

# Package ‘sangeranalyseR’

March 26, 2024

**Type** Package

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

**Version** 1.12.0

**Date** 2020-04-22

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**biocViews** Genetics, Alignment, Sequencing, SangerSeq, Preprocessing, QualityControl, Visualization, GUI

**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 output detailed HTML reports, including chromatograms.

**License** GPL-2

**Encoding** UTF-8

**Depends** R (>= 4.0.0), stringr, ape, Biostrings, DECIPHER, parallel, reshape2, phangorn, sangerseqR, gridExtra, shiny, shinydashboard, shinyjs, data.table, plotly, DT, zeallot, excelR, shinycssloaders, ggdendro, shinyWidgets, openxlsx, tools, rmarkdown (>= 2.9), knitr (>= 1.33), seqinr, BiocStyle, logger

**RoxygenNote** 7.2.1

**VignetteBuilder** knitr

**Suggests** testthat (>= 2.1.0)

**Collate** 'AllGenerics.R' 'ClassChromatogramParam.R'  
'ClassObjectResults.R' 'ClassQualityReport.R'  
'ClassSangerRead.R' 'ClassSangerAlignment.R'  
'ClassSangerContig.R' 'Constructors.R' 'LoadMessage.R'

'MethodSangerAlignment.R' 'MethodSangerContig.R'  
 'MethodSangerRead.R' 'MethodShared.R' 'MethodsQualityReport.R'  
 'ShinySangerAlignmentServer.R' 'ShinySangerAlignmentUI.R'  
 'ShinySangerContigServer.R' 'ShinySangerContigUI.R'  
 'ShinyServerModule.R' 'UtilitiesFunc.R'  
 'UtilitiesFuncInputChecker.R' 'data.R'  
 'sangeranalyseR\_package.R' 'sangeranalyseR\_show\_method.R'

**git\_url** <https://git.bioconductor.org/packages/sangeranalyseR>

**git\_branch** RELEASE\_3\_18

**git\_last\_commit** dd9c501

**git\_last\_commit\_date** 2023-10-24

**Repository** Bioconductor 3.18

**Date/Publication** 2024-03-25

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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)
```

---

generateReport      *Method generateReport*

---

### 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)
## Not run:
generateReport(sangerReadFData)
generateReport(sangerReadFData, colors="cb_friendly")
generateReport(sangerContigData)
generateReport(sangerContigData, colors="cb_friendly")
generateReport(sangerAlignmentData)
generateReport(sangerAlignmentData, colors="cb_friendly")
## End(Not run)

```

---

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

**Description**

Method generateReportSA

**Usage**

```

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

```

**Arguments**

<code>object</code>	A SangerAlignment S4 instance.
<code>outputDir</code>	The output directory of the generated HTML report.
<code>includeSangerContig</code>	The parameter that decides whether to include SangerContig level report. The value is TRUE or FALSE and the default is TRUE.
<code>includeSangerRead</code>	The parameter that decides whether to include SangerRead level report. The value is TRUE or FALSE and the default is TRUE.
<code>colors</code>	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.
<code>...</code>	Further generateReportSA-related parameters.

**Value**

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

**Examples**

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

---

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

**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)
## Not run:
generateReportSC(sangerContigData)
## End(Not run)
```

---

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

## 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)
## Not run:
generateReportSR(sangerReadFData)
## End(Not run)
```

---

launchApp	<i>Method launchApp</i>
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### 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>
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---

**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

*Method MakeBaseCalls*

---

**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(sangerReadFData)
MakeBaseCalls(sangerReadFData, signalRatioCutoff = 0.22)
```

---

ObjectResults-class    *ObjectResults*

---

**Description**

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

**Slots**

printLevel

**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")
```

---

qualityBasePlot    *Method qualityBasePlot*

---

**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    *QualityReport*

---

**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**

```

inputFilesPath <- system.file("extdata/", package = "sangeranalyseR")
A_chloroticaFFN <- file.path(inputFilesPath,
                             "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")
## Not run:
qualityBasePlot(qualityReportData)
## End(Not run)

```

---

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	<i>QualityReport instance</i>
-------------------	-------------------------------

---

**Description**

QualityReport instance

**Usage**

```
data(qualityReportData)
```

**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)
data(sangerAlignmentData)
## Not run:
readTable(sangerReadFData)
readTable(sangerContigData)
readTable(sangerAlignmentData)

## End(Not run)
```

---

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
)
```

## Arguments

inputSource	The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".
ABIF_Directory	The parent directory of all of the reads contained in ABIF format you wish to analyse. In SangerAlignment, all reads in subdirectories will be scanned recursively.
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.
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 "".

