

Package ‘Rolexa’

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Type Package

Title Statistical analysis of Solexa sequencing data

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Author Jacques Rougemont, Arnaud Amzallag, Christian Iseli, Laurent Farinelli, Ioannis Xenarios, Felix Naef

Maintainer Jacques Rougemont <jacques.rougemont@epfl.ch>

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Imports mclust, Biostrings, graphics, grDevices, IRanges, methods, ShortRead, stats

Enhances fork

Description

Provides probabilistic base calling, quality checks and diagnostic plots for Solexa sequencing data

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biocViews Sequencing, DataImport, Preprocessing, QualityControl

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BatchAnalysis

Batch Analysis

Description

Generate summary plots of the results of a base calling batch

Usage

```
## S4 method for signature RolexaRun
PlotCycles(run=Rolexa.env, int, seq,
cycles=c(1,11,21,31), par=list())
PlotCycles(run,...)
## S4 method for signature RolexaRun
BatchAnalysis(run=Rolexa.env, seq, scores, what=c("length","information","base","ratio","iupac"), main, par)
BatchAnalysis(run,...)
QualityBoxPlots(run=Rolexa.env, seq, cycles, par=list(las=2))
```

Arguments

run	a RolexaRun object defining the run parameters
int	a SolexaIntensity object
seq	a DNAStrngSet object
scores	a matrix of base quality scores (one column per base, one row per sequence)
what	select one the plot types
main	a title for the plot
cycles	the cycles to plot
par	parameters for the plotting functions
...	additional arguments, ignored

Details

Four types of diagnostic plots can be selected with the what argument of BatchAnalysis:

- lengthshows the histogram of tag lengths,
- informationthe distribution of information content per sequenced base, namely $((2 \times \text{length}(\text{tag}) - \text{total_entropy}(\text{tag})) / \text{length}(\text{tag}))$,
- basethe base composition of the sequences,
- ratiothe ratio of complementary bases,
- iupacthe proportion of the different classes of ambiguous bases along the sequences.

QualityBoxPlots makes boxplots of quality scores along the sequences. PlotCycles will execute [SeqScore](#) with plot=TRUE.

Author(s)

Jacques Rougemont, Arnaud Amzallag, Christian Iseli, Laurent Farinelli, Ioannis Xenarios, Felix Naef

References

Probabilistic base calling of Solexa sequencing data, BMC Bioinformatics 2008, 9:431

See Also

[SaveResults](#) to save the results produced by [SeqScore](#) or [FilterResults](#).

Examples

```
path = SolexaPath(system.file("extdata", package="ShortRead"))
rolenv = SetModel(idsep="_")
int = readIntensities(path,pattern="s_1_0001",withVariability=FALSE)
seq = CombineReads(run=rolenv,path=path,pattern="s_1_0001_seq*")
results = SeqScore(run=rolenv,int=int,seqInit=seq,cycles=1:36)
PlotCycles(run=rolenv,int=int,seq=seq,cycles=1:4)
par(ask=TRUE)
BatchAnalysis(rolenv,sread(seq),matrix(),what="iupac")
BatchAnalysis(rolenv,sread(seq),results$entropy,what="information")
results = FilterResults(run=rolenv,results=results)
BatchAnalysis(rolenv,sread(seq),results,what="length")
seq = readFastq(path)
par(mar=c(4,4,1,1),cex=1.5,lwd=2)
QualityBoxPlots(rolenv,seq,cycles=10:36)
```

CombinedPlot

Diagnostic plots

Description

Generate plots to visually assess the quality of select colonies or sequencing cycles

Usage

```
## S4 method for signature RolexaRun
CombinedPlot(run=Rolexa.env, int, seq, scores, colonies = 1:4, par = list())
CombinedPlot(run,...)
## S4 method for signature SolexaIntensity
ChannelHistogram(int, cycles = c(1,18,36),
threeModes = FALSE, par = list())
ChannelHistogram(int,...)
```

Arguments

run	a RoLexaRun object defining the run parameters
int	a SolexaIntensity object
seq	a ShortRead object
scores	a matrix of base quality scores (one column per base, one row per sequence)
cycles	the list of cycles to plot
colonies	the list of rows to select for plotting
threemodes	fit and plot a mixture of 3 gaussians (2 by default)
par	parameters for the plotting function
...	additional arguments, ignored

Details

CombinedPlot creates one plot for each selected colony with the sequence along the x axis, the four intensities plotted as barplots above each base and the quality scores as a line plot below the sequence.

