

# 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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**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 (>= 3.6.0), stringr, ape, Biostrings, DECIPHER, parallel, reshape2, phangorn, sangerseqR, gridExtra, shiny, shinydashboard, shinyjs, data.table, plotly, DT, zeallot, excelR, shinycssloaders, gg dendro, shinyWidgets, openxlsx, tools, rmarkdown, kableExtra, seqinr, BiocStyle, logger

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**VignetteBuilder** knitr

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'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'

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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, ...)
```

**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.
...	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(sangerContigData)
generateReport(sangerAlignmentData)
## End(Not run)
```

---

generateReportSA      *Method generateReportSA*

---

**Description**

Method generateReportSA

**Usage**

```
generateReportSA(object, outputDir = NULL, includeSangerContig = TRUE,
  includeSangerRead = TRUE, ...)
```

**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.
...
    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,
... )

```

**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.
...
    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      *Method generateReportSR*

---

### Description

Method generateReportSR

### Usage

```
generateReportSR(object, outputDir = NULL, ...)
```

### Arguments

object	A SangerRead S4 instance.
outputDir	The output directory of the generated HTML report.
...	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      *Method launchApp*

---

### Description

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

### Usage

```
launchApp(object, outputDir = NULL)
```

### Arguments

object	A SangerContig or SangerAlignment S4 instance.
outputDir	The output directory of the saved new SangerContig or SangerAlignment S4 instance.

### Value

A SangerContig or SangerAlignment object.

**Author(s)**

Kuan-Hao Chao

**Examples**

```
data(sangerContigData)
data(sangerAlignmentData)
## Not run:
launchApp(sangerContigData)
launchApp(sangerAlignmentData)
## End(Not run)
```

---

launchAppSA

*Method launchAppSA*

---

**Description**

Method launchAppSA

**Usage**

```
launchAppSA(object, outputDir = NULL)
```

**Arguments**

object	A SangerAlignment S4 instance.
outputDir	The output directory of the saved new SangerAlignment S4 instance.

**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)
```

**Arguments**

object	A SangerContig S4 instance.
outputDir	The output directory of the saved new SangerContig S4 instance.

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

---

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

**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>
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---

**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_ACHL0006-09_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>
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---

**Description**

QualityReport instance

**Usage**

```
data(qualityReportData)
```

**Author(s)**

Kuan-Hao Chao

---

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

---

**Description**

Method readTable

**Usage**

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

**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

*SangerAlignment*


---

**Description**

the wrapper function for SangerAlignment

**Usage**

```

SangerAlignment(inputSource = "ABIF", fastaFileName = "",
namesConversionCSV = NULL, parentDirectory = "",
suffixForwardRegExp = "_F.ab1", suffixReverseRegExp = "_R.ab1",
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,
geneticCode = GENETIC_CODE, acceptStopCodons = TRUE,
readingFrame = 1, minFractionCallSA = 0.5, maxFractionLostSA = 0.5,
processorsNum = NULL)

```

**Arguments**

- inputSource** The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".
- fastaFileName** 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.
- namesConversionCSV**  
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.
- parentDirectory**  
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.
- suffixForwardRegExp**  
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".

suffixReverseRegExp	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".
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.
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.

<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>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.
<code>processorsNum</code>	The number of processors to use, or NULL (the default) for all available processors.

### Value

A `SangerAlignment` instance.

### Author(s)

Kuan-Hao Chao

### Examples

```
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, "Allolobophora_chlorotica", "RBNI")
suffixForwardRegExp <- "_[0-9]*_F.ab1"
suffixReverseRegExp <- "_[0-9]*_R.ab1"
sangerAlignment <- SangerAlignment(
  inputSource          = "ABIF",
  parentDirectory      = parentDir,
  suffixForwardRegExp  = suffixForwardRegExp,
  suffixReverseRegExp  = suffixReverseRegExp,
  refAminoAcidSeq     = "SRQWLFSTNHKDIGTLYIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIIVTAHAFIMIFFMVPIMI",
  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

- `inputSource` The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".
- `fastaFileName` 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.
- `namesConversionCSV` 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.
- `parentDirectory` If `inputSource` is "ABIF", then this value is the path of the parent directory storing all reads in ABIF format you wish to analyse and cannot be NULL. In `SangerAlignment`, all reads in subdirectories will be scanned recursively. If `inputSource` is "FASTA", then this value is NULL by default.
- `suffixForwardRegExp` 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".
- `suffixReverseRegExp` 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".
- `trimmingMethodSA` The read trimming method for all `SangerRead` S4 instances in `SangerAlignment`. The value must be "M1" (the default) or 'M2'. All `SangerReads` must have the same trimming method.
- `minFractionCallSA` Minimum fraction of the sequences required to call a consensus sequence for `SangerAlignment` 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.
- `maxFractionLostSA` Numeric giving the maximum fraction of sequence information that can be lost in the consensus sequence for `SangerAlignment` (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.
- `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