<code>minReadsNum</code>	The minimum number of reads required to make a consensus sequence, must be 2 or more. The default value is 2.
<code>minReadLength</code>	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.
<code>minFractionCall</code>	Minimum fraction of the sequences required to call a consensus sequence for <code>SangerContig</code> at any given position (see the <code>ConsensusSequence()</code> 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.
<code>maxFractionLost</code>	Numeric giving the maximum fraction of sequence information that can be lost in the consensus sequence for <code>SangerContig</code> (see the <code>ConsensusSequence()</code> 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.
<code>acceptStopCodons</code>	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).
<code>readingFrame</code>	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.
<code>processorsNum</code>	The number of processors to use, or NULL (the default) for all available processors.
<code>minFractionCallSA</code>	Minimum fraction of the sequences required to call a consensus sequence for <code>SangerAlignment</code> at any given position (see the <code>ConsensusSequence()</code> 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.
<code>maxFractionLostSA</code>	Numeric giving the maximum fraction of sequence information that can be lost in the consensus sequence for <code>SangerAlignment</code> (see the <code>ConsensusSequence()</code> 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.

**Value**

A `SangerAlignment` instance.

**Author(s)**

Kuan-Hao Chao

**Examples**

```

rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, "Allolobophora_chlorotica", "RBNI1")
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     = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHA FIMIFFMVMPI MIGGF
  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 = "SRQWLFSTNHKDIGTLYIFIGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFAIMIFFMVMPIGIGF
        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 = "SRQWLFSTNHKDIGTLYIFIGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFAIMIFFMVMPIGIGF
        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 = "SRQWLFSTNHKDIGTLYFIGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFAIMIFFMVMPIMIGG
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 = "SRQWLFSTNHKDIGTLYFIGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFAIMIFFMVMPIMIGG
                        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")
## Not run:
generateReportSA(sangerAlignmentData)
generateReportSA(sangerAlignmentData, colors="cb_friendly")
## End(Not run)
```

---

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")
## Not run:
updateQualityParam(sangerAlignmentData,
                   TrimmingMethod      = "M2",
                   M1TrimmingCutoff    = NULL,
                   M2CutoffQualityScore = 40,
                   M2SlidingWindowSize = 15)
## End(Not run)

```

---

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**

SangerAlignment instance

**Usage**

```
data(sangerAlignmentData)
```

**Author(s)**

Kuan-Hao Chao

---

sangeranalyseR    *sangeranalyseR-package*

---

**Description**

sangeranalyseR-package

---

SangerContig    *SangerContig*

---

**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
)

```

**Arguments**

<code>inputSource</code>	The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".
<code>ABIF_Directory</code>	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.
<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.
<code>contigName</code>	The contig name of all the reads in <code>ABIF_Directory</code> .
<code>geneticCode</code>	Named character vector in the same format as <code>GENETIC_CODE</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 <code>getGeneticCode()</code> function. The default is the standard code.
<code>TrimmingMethod</code>	<code>TrimmingMethod</code> The read trimming method for this <code>SangerRead</code> . The value must be "M1" (the default) or 'M2'.
<code>M1TrimmingCutoff</code>	The trimming cutoff for the Method 1. If <code>TrimmingMethod</code> is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
<code>M2CutoffQualityScore</code>	The trimming cutoff quality score for the Method 2. If <code>TrimmingMethod</code> is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with <code>M2SlidingWindowSize</code> .
<code>M2SlidingWindowSize</code>	The trimming sliding window size for the Method 2. If <code>TrimmingMethod</code> is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with <code>M2CutoffQualityScore</code> .
<code>baseNumPerRow</code>	It defines maximum base pairs in each row. The default value is 100.
<code>heightPerRow</code>	It defines the height of each row in chromatogram. The default value is 200.
<code>signalRatioCutoff</code>	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.
<code>showTrimmed</code>	The logical value storing whether to show trimmed base pairs in chromatogram. The default value is TRUE.
<code>refAminoAcidSeq</code>	An amino acid reference sequence supplied as a string or an <code>AAString</code> 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 "".
<code>minReadsNum</code>	The minimum number of reads required to make a consensus sequence, must be 2 or more. The default value is 2.
<code>minReadLength</code>	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.
<code>minFractionCall</code>	Minimum fraction of the sequences required to call a consensus sequence for <code>SangerContig</code> at any given position (see the <code>ConsensusSequence()</code> 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.

