Rolexa

April 19, 2010

`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,outpath="./",prefix="rs_",nthreads=3,nfiles=2,lane
## S4 method for signature 'RolexaRun':
OneBatch(run,path,lane,tiles,outpath,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,outpath,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
CombineFastQ(run,path,...)
```

Arguments

run	a RolexaRun object defining the run parameters
results	a results list, as given by FilterResults or SeqScore
outpath	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

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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(0.8806
## S4 method for signature 'array':
DeCorrelateChannels