ChannelHistogram plots histograms and signal-noise thresholds for each of the four intensity channels on selected cycles. Fits to 2 or 3 gaussians are overlaid on the histograms.

Author(s)

Jacques Rougemont, Arnaud Amzallag, Christian Iseli, Laurent Farinelli, Ioannis Xenarios, Felix Naef

References

Probabilistic base calling of Solexa sequencing data, BMC Bioinformatics 2008, 9:431

Examples

```
path = SolexaPath(system.file("extdata", package="ShortRead"))
rolenv = SetModel(idsep="_")
int = readIntensities(path,pattern="s_1_0001",withVariability=FALSE)
seq = CombineFastQ(run=rolenv,path=path)
CombinedPlot(run=rolenv,int=int,seq=seq,scores=as(quality(seq),"matrix"),colonies=1)
```

DeCorrelateChannels *Correct for global correlations and biases*

Description

Functions to correct for global correlations between color channels or between successive sequencing cycles

Usage

```

## S4 method for signature SolexaIntensity
DeCorrelateChannels(int,cycles=seq(1,dim(int)[3],by=1),theta=matrix(rep(c(0.8806742,1.3727418,0.883
## S4 method for signature array
DeCorrelateChannels(int,cycles=seq(1,dim(int)[3],by=1),theta=matrix(rep(c(0.8806742,1.3727418,0.883
DeCorrelateChannels(int,...)
## S4 method for signature SolexaIntensity
OptimizeAngle(int,cycles=seq(1,dim(int)[3],by=1),...)
OptimizeAngle(int,...)
## S4 method for signature SolexaIntensity
DeCorrelateCycles(int,ncycles=dim(int)[3],rate=1.8e-2)
## S4 method for signature array
DeCorrelateCycles(int,ncycles=dim(int)[3],rate=1.8e-2)
DeCorrelateCycles(int,...)
## S4 method for signature SolexaIntensity
OptimizeRate(int,ncycles=dim(int)[3],...)
OptimizeRate(int,...)
## S4 method for signature RolexaRun
TileNormalize(run=Rolexa.env,int,cycles=seq(1,dim(int)[3],by=1))
TileNormalize(run,...)

```

Arguments

run	a RolexaRun object defining the run parameters
int	a SolexaIntensity object or an array
cycles, ncycles	the cycles or the number of cycles (starting from 1) to apply the correction to
theta	a $\text{length}(\text{cycles}) \times 4$ matrix with four angles per cycle defining the coordinate changes
rate	the rate of nucleotide mis-incorporation at each cycle
...	additional arguments passed to optim

Details

DeCorrelateChannels applies to coordinate transforms: one transforming the axes 1,2 to the axes with angles $\theta[1:2]$ relative to axis 1, and similarly with axes 3,4 and angles $\theta[3:4]$. These angles can be calculated with `OptimizeAngle` which minimizes the correlations between channel 1 and 2, and between channel 3 and 4, for each cycle. DeCorrelateCycles assumes that at each cycles, a fraction rate of sequences fail to incorporate any nucleotides and therefore the sequence lengths at each colony display a binomial distribution which is corrected for by taking into account the intensity measured at previous cycles. OptimizeRate calculates a rate that minimizes correlations between consecutive cycles.

TileNormalize estimates the local trend by [loess](#) fitting of the model $\text{int} \sim x+y$ and subtracts it from the intensity matrix.

Value

TileNormalize, DeCorrelateChannels and DeCorrelateCycles return an object of the same type as int corrected for spurious correlations. OptimizeAngle returns an length(cycles)*4 matrix and OptimizeRate returns a single positive real number.

Author(s)

Jacques Rougemont, Arnaud Amzallag, Christian Iseli, Laurent Farinelli, Ioannis Xenarios, Felix Naef

References

Probabilistic base calling of Solexa sequencing data, BMC Bioinformatics 2008, 9:431

See Also

TileNormalize

Examples

```
path = SolexaPath(system.file("extdata", package="ShortRead"))
rolenv = SetModel(idsep="_")
int = readIntensities(path,pattern="s_1_0001",withVariability=FALSE)

int1 = DeCorrelateChannels(int=int,cycles=1:5,theta=OptimizeAngle(int=int,cycles=1:5))
int2 = DeCorrelateCycles(int=int1,ncycles=5,rate=OptimizeRate(int=int1))
int3 = TileNormalize(run=rolenv,int=int,cycles=1)
seq = CombineReads(run=rolenv,path=path,pattern="s_1_0001_seq*")
PlotCycles(run=rolenv,int=int3,seq=seq,cycles=1:4)
```

FilterResults

FilterResults

Description

Filter basecalling results to keep only high-quality bases

Usage

```
## S4 method for signature RolexaRun
FilterResults(run=Rolexa.env,results)
FilterResults(run,...)
```

Arguments

run	a RolexaRun object defining the run parameters
results	a results object from SeqScore
...	additional arguments, ignored

Details

FilterResults filters the sequences according to the entropy thresholds set by [IThresholds](#) and applies the tag length cutoff [MinimumTagLength](#).