**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_ACHLO006-09"
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 = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAEALGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPIIMIGGFN
  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", "RBNI")
contigName <- "Achl_RBNI384-13"
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 <- "Achl_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 = "SRQWLFSTNHKDIGTLYIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPI MIGGFN",
                    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", "RBNI")
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          = "Achl_RBNI384-13",
                    refAminoAcidSeq = "SRQWLFSTNHKDIGTLYIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPI MIGGFN",
                    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  = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVPIMI",
                      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  = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVPIMI",
                      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")
## Not run:
generateReportSC(sangerContigData)
generateReportSC(sangerContigData, colors="cb_friendly")
## End(Not run)

```

---

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)
data(sangerAlignmentData)
## Not run:
readTable(sangerReadFData)
readTable(sangerContigData)
readTable(sangerAlignmentData)

## End(Not run)

```

---

```

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")
## Not run:
updateQualityParam(sangerContigData,
                   TrimmingMethod      = "M2",
                   M1TrimmingCutoff    = NULL,
                   M2CutoffQualityScore = 40,
                   M2SlidingWindowSize = 15)
## End(Not run)
```

---

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`      *SangerContig instance*

---

**Description**

SangerContig instance

**Usage**

```
data(sangerContigData)
```

**Author(s)**

Kuan-Hao Chao

---

`SangerRead`      *SangerRead*

---

**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
)

```

**Arguments**

<code>inputSource</code>	The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".
<code>readFeature</code>	The direction of the Sanger read. The value must be "Forward Read" or "Reverse Read".
<code>readFileName</code>	The filename of the target ABIF file.
<code>fastaReadName</code>	If <code>inputSource</code> is "FASTA", then this value has to be the name of the read inside the FASTA file; if <code>inputSource</code> is "ABIF", then this value is "" by default.
<code>geneticCode</code>	Named character vector in the same format as <code>GENETIC_CODE</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 <code>getGeneticCode()</code> function. The default is the standard code.
<code>TrimmingMethod</code>	<code>TrimmingMethod</code> The read trimming method for this <code>SangerRead</code> . 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 <code>trimomatic</code> 's sliding window method.
<code>M1TrimmingCutoff</code>	The trimming cutoff for the Method 1. If <code>TrimmingMethod</code> is "M1", then the default value is 0.0001. Otherwise, the value must be NULL.
<code>M2CutoffQualityScore</code>	The trimming cutoff quality score for the Method 2. If <code>TrimmingMethod</code> is 'M2', then the default value is 20. Otherwise, the value must be NULL. It works with <code>M2SlidingWindowSize</code> .
<code>M2SlidingWindowSize</code>	The trimming sliding window size for the Method 2. If <code>TrimmingMethod</code> is 'M2', then the default value is 10. Otherwise, the value must be NULL. It works with <code>M2CutoffQualityScore</code> .

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.

**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_ACHL0006-09_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

*SangerRead*

---

**Description**

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





```

sangerReadF <- new("SangerRead",
  readFeature      = "Forward Read",
  readFileName     = A_chloroticaFFN)

## Input From ABIF file format
# Forward Read
A_chloroticaFFN <- file.path(inputFilesPath,
  "Allolobophora_chlorotica",
  "ACHLO",
  "Ach1_ACHLO006-09_1_F.ab1")
sangerReadF <- new("SangerRead",
  printLevel      = "SangerRead",
  inputSource     = "ABIF",
  readFeature     = "Forward Read",
  readFileName    = A_chloroticaFFN,
  fastaReadName  = NULL,
  geneticCode     = GENETIC_CODE,
  TrimmingMethod = "M1",
  M1TrimmingCutoff = 0.0001,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  baseNumPerRow  = 100,
  heightPerRow   = 200,
  signalRatioCutoff = 0.33,
  showTrimmed    = TRUE)

# Reverse Read
A_chloroticaRFN <- file.path(inputFilesPath,
  "Allolobophora_chlorotica",
  "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_ACHL0006-09_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_ACHL0006-09_2_R.fa")
readNameRfa <- "Ach1_ACHL0006-09_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")
## Not run:
generateReportSR(sangerReadFData, "~/Documents")
generateReportSR(sangerReadFData, colors="cb_friendly")
## End(Not run)
```

---

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")  
## Not run:  
qualityBasePlot(sangerReadFData)  
## End(Not run)
```

---

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)
data(sangerAlignmentData)
## Not run:
readTable(sangerReadFData)
readTable(sangerContigData)
readTable(sangerAlignmentData)

## End(Not run)

```

---

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**

SangerRead instance

**Usage**

```
data(sangerReadFData)
```

**Author(s)**

Kuan-Hao Chao

---

updateQualityParam	<i>Method updateQualityParam</i>
--------------------	----------------------------------

---

**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)
## Not run:
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)
## End(Not run)

```

---

writeFasta	<i>Method writeFasta</i>
------------	--------------------------

---

**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)  
## Not run:  
writeFasta(sangerReadFData)  
writeFasta(sangerContigData)
```

```
writeFasta(sangerAlignmentData)
## End(Not run)
```

---

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>
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**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)
```

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