```
## Input From ABIF file format (Regex)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, 'Allolobophora_chlorotica', 'ACHLO')
suffixForwardRegExp <- "_[0-9]*_F.ab1"
suffixReverseRegExp <- "_[0-9]*_R.ab1"
sangerAlignment <- new("SangerAlignment",
  inputSource = "ABIF",
  parentDirectory = parentDir,
  suffixForwardRegExp = suffixForwardRegExp,
  suffixReverseRegExp = suffixReverseRegExp,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPIMI",
  TrimmingMethod = "M1",
  M1TrimmingCutoff = 0.0001,
  M2CutoffQualityScore = NULL,
  M2SlidingWindowSize = NULL,
  baseNumPerRow = 100,
  heightPerRow = 200,
  signalRatioCutoff = 0.33,
  showTrimmed = TRUE,
  processorsNum = 2)

## Input From ABIF file format (Csv three column)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, 'Allolobophora_chlorotica', 'ACHLO')
namesConversionCSV <- file.path(rawDataDir, "ab1", "SangerAlignment",
  "names_conversion.csv")
sangerAlignment <- new("SangerAlignment",
  inputSource = "ABIF",
  parentDirectory = parentDir,
  namesConversionCSV = namesConversionCSV,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPIMI",
  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")
suffixForwardRegExpFa <- "_[0-9]*_F$"
suffixReverseRegExpFa <- "_[0-9]*_R$"
sangerAlignmentFa <- new("SangerAlignment",
                        inputSource      = "FASTA",
                        fastaFileName    = fastaFN,
                        suffixForwardRegExp = suffixForwardRegExpFa,
                        suffixReverseRegExp = suffixReverseRegExpFa,
                        refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPIN",
                        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")
namesConversionCSV <- file.path(rawDataDir, "fasta",
                                "SangerAlignment", "names_conversion.csv")
sangerAlignmentFa <- new("SangerAlignment",
                        inputSource      = "FASTA",
                        fastaFileName    = fastaFN,
                        namesConversionCSV = namesConversionCSV,
                        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)

```

## 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.

## Value

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

**Examples**

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

**Arguments**

object            A SangerAlignment S4 instance.  
outputDir        The output directory of the saved new SangerContig S4 instance.

**Value**

A shiny.appobj object.

**Examples**

```
data("sangerAlignmentData")
RShinySA <- launchAppSA(sangerAlignmentData)
```

---

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(inputSource = "ABIF", fastaFileName = "",
  namesConversionCSV = NULL, parentDirectory = "", contigName = "",
  suffixForwardRegExp = "_F.ab1", suffixReverseRegExp = "_R.ab1",
  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,
  geneticCode = GENETIC_CODE, acceptStopCodons = TRUE,
  readingFrame = 1, processorsNum = NULL)
```

## Arguments

- inputSource**      The input source of the raw file. It must be "ABIF" or "FASTA". The default value is "ABIF".
- fastaFileName**    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.
- namesConversionCSV**  
                       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.
- parentDirectory**  
                       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.
- contigName**        The contig name of all the reads in parentDirectory.
- suffixForwardRegExp**  
                       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".
- suffixReverseRegExp**  
                       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".
- 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.
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.
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_ACHL0006-09"
suffixForwardRegExp <- "_F.ab1"
suffixReverseRegExp <- "_R.ab1"
sangerContig <- SangerContig(
  inputSource          = "ABIF",
  parentDirectory     = parentDir,
  contigName          = contigName,
  suffixForwardRegExp = suffixForwardRegExp,
  suffixReverseRegExp = suffixReverseRegExp,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVMPIMIG
  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**