The algorithm works as follows: for each tag the base entropies are searched for a sub-vector $k+1:l$ such that $\text{sum}(\text{entropy}[n, 5+k+1:l]) \leq \text{IThresholds}[l]$ where $l = \text{MinimumTagLength}$. If such a sub-vector exists, it is then extended in both direction until the total entropy exceeds the threshold: $\text{sum}(\text{results}[n, 5+k1:k2]) > \text{IThresholds}[k2-k1+1]$.

The tag is then shortened: `substr(results[n,5],k1,k2)`, but [ACGT] bases to left of $k1$ and to the right of $k2$ are added. The [Barcode](#) first bases of the tags will always be included in a separate column if this parameter has been set. If `PET=TRUE` then the whole procedure is applied independently to each half of the sequence (and two separate sets of tags and scores are returned) and the barcode (if any) is assumed to be in-between the two paired tags.

Value

FilterResults returns an object suitable for [SaveResults](#)

Author(s)

Jacques Rougemont, Arnaud Amzallag, Christian Iseli, Laurent Farinelli, Ioannis Xenarios, Felix Naef

References

Probabilistic base calling of Solexa sequencing data, BMC Bioinformatics 2008, 9:431

See Also

[readFastq](#) to read fastq files, [SeqScore](#) and [FilterResults](#) to produce results for [SaveResults](#)

ForkBatch

Multi-threaded Probabilistic Base Calling

Description

Performs multi-threaded base calling on a collection of intensity files generated by the Solexa image analysis software

Usage

```
ForkBatch(run=Rolexa.env,path,outputpath="./",prefix="rs_",nthreads=3,nfiles=2,lane=1,tiles=1:100,...)
## S4 method for signature RolexaRun
OneBatch(run,path,lane,tiles,outputpath,prefix)
OneBatch(run,...)
```

Arguments

run	a RolexaRun object defining the run parameters
path	a SolexaPath object defining providing the input paths
outpath	the path to the output directory
prefix	output file prefix, see SaveResults
nthreads	number of threads to use
nfiles	number of input files to concatenate in one batch
lane	the lane number to analyze
tiles	a subset of tiles to read
...	further arguments passed to the RolexaRun constructor

Details

The function [ForkBatch](#) runs through the list of input files, concatenates them by batches of `nfiles`, then calls [OneBatch](#) in each of the `nthreads` threads until all batches have been processed. Each batch results are passed to [FilterResults](#) and saved in an output file inside `outpath`.

Author(s)

Jacques Rougemont, Arnaud Amzallag, Christian Iseli, Laurent Farinelli, Ioannis Xenarios, Felix Naef

References

Probabilistic base calling of Solexa sequencing data, BMC Bioinformatics 2008, 9:431

See Also

[CombineFastQ](#), [CombineReads](#) and [SaveResults](#)

Examples

```
path = SolexaPath(system.file("extdata", package="ShortRead"))
rolenv = SetModel(idsep="_")
## Not run:
#This will take some time to complete:
library(fork)
ForkBatch(run=rolenv,path=path,tiles=1)

## End(Not run)
```


SaveResults

*SaveResults***Description**

Read and write data in a convenient form for Rolexa base-calling

Usage

```
## S4 method for signature RolexaRun
SaveResults(run=Rolexa.env,results,outputpath,prefix="rs_")
SaveResults(run,...)
## S4 method for signature RolexaRun,SolexaPath
CombineReads(run=Rolexa.env,path,pattern="s_[1-8]_0[01][0-9]*_seq*")
CombineReads(run,path,...)
## S4 method for signature RolexaRun,SolexaPath
CombineFastQ(run=Rolexa.env,path,pattern="s_[1-8]_0[01][0-9]*",sext="_seq*",pext="_prb*")
CombineFastQ(run,path,...)
```

Arguments

run	a RolexaRun object defining the run parameters
results	a results list, as given by FilterResults or SeqScore
outputpath	a directory name for the output files
path	a SolexaPath object
prefix	a prefix string for output file names
pattern	a pattern for selecting Solexa output files, see readXStringColumns
sext	file extension tag for sequence files readPrb
pext	file extension tag for prb files, see
...	additional arguments, ignored

Details

CombineReads reads "_seq" files and splits the columns to create a [ShortRead](#) object, CombineFastQ reads "_seq" and "_prb" files and combines them into a [ShortReadQ](#) object, SaveResults creates a [ShortReadQ](#) objects from the output of [FilterResults](#) and writes it to a file using [writeFastq](#).

