the first nucleic acid.


```

                                "ACHLO",
                                "Ach1_ACHLO006-09_2_R.ab1")
sangerReadR <- new("SangerRead",
  inputSource      = "ABIF",
  readFeature      = "Reverse Read",
  readFileName     = A_chloroticaRFN,
  geneticCode      = GENETIC_CODE,
  TrimmingMethod  = "M1",
  M1TrimmingCutoff = 0.0001,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  baseNumPerRow    = 100,
  heightPerRow     = 200,
  signalRatioCutoff = 0.33,
  showTrimmed      = TRUE)

## Input From FASTA file format
# Forward Read
inputFilesPath <- system.file("extdata/", package = "sangeranalyseR")
A_chloroticaFFNfa <- file.path(inputFilesPath,
  "fasta",
  "SangerRead",
  "Ach1_ACHLO006-09_1_F.fa")
readNameFfa <- "Ach1_ACHLO006-09_1_F"
sangerReadFfa <- new("SangerRead",
  inputSource      = "FASTA",
  readFeature      = "Forward Read",
  readFileName     = A_chloroticaFFNfa,
  fastaReadName    = readNameFfa,
  geneticCode      = GENETIC_CODE)

# Reverse Read
A_chloroticaRFNfa <- file.path(inputFilesPath,
  "fasta",
  "SangerRead",
  "Ach1_ACHLO006-09_2_R.fa")
readNameRfa <- "Ach1_ACHLO006-09_2_R"
sangerReadRfa <- new("SangerRead",
  inputSource      = "FASTA",
  readFeature      = "Reverse Read",
  readFileName     = A_chloroticaRFNfa,
  fastaReadName    = readNameRfa,
  geneticCode      = GENETIC_CODE)

```

SangerRead-class-generateReportSR

generateReportSR

Description

A SangerRead method which generates final reports of the SangerRead instance.

Usage

```
## S4 method for signature 'SangerRead'
generateReportSR(
  object,
  outputDir,
  colors,
  navigationContigFN = NULL,
  navigationAlignmentFN = NULL
)
```

Arguments

object	A SangerRead S4 instance.
outputDir	The output directory of the generated HTML report.
colors	A vector for users to set the colors of (A, T, C, G, else). There are three options for users to choose from. 1. "default": (green, blue, black, red, purple). 2. "cb_friendly": ((0, 0, 0), (199, 199, 199), (0, 114, 178), (213, 94, 0), (204, 121, 167)). 3. Users can set their own colors with a vector with five elements.
navigationContigFN	The internal parameter passed to HTML report. Users should not modify this parameter on their own.
navigationAlignmentFN	The internal parameter passed to HTML report. Users should not modify this parameter on their own.

Value

The output absolute path to the SangerRead's HTML file.

Examples

```
data("sangerReadFData")

generateReportSR(sangerReadFData, "~/Documents")
generateReportSR(sangerReadFData, colors="cb_friendly")
```

SangerRead-class-MakeBaseCalls
MakeBaseCalls

Description

A SangerRead method which does base calling on SangerRead instance

Usage

```
## S4 method for signature 'SangerRead'
MakeBaseCalls(object, signalRatioCutoff = 0.33)
```

Arguments

`object` A SangerRead S4 instance.

`signalRatioCutoff` The ratio of the height of a secondary peak to a primary peak. Secondary peaks higher than this ratio are annotated. Those below the ratio are excluded. The default value is 0.33.

Value

A SangerRead instance.

Examples

```
data("sangerReadFData")
newSangerReadFData <- MakeBaseCalls(sangerReadFData, signalRatioCutoff = 0.22)
```

SangerRead-class-qualityBasePlot
qualityBasePlot

Description

A SangerRead method which creates quality base interactive plot.

Usage

```
## S4 method for signature 'SangerRead'
qualityBasePlot(object)
```

Arguments

`object` A SangerRead S4 instance.

Value

A quality plot.

Examples

```
data("sangerReadFData")
qualityBasePlot(sangerReadFData)
```

SangerRead-class-readTable
readTable

Description

A SangerRead method which generates summary table for SangerRead instance

Usage

```
## S4 method for signature 'SangerRead'  
readTable(object, indentation = 0)
```

Arguments

object A SangerRead S4 instance.
indentation The indentation for different level printing.

