Package 'MethTargetedNGS'

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Type Package

Title Perform Methylation Analysis on Next Generation Sequencing Data

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Description Perform step by step methylation analysis of Next Generation Sequencing data.

License Artistic-2.0

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`MethTargetedNGS-package`

Methylation Analysis of Next Generation Sequencing data.

Description

This package helps in visualizing methylation in CpG sites in NGS data for given datasets (normal/tumor) and to identify differentially methylated CpG sites in normal/tumor. This package to help in perform profile hidden markov modelling of given sequences.

NOTE: For profile hidden markov model HMMER software is required

Details

Package:	MethTargetedNGS
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Compare methylation status/pattern between samples.

*`compare_samples(healthy,tumor)`

Sequence alignment and create methylation pattern

*`methAlign(sequence_fasta, ref_seq)`

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bconv *Convert non-bisulfite sequences to bisulfite sequences.*

Description

Bisulfite sequences are the bisulfite treated DNA sequences where all cytosines except cytosine from CpG sites are converted to thymie. This technique is used to determine pattern of methylation. This function convert all cytosine except cytosines from CpG sites to thymine.

Usage

```
bconv(fasta_file, out_file = "output.fasta")
```

Arguments

fasta_file	: Input fasta file for conversion
out_file	: String value naming an output file. Default is output.fasta

Value

Fasta File

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Examples

```
input =  system.file("extdata", "bisulfite.fasta", package = "MethTargetedNGS")
bconv(fasta_file = input, out_file = "output.fasta")
```

compare_samples *Complete Methylation Analysis of Next Generation Sequencing Data*

Description

This function perform complete methylation analysis of the data.

1. Visualize methylation pattern
2. Calculate methylation average
3. Calculate methylation entropy
4. Perform fisher exact test on the samples to identify significant CpG sites.

Usage

```
compare_samples(healthy, tumor)
```

Arguments

healthy	: Output Matrix from methAlign
tumor	: Output Matrix from methAlign

Value

Generate a plot of Methylation Average, Methylation Entropy, Fisher Exact Test and Log Odd Ratio

Note

This function needs time to process depending on the number of sequences in fasta file

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See Also

methAlign, methAvg, methEntropy, odd_ratio, fishertest_cpg,

Examples

```
healthy = system.file("extdata", "Healthy.fasta", package = "MethTargetedNGS")
tumor = system.file("extdata", "Tumor.fasta", package = "MethTargetedNGS")
reference =  system.file("extdata", "Reference.fasta", package = "MethTargetedNGS")

healthy = methAlign(healthy,reference)
tumor = methAlign(tumor,reference)
compare_samples(healthy,tumor)
```

---

fishertest_cpg *Perform Fisher Exact Test on Methylation Data.*

Description

Fisher exact test is a test to calculate the statistical significance using contingency table. It was used to find the statistically significant differences in the methylation status of one particular CpG site between healthy and tumor sample. Contingency matrix was created for each CpG site. P-value was corrected for multiple testing using Benjamini-Hochberg method to calculate False Discovery Rate (FDR)

Usage

```
fishertest_cpg(healthy, tumor, plot = TRUE, main = "Fisher Exact Test")
```

Arguments

healthy	Matrix from methAlign. Also matrix where columns represents Cytosine of CpG sites and rows represents sequences.
tumor	Matrix from methAlign. Also matrix where columns represents Cytosine of CpG sites and rows represents sequences.
plot	Boolean. TRUE if need a plot after calculation. Default TRUE
main	Title of the plot. Default "Fisher Exact Test"

Value

Vector containing p-values.

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See Also

methAlign, compare_samples

Examples

```
healthy = system.file("extdata", "Healthy.fasta", package = "MethTargetedNGS")
tumor = system.file("extdata", "Tumor.fasta", package = "MethTargetedNGS")
reference =  system.file("extdata", "Reference.fasta", package = "MethTargetedNGS")

healthy = methAlign(healthy,reference)
tumor = methAlign(tumor,reference)
fisherexacttest <- fishertest_cpg(healthy,tumor)
```

---

hmmbuild *Create Profile Hidden Markov Model of given aligned sequences*

Description

This function creates profile hidden markov model of the given aligned sequences using HMMER algorithm.[1]