Value

CombineReads returns a [ShortRead](#) object, CombineFastQ returns a [ShortReadQ](#) object,

Author(s)

Jacques Rougemont, Arnaud Amzallag, Christian Iseli, Laurent Farinelli, Ioannis Xenarios, Felix Naef

References

Probabilistic base calling of Solexa sequencing data, BMC Bioinformatics 2008, 9:431

See Also

[readFastq](#) to read fastq files, [SeqScore](#) and [FilterResults](#) to produce results for SaveResults

 SeqScore

Fit and Plot intensities

Description

Model-based classification of intensity data points, to either perform a base calling or generate diagnostic plots

Usage

```
## S4 method for signature RolexaRun
SeqScore(run=Rolexa.env,int,seqInit,colonies,cycles,plot=FALSE)
SeqScore(run,...)
```

Arguments

run	a RolexaRun object defining the run parameters
int	a SolexaIntensity object
seqInit	a ShortRead object
colonies	which colonies to select
cycles	which cycles to select
plot	if TRUE do a plot rather than perform a base-calling
...	additional arguments, ignored

Details

This will use the EEV model of [mclust](#) to fit the data clouds with a mixture of 4 gaussian distributions. and generate a list of tags and entropy scores for each sequenced colony (if plot is FALSE) or plots two 2-dimensional projections for each selected cycle with gaussian parameters represented by standard ellipses and data points colored according to the induced classification.

If [fit](#) is TRUE, then the [EM](#) algorithm is run to convergence, otherwise only an [E-step](#) and an [M-step](#) are performed to evaluate the probabilities.

The fitting procedure then uses [HThresholds](#) to decide if a base is unambiguous and if degenerate IUPAC codes will be used.

Value

if plot is FALSE, SeqScore returns a list with an id slot containing the colonies coordinates, an sread slot which is a [DNAStrngSet](#) object and an entropy matrix

Author(s)

Jacques Rougemont, Arnaud Amzallag, Christian Iseli, Laurent Farinelli, Ioannis Xenarios, Felix Naef

References

Probabilistic base calling of Solexa sequencing data, BMC Bioinformatics 2008, 9:431

Examples

```
path = SolexaPath(system.file("extdata", package="ShortRead"))
rolenv = SetModel(idsep="_")
int = readIntensities(path,pattern="s_1_0001",withVariability=FALSE)
seq = CombineReads(run=rolenv,path=path,pattern="s_1_0001_seq*")
results = SeqScore(run=rolenv,int=int,seqInit=seq,cycles=1:10)
results$sread
```

TileImage

Reconstruct tile image

Description

Generate an image of the local intensity average

Usage

```
## S4 method for signature SolexaIntensity
TileImage(int,cycle,tile,channel=c(A,C,G,T),ncell=30)
TileImage(int,...)
```

Arguments

int	a SolexaIntensity object
cycle	the cycle to make an image of
tile	the tile to make an image of
channel	the channel ('A', 'C', 'G' or 'T') to make an image of
ncell	the number of divisions in each dimension for the image
...	additional arguments, ignored

Details

TileImage creates an image of the intensity on a tile, in a given channel and at a given cycle. The tile is divided into ncell*ncell cells and the average intensity in each cell is represented on a color scale.

Author(s)

Jacques Rougemont, Arnaud Amzallag, Christian Iseli, Laurent Farinelli, Ioannis Xenarios, Felix Naef

References

Probabilistic base calling of Solexa sequencing data, BMC Bioinformatics 2008, 9:431

Examples

```
path = SolexaPath(system.file("extdata", package="ShortRead"))
rolenv = SetModel(idsep="_")
int = readIntensities(path,pattern="s_1_0001",withVariability=FALSE)
par(mfrow=c(2,2))
for (c in c(A,C,G,T))
  TileImage(int=int,cycle=1,tile=readInfo(int)$tile[1],channel=c,ncell=5)
int2 = TileNormalize(rolenv,int=int,cycles=1)
x11()
par(mfrow=c(2,2))
for (c in c(A,C,G,T))
  TileImage(int=int2,cycle=1,tile=readInfo(int)$tile[1],channel=c,ncell=5)
```

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