Value

None

Examples

```
data(sangerReadFData)  
data(sangerContigData)  
  
readTable(sangerReadFData)  
readTable(sangerContigData)
```

SangerRead-class-updateQualityParam
updateQualityParam

Description

A SangerRead method which updates QualityReport parameter inside the SangerRead.

Usage

```
## S4 method for signature 'SangerRead'  
updateQualityParam(  
  object,  
  TrimmingMethod = "M1",  
  M1TrimmingCutoff = 1e-04,  
  M2CutoffQualityScore = NULL,  
  M2SlidingWindowSize = NULL  
)
```

Arguments

object	A SangerRead S4 instance.
TrimmingMethod	The read trimming method for this SangerRead. The value must be "M1" (the default) or 'M2'.
M1TrimmingCutoff	The trimming cutoff for the Method 1. If TrimmingMethod is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
M2CutoffQualityScore	The trimming cutoff quality score for the Method 2. If TrimmingMethod is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with M2SlidingWindowSize.
M2SlidingWindowSize	The trimming sliding window size for the Method 2. If TrimmingMethod is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with M2CutoffQualityScore.

Value

A SangerRead instance.

Examples

```
data("sangerReadFData")
updateQualityParam(sangerReadFData,
  TrimmingMethod      = "M2",
  M1TrimmingCutoff    = NULL,
  M2CutoffQualityScore = 40,
  M2SlidingWindowSize = 15)
```

SangerRead-class-writeFastaSR
writeFastaSR

Description

A SangerRead method which writes the sequence into Fasta files.

Usage

```
## S4 method for signature 'SangerRead'
writeFastaSR(
  object,
  outputDir = NULL,
  compress = FALSE,
  compression_level = NA
)
```

Arguments

object	A SangerRead S4 instance.
outputDir	The output directory of the generated FASTA file.
compress	Like for the save function in base R, must be TRUE or FALSE (the default), or a single string specifying whether writing to the file is to use compression. The only type of compression supported at the moment is "gzip". This parameter will be passed to writeXStringSet function in Biostrings package.
compression_level	This parameter will be passed to writeXStringSet function in Biostrings package.

Value

The output absolute path to the FASTA file.

Examples

```
data("sangerReadFData")
writeFastaSR(sangerReadFData)
```

sangerReadFData	<i>SangerRead instance</i>
-----------------	----------------------------

Description

A pre-built SangerRead S4 object for one forward ABIF read from the ACHLO fixture.

Usage

```
data(sangerReadFData)
```

Format

A [SangerRead-class](#) S4 object with populated primarySeq, secondarySeq, traceMatrix, and nested QualityReport / ChromatogramParam.

Author(s)

Kuan-Hao Chao

updateQualityParam *Method updateQualityParam*

Description

Method updateQualityParam

Usage

```
updateQualityParam(
    object,
    TrimmingMethod = "M1",
    M1TrimmingCutoff = 1e-04,
    M2CutoffQualityScore = NULL,
    M2SlidingWindowSize = NULL,
    ...
)
```

Arguments

object	A QualityReport, SangerRead, SangerContig, or SangerAlignment S4 instance.
TrimmingMethod	The read trimming method for this SangerRead. The value must be "M1" (the default) or 'M2'.
M1TrimmingCutoff	The trimming cutoff for the Method 1. If TrimmingMethod is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
M2CutoffQualityScore	The trimming cutoff quality score for the Method 2. If TrimmingMethod is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with M2SlidingWindowSize.
M2SlidingWindowSize	The trimming sliding window size for the Method 2. If TrimmingMethod is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with M2CutoffQualityScore.
...	Further updateQualityParam-related parameters.

Value

A QualityReport, SangerRead, SangerContig, or SangerAlignment instance.