Usage

```
hmmbuild(file_seq, file_out,pathHMMER="")
```

Arguments

file_seq	Multiple sequence aligned fasta file
file_out	Output hidden markov model file
pathHMMER	Path where HMMER software is installed. Note: Windows user must setup cygwin to use this feature and set path to HMMER binaries (~hmmer/binaries/)

Value

Create Profile Hidden Markov Model in local directory

Note

Require HMMER software

Windows User: Please download HMMER from http://hmmer.janelia.org/

Setup cygwin from http://www.cygwin.com

Linux/Mac User: Download binaries or compile HMMER from http://hmmer.janelia.org/

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References

[1]Finn, Robert D., Jody Clements, and Sean R. Eddy. "HMMER web server: interactive sequence similarity searching." Nucleic acids research (2011): gkr367.

See Also

nhmmer

Examples

```
msa = system.file("extdata", "msa.fasta", package = "MethTargetedNGS")
if (file.exists("/usr/bin/hmmbuild"))
  hmmbuild(file_seq=msa,file_out="hmm",pathHMMER = "/usr/bin")
```

methAlign *Align sequences with the reference sequence using pairwiseAlignment function from the pwalign package*

Description

This function allow users to align pool of sequences to the reference sequence.

Usage

```
methAlign(sequence_fasta, ref_seq, sub_mat = FALSE, align_type = "local")
```

Arguments

sequence_fasta	String value naming an input fasta file. Single sequence or Multiple sequences in a single fasta file
ref_seq	String value naming an input fasta file. Single reference sequence is requried. If multiple sequences were passed only first sequence will be considered as reference.
sub_mat	Substitution matrix for the alignment.
align_type	type of alignment. One of "global", "local", "overlap", "global-local", and "local-global" where "global" = align whole strings with end gap penalties, "local" = align string fragments, "overlap" = align whole strings without end gap penalties, "global-local" = align whole strings in pattern with consecutive subsequence of subject, "local-global" = align consecutive subsequence of pattern with whole strings in subject. Default is "local"

Value

Methylation Matrix. Number of rows represents number of reads in sequence fasta file and number of columns represents number of CpG sites in reference fasta sequence. Only Cytosine of CpG site was observed in the table whether it is methylated or unmethylated.

Note

This function need some time to process depending on the number of sequences in fasta file

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See Also

compare_samples

Examples

```
healthy = system.file("extdata", "Healthy.fasta", package = "MethTargetedNGS")
reference = system.file("extdata", "Reference.fasta", package = "MethTargetedNGS")
methAlign(healthy,reference)
```

---

methAvg *Calculate Methylation Average of given methylation matrix*

Description

Methylation average of a CpG site is the percentage of unmethylated cytosine or methylated cytosine in a particular CpG site. The methylation average of a particular CpG site was calculated by number of cytosine divided by sum of total number of methylated and unmethylated cytosine at particular CpG site in a group of reads.

average = NC/(NC + NT)

Usage

```
methAvg(Sample, plot = FALSE)
```

Arguments

Sample	Matrix from methAlign. Also matrix where columns represents Cytosine of CpG sites and rows represents sequences.
plot	Boolean. TRUE if need a plot after calculation. Default FALSE

Value

Vector containing average methylation of given methylation matrix. Length of the vector represents the number of CpG sites in methylation matrix.

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See Also

methAlign, compare_samples

Examples

```
healthy = system.file("extdata", "Healthy.fasta", package = "MethTargetedNGS")
reference = system.file("extdata", "Reference.fasta", package = "MethTargetedNGS")
methP <- methAlign(healthy,reference)
avgMeth <- methAvg(methP,plot=TRUE)
```

`methEntropy` *Calculate Methylation Entropy*

Description

Entropy comparison between healthy and tumor samples can identify significant CpG sites which are contributing most in the tumor development either by hypomethylation or hypermethylation. Also such way can help in understanding the randomness in methylation status. Sliding window of 4 was used to calculate the entropy in the sample, which can analyze 16 different pattern for entropy calculation.

Usage

```
methEntropy(x)
```

Arguments

`x`	Matrix from methAlign. Also matrix where columns represents Cytosine of CpG sites and rows represents sequences

Value

Matrix containing entropy for every sequence and group of 4 cpg sites.