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



- fastaFileName** If `inputSource` is "FASTA", then this value has to be the FASTA file; if `inputSource` is "ABIF", then this value is NULL by default.
- namesConversionCSV** 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.
- parentDirectory** If `inputSource` is "ABIF", then this value is the path of the parent directory storing all reads in ABIF format you wish to analyse and cannot be NULL. In SangerContig, all reads must be in the first layer in this directory. If `inputSource` is "FASTA", then this value is NULL by default.
- contigName** The contig name of all the reads in `parentDirectory`.
- suffixForwardRegExp** 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".
- suffixReverseRegExp** 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".
- 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.
- trimmingMethodSC** The read trimming method for all SangerRead S4 instances in SangerContig. The value must be "M1" (the default) or 'M2'. All SangerRead must have the same trimming method.
- 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 AAStrng 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

```
## Input From ABIF file format (Regex)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, "Allolobophora_chlorotica", "RBNI1")
contigName <- "Ach1_RBNI1384-13"
suffixForwardRegExp <- "_[0-9]*_F.ab1"
suffixReverseRegExp <- "_[0-9]*_R.ab1"
sangerContig <- new("SangerContig",
                    inputSource           = "ABIF",
                    parentDirectory       = parentDir,
                    contigName            = contigName,
                    suffixForwardRegExp   = suffixForwardRegExp,
                    suffixReverseRegExp   = suffixReverseRegExp,
                    refAminoAcidSeq      = "SRQWLFSTNHKDIGTLYIFGAWAGMVGTSLSILIRAELGHPGALIGDDQIYNVIIVTAHAFAIMIFFMVPIMIG",
                    TrimmingMethod        = "M1",
                    M1TrimmingCutoff      = 0.0001,
                    M2CutoffQualityScore  = NULL,
                    M2SlidingWindowSize  = NULL,
                    baseNumPerRow         = 100,
                    heightPerRow          = 200,
                    signalRatioCutoff     = 0.33,
                    showTrimmed           = TRUE,
```

```

processorsNum = 2)

## Input From ABIF file format (Csv three column method)
rawDataDir <- system.file("extdata", package = "sangeranalyseR")
parentDir <- file.path(rawDataDir, "Allolobophora_chlorotica", "RBNII")
namesConversionCSV <- file.path(rawDataDir, "ab1", "SangerContig", "names_conversion_2.csv")
sangerContig <- new("SangerContig",
  inputSource = "ABIF",
  parentDirectory = parentDir,
  namesConversionCSV = namesConversionCSV,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVPIMIG",
  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",
  "SangerContig", "Ach1_ACHL0006-09.fa")
contigName <- "Ach1_ACHL0006-09"
suffixForwardRegExpFa <- "_[0-9]*_F$"
suffixReverseRegExpFa <- "_[0-9]*_R$"
sangerContigFa <- new("SangerContig",
  inputSource = "FASTA",
  fastaFileName = fastaFN,
  contigName = contigName,
  suffixForwardRegExp = suffixForwardRegExpFa,
  suffixReverseRegExp = suffixReverseRegExpFa,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVPIMIG",
  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")
namesConversionCSV <- file.path(rawDataDir, "fasta", "SangerContig", "names_conversion_1.csv")
sangerContigFa <- new("SangerContig",
  inputSource = "FASTA",
  fastaFileName = fastaFN,
  namesConversionCSV = namesConversionCSV,
  refAminoAcidSeq = "SRQWLFSTNHKDIGTLYFIFGAWAGMVGTSLSILIRAE LGHPGALIGDDQIYNVIVTAHAFIMIFFMVPIMIG",
  processorsNum = 2)

```

**Description**

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

**Usage**

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

**Arguments**

object	A SangerContig S4 instance.
outputDir	The output directory of the saved new SangerContig S4 instance.

**Value**

A shiny.appobj object.

**Examples**

```
data("sangerContigData")
RShinySC <- launchAppSC(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")
## 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	<i>SangerContig instance</i>
------------------	------------------------------

---

**Description**

SangerContig instance

**Usage**

```
data(sangerContigData)
```

**Author(s)**

Kuan-Hao Chao

---

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

---

**Description**

the wrapper function for SangerRead

**Usage**

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

**Arguments**

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'.

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.

**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(
  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

`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. It can be "ABIF" or "FASTA" 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.

`abifRawData` A S4 class containing all fields in the ABIF file. It is 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.

`primaryAASeqS2` A polypeptide translated from primary DNA sequence starting from the second nucleic acid.

`primaryAASeqS3` A polypeptide translated from primary DNA sequence starting from the third nucleic acid.

`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.

`primarySeqRaw` The raw primary sequence from sangerseq class in sangerseqR package before base calling.

`secondarySeqRaw` The raw secondary sequence from sangerseq class in sangerseqR package before base calling.

`peakPosMatrixRaw` The raw peak position matrix from sangerseq class in sangerseqR package before base calling.

`peakAmpMatrixRaw` The raw peak amplitude matrix from sangerseq class in sangerseqR package before base calling.

### Author(s)

Kuan-Hao Chao

**Examples**

```

## Input From ABIF file format
# Forward Read
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)

# 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_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,
                 navigationContigFN = NULL, navigationAlignmentFN = NULL)

```

## Arguments

object	A SangerRead S4 instance.
outputDir	The output directory of the generated HTML report.
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)
## 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      *SangerRead instance*

---

**Description**

SangerRead instance

**Usage**

```
data(sangerReadFData)
```

**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)
## 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

*Method writeFastaSA*


---

**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)
```

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