Examples

```
data(qualityReportData)
data(sangerReadFData)
data(sangerContigData)
data(sangerAlignmentData)

updateQualityParam(qualityReportData,
                   TrimmingMethod      = "M2",
                   M1TrimmingCutoff    = NULL,
                   M2CutoffQualityScore = 40,
```

```

        M2SlidingWindowSize = 15)
updateQualityParam(sangerReadFData,
  TrimmingMethod = "M2",
  M1TrimmingCutoff = NULL,
  M2CutoffQualityScore = 40,
  M2SlidingWindowSize = 15)
updateQualityParam(sangerContigData,
  TrimmingMethod = "M2",
  M1TrimmingCutoff = NULL,
  M2CutoffQualityScore = 40,
  M2SlidingWindowSize = 15)
updateQualityParam(sangerAlignmentData,
  TrimmingMethod = "M2",
  M1TrimmingCutoff = NULL,
  M2CutoffQualityScore = 40,
  M2SlidingWindowSize = 15)

```

writeFasta

Method writeFasta

Description

A method which writes FASTA files of the SangerRead, SangerContig, and SangerAlignment instance.

Usage

```

writeFasta(
  object,
  outputDir = NULL,
  compress = FALSE,
  compression_level = NA,
  selection = "all"
)

```

Arguments

object	A SangerRead, SangerContig, or SangerAlignment S4 instance.
outputDir	The output directory of generated FASTA files.
compress	Like for the save function in base R, must be TRUE or FALSE (the default), or a single string specifying whether writing to the file is to use compression. The only type of compression supported at the moment is "gzip". This parameter will be passed to writeXStringSet function in Biostrings package.
compression_level	This parameter will be passed to writeXStringSet function in Biostrings package.
selection	This parameter will be passed to writeFastaSC or writeFastaSA.

Value

A SangerRead, SangerContig, or SangerAlignment object.

Author(s)

Kuan-Hao Chao

Examples

```

data(sangerReadFData)
data(sangerContigData)
data(sangerAlignmentData)

writeFasta(sangerReadFData)
writeFasta(sangerContigData)
writeFasta(sangerAlignmentData)

```

writeFastaSA	<i>Method writeFastaSA</i>
--------------	----------------------------

Description

Method writeFastaSA

Usage

```

writeFastaSA(
  object,
  outputDir = NULL,
  compress = FALSE,
  compression_level = NA,
  selection = "all"
)

```

Arguments

object	A SangerAlignment S4 instance.
outputDir	The output directory of generated FASTA files.
compress	Like for the save function in base R, must be TRUE or FALSE (the default), or a single string specifying whether writing to the file is to use compression. The only type of compression supported at the moment is "gzip". This parameter will be passed to writeXStringSet function in Biostrings package.
compression_level	This parameter will be passed to writeXStringSet function in Biostrings package.
selection	This value can be all, contigs_alignment, contigs_unalignment or all_reads. It generates reads and contigs FASTA files.

Value

The output directory of FASTA files.

Examples

```

data(sangerAlignmentData)
writeFastaSA(sangerAlignmentData)

```

writeFastaSC	<i>Method writeFastaSC</i>
--------------	----------------------------

Description

Method writeFastaSC

Usage

```
writeFastaSC(
  object,
  outputDir = NULL,
  compress = FALSE,
  compression_level = NA,
  selection = "all"
)
```

Arguments

object	A SangerContig S4 instance.
outputDir	The output directory of generated FASTA files.
compress	Like for the save function in base R, must be TRUE or FALSE (the default), or a single string specifying whether writing to the file is to use compression. The only type of compression supported at the moment is "gzip". This parameter will be passed to writeXStringSet function in Biostrings package.
compression_level	This parameter will be passed to writeXStringSet function in Biostrings package.
selection	This value can be all, reads_alignment, reads_unalignment or contig. It generates reads and the contig FASTA files.

Value

The output directory of FASTA files.

Examples

```
data(sangerContigData)
writeFastaSC(sangerContigData)
```

writeFastaSR	<i>Method writeFastaSR</i>
--------------	----------------------------

Description

Method writeFastaSR

Usage

```
writeFastaSR(  
  object,  
  outputDir = NULL,  
  compress = FALSE,  
  compression_level = NA  
)
```

Arguments

object	A SangerRead S4 instance.
outputDir	The output directory of the generated FASTA file.
compress	Like for the save function in base R, must be TRUE or FALSE (the default), or a single string specifying whether writing to the file is to use compression. The only type of compression supported at the moment is "gzip". This parameter will be passed to writeXStringSet function in Biostrings package.
compression_level	This parameter will be passed to writeXStringSet function in Biostrings package.

