

The RSeqMeth Package

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Type Package

Title Package for analysis of Sequenom EpiTYPER Data

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Description Package for analysis of Sequenom EpiTyper Data

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R topics documented:

RSeqMeth-package	1
ampliconReport	2
analyzeSequenom	3

Index	6
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RSeqMeth-package *Package for analysis of Sequenom EpiTYPER Data*

Description

Package for analysis of Sequenom EpiTyper Data

Details

Package: RSeqMeth
Type: Package
Version: 1.0.1
Date: 2007-08-13
License: GPL (Version 2 or later)

Author(s)

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References

Coolen MW, Statham AL, Gardiner-Garden M, Clark SJ. (2007) Nucleic Acids Research 35(18):e119
Genomic profiling of CpG methylation and allelic specificity using quantitative high-throughput mass spectrometry: critical evaluation and improvements.

Examples

```
#ampliconReport ()  
  
#analyzeSequenom ()
```

ampliconReport *Generate report files*

Description

Specified sequence files are read and reports generated.

Sequence files must be plaintext - no header. Whitespace is allowed.

Four files are generated:

<SEQUENCE NAME> T/C Report.csv - analysis of the CpG containing fragments

<SEQUENCE NAME> T/C Spectra.pdf - illustration of the predicted spectra

Usage

```
ampliconReport (fnames = NA, minMass = 1500, maxMass = 7000)
```

Arguments

fnames	A character vector of file names of sequences to be analyzed. If left to default, files are chosen interactively.
minMass	The minimal mass of a peak to be included in the analysis.
maxMass	The maximal mass of a peak to be included in the analysis.

Details

Fragmentation is analyzed for both the C and T Cleavage reactions.

Value

No value returned - reports generated are written to the directory the sequence files are read from.

Author(s)

Aaron Statham

References

Coolen MW, Statham AL, Gardiner-Garden M, Clark SJ. (2007) Nucleic Acids Research 35(18):e119
Genomic profiling of CpG methylation and allelic specificity using quantitative high-throughput mass spectrometry: critical evaluation and improvements.

See Also[analyzeSequenom](#)**Examples**

```
## choose sequence files interactively
#ampliconReport()

## generate report files from EN1.txt and SCTR.txt in the current working directory
#ampliconReport(c("EN1.txt", "SCTR.txt"))
```

analyzeSequenom	<i>Calculates methylation ratios and proportions</i>
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Description

The user is interactively asked to specify

Usage

```
analyzeSequenom(matchedName = NA, methName = NA, seqNames = NA, cull=TRUE,
  writeOut = TRUE, quiet = FALSE, minMass = 1500, maxMass = 7000)
```

Arguments

matchedName	Name of the file to read the matched peak data from - if left to default then the user is asked to interactively choose the matched peaks table.
methName	If <code>cull</code> is <code>TRUE</code> then the name of the file to read methylation grid data from - if left to default then the user is asked to interactively choose the methylation grid data. If <code>cull</code> is <code>FALSE</code> this value is ignored.
seqNames	A character vector of file names to read sequences from. The sequences are specified in the same order that their amplicons appear in the matched peaks table. If left to default then the user is asked to interactively choose the sequence files used in analysis.

cull	logical: if TRUE (default) then methylation grid data will be read from <code>methName</code> and missing values from this grid will be used to cull methylation ratios that did not meet the EpiTyper Probability Threshold setting at the time the methylation grid was exported. if FALSE no culling will occur and the value of <code>methName</code> is ignored.
writeOut	logical: if TRUE (default) then the calculated methylation values are written to tab separated text files in the same directory as <code>matchedName</code> . Two files are written: <matchedName> Weighted - contains for each informative CpGUnit (excluding overlaps) the methylation ratio calculated using the weighted formula. <matchedName> Proportion - contains for each informative CpGUnits (including overlaps) the proportion of each peak eg (0/2 CpGs methylated, 1/2 CpGs methylated, 2/2 CpGs methylated)
quiet	logical: if FALSE no output is written to the screen
minMass	The minimal mass of a peak to be included in the analysis.
maxMass	The maximal mass of a peak to be included in the analysis.

Details

Currently, only T cleavage data is interpreted. Matched peak files containing C cleavage data have not been tested.

Value

A list containing three elements:

Sequenom - Reproduces the calculations made by EpiTyper.

Weighted - Ratio for each CpGUnits (excluding overlaps) calculated using the weighted formula.

Proportion - Proportion for each peak in each informative CpGUnit (including overlaps).

Each of these is a list which contains an element for each amplicon in the input matched peaks table.

Each of these amplicon elements contains two elements:

Name - The name of the amplicon as specified in the matched peaks table.

Ratios - A data frame containing for each sample in the matched peaks table the methylation ratio or proportion as given above.

Author(s)

Aaron Statham

References

Coolen MW, Statham AL, Gardiner-Garden M, Clark SJ. (2007) Nucleic Acids Research 35(18):e119
 Genomic profiling of CpG methylation and allelic specificity using quantitative high-throughput mass spectrometry: critical evaluation and improvements.

See Also

[ampliconReport](#)

Examples

```
## run completely interactively, everything obtained from the user
#meth <- analyzeSequenom()

## specified matched peaks table, do not cull, sequences will be specified
## interactively by the user
#meth <- analyzeSequenom(matchedName = "Plate1 matched.txt", cull=FALSE)

## runs completely without user intervention - output is not written to files
#meth <- analyzeSequenom(matchedName = "Plate1 matched.txt", cull=FALSE, seqNames
# = c("EN1.txt", "EN1.txt", "SCTR.txt", "SCTR.txt"), quiet=TRUE, writeOut=FALSE)
```

Index

*Topic **manip**

ampliconReport, [2](#)

analyzeSequenom, [3](#)

*Topic **package**

RSeqMeth-package, [1](#)

ampliconReport, [2](#), [4](#)

analyzeSequenom, [3](#), [3](#)

RSeqMeth (*RSeqMeth-package*), [1](#)

RSeqMeth-package, [1](#)