Note

This function needs time to process depending on the number of rows in matrix

Author(s)

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References

Xie, H., Wang, M., de Andrade, A., Bonaldo, M.d.F., Galat, V., Arndt, K., Rajaram, V., Goldman, S., Tomita, T. and Soares, M.B. (2011) Genome-wide quantitative assessment of variation in DNA methylation patterns. Nucleic Acids Research, 39, 4099-4108.

See Also

methAlign

Examples

```
healthy = system.file("extdata", "Healthy.fasta", package = "MethTargetedNGS")
reference = system.file("extdata", "Reference.fasta", package = "MethTargetedNGS")
methP <- methAlign(healthy,reference)
entMeth <- methEntropy(methP)
plot(entMeth,type="l")
```

---

methHeatmap *Generate Heatmap of the given methylation data.*

Description

Heatmaps are the way of visualizing methylation statuses of a sample. This function allows user to visualize methylation statuses at each CpG site for every sequence available in pool.

Usage

```
methHeatmap(Sample, yl = "", plot = TRUE, title = "")
```

Arguments

Sample	Matrix from methAlign. Also matrix where columns represents Cytosine of CpG sites and rows represents sequences.
yl	Ylabel for heatmap
plot	Boolean. If plot == FALSE, function will return a matrix of 1s and 0s. If plot == TRUE, function will create a heatmap as well as return a matrix of 1s and 0s
title	Title of the heatmap

Value

Heatmap

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See Also

methAlign

Examples

```
healthy = system.file("extdata", "Healthy.fasta", package = "MethTargetedNGS")
reference = system.file("extdata", "Reference.fasta", package = "MethTargetedNGS")
healthy = methAlign(healthy,reference)
hHeatmap = methHeatmap(healthy,plot=TRUE)
```

---

nhmmer *Calculate likelihood of the given profile hidden markov model against group of sequences*

Description

This function calculates likelihood score of given pool of sequences against given profile hidden markov model using HMMER algorithm.[1]

Usage

```
nhmmer(file_hmm, file_seq, pathHMMER="")
```

Arguments

file_hmm	HMM file from hmmbuild function
file_seq	Sequence fasta file for calculating likelihood
pathHMMER	Path where HMMER software is installed. Note: Windows user must setup cygwin to use this feature and set path to HMMER binaries (~hmmer/binaries/)

Value

Matrix containing likelihood scores

Note

Require HMMER software

Windows User: Please download HMMER from http://hmmer.janelia.org/

Setup cygwin from http://www.cygwin.com

Linux/Mac User: Download binaries or compile HMMER from http://hmmer.janelia.org/

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References

[1]Finn, Robert D., Jody Clements, and Sean R. Eddy. "HMMER web server: interactive sequence similarity searching." Nucleic acids research (2011): gkr367.

See Also

hmmbuild

Examples

```
msa = system.file("extdata", "msa.fasta", package = "MethTargetedNGS")
tumor = system.file("extdata", "Tumor.fasta", package = "MethTargetedNGS")
if (file.exists("/usr/bin/hmmbuild"))
{hmmbuild(file_seq=msa,file_out="hmm",pathHMMER = "/usr/bin")
res <- nhmmer("hmm",tumor,pathHMMER = "/usr/bin")
res}
```

---

odd_ratio *Calculate log odd ratio of the given samples (healthy/tumor)*

Description

Log Odd ratio defines the hypomethylation and hypermethylation of a sample in comparison to the other sample.

Usage

```
odd_ratio(SampA, SampB, plot = TRUE, main = "Log Odd Ratio")
```

Arguments

SampA	Matrix from methAlign. Also matrix where columns represents Cytosine of CpG sites and rows represents sequences.
SampB	Matrix from methAlign. Also matrix where columns represents Cytosine of CpG sites and rows represents sequences.
plot	Boolean. TRUE if need a plot after calculation. Default TRUE
main	Title of the plot

Value

Vector containing log odd ratios.

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See Also

methAlign

Examples

```
healthy = system.file("extdata", "Healthy.fasta", package = "MethTargetedNGS")
tumor = system.file("extdata", "Tumor.fasta", package = "MethTargetedNGS")
reference =  system.file("extdata", "Reference.fasta", package = "MethTargetedNGS")

healthy = methAlign(healthy,reference)
tumor = methAlign(tumor,reference)
odd_ratio(healthy,tumor)
```

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