Value

The output absolute path to the FASTA file.

Examples

```
data(sangerReadFData)  
writeFastaSR(sangerReadFData)
```

Index

- * **datasets**
 - qualityReportData, 18
 - sangerAlignmentData, 29
 - sangerContigData, 41
 - sangerReadFData, 50
- chromatogram_overwrite, 4, 5
- chromatogram_plotly, 4, 5
- ChromatogramParam-class, 3
- generateReport, 6
- generateReportSA, 7
- generateReportSA, SangerAlignment-method (SangerAlignment-class-generateReportSA), 26
- generateReportSC, 8
- generateReportSC, SangerContig-method (SangerContig-class-generateReportSC), 36
- generateReportSR, 9
- generateReportSR, SangerRead-method (SangerRead-class-generateReportSR), 45
- globalTrimApp, 9
- launchApp, 10
- launchAppSA, 11
- launchAppSA, SangerAlignment-method (SangerAlignment-class-launchAppSA), 27
- launchAppSC, 11
- launchAppSC, SangerContig-method (SangerContig-class-launchAppSC), 37
- MakeBaseCalls, 12
- MakeBaseCalls, SangerRead-method (SangerRead-class-MakeBaseCalls), 46
- ObjectResults-class, 12
- primaryAASeqS1, 13
- primaryAASeqS1, SangerRead-method (primaryAASeqS1), 13
- primaryAASeqS2, 14
- primaryAASeqS2, SangerRead-method (primaryAASeqS2), 14
- primaryAASeqS3, 14
- primaryAASeqS3, SangerRead-method (primaryAASeqS3), 14
- qualityBasePlot, 15
- qualityBasePlot, QualityReport-method (QualityReport-class-qualityBasePlot), 17
- qualityBasePlot, SangerRead-method (SangerRead-class-qualityBasePlot), 47
- QualityReport-class, 15
- QualityReport-class-qualityBasePlot, 17
- QualityReport-class-updateQualityParam, 17
- qualityReportData, 18
- readTable, 19
- readTable, SangerContig-method (SangerContig-class-readTable), 38
- readTable, SangerRead-method (SangerRead-class-readTable), 48
- SangerAlignment, 19
- SangerAlignment-class, 23
- SangerAlignment-class-generateReportSA, 26
- SangerAlignment-class-launchAppSA, 27
- SangerAlignment-class-updateQualityParam, 27
- SangerAlignment-class-writeFastaSA, 28
- sangerAlignmentData, 29
- sangeranalyseR, 29
- SangerContig, 30
- SangerContig-class, 33
- SangerContig-class-generateReportSC, 36
- SangerContig-class-launchAppSC, 37

SangerContig-class-readTable, [38](#)
SangerContig-class-updateQualityParam,
[39](#)
SangerContig-class-writeFastaSC, [40](#)
sangerContigData, [41](#)
SangerRead, [41](#)
SangerRead-class, [43](#)
SangerRead-class-generateReportSR, [45](#)
SangerRead-class-MakeBaseCalls, [46](#)
SangerRead-class-qualityBasePlot, [47](#)
SangerRead-class-readTable, [48](#)
SangerRead-class-updateQualityParam,
[48](#)
SangerRead-class-writeFastaSR, [49](#)
sangerReadFData, [50](#)

updateQualityParam, [51](#)
updateQualityParam,QualityReport-method
(QualityReport-class-updateQualityParam),
[17](#)
updateQualityParam,SangerAlignment-method
(SangerAlignment-class-updateQualityParam),
[27](#)
updateQualityParam,SangerContig-method
(SangerContig-class-updateQualityParam),
[39](#)
updateQualityParam,SangerRead-method
(SangerRead-class-updateQualityParam),
[48](#)

writeFasta, [52](#)
writeFastaSA, [53](#)
writeFastaSA,SangerAlignment-method
(SangerAlignment-class-writeFastaSA),
[28](#)
writeFastaSC, [54](#)
writeFastaSC,SangerContig-method
(SangerContig-class-writeFastaSC),
[40](#)
writeFastaSR, [54](#)
writeFastaSR,SangerRead-method
(SangerRead-class-writeFastaSR),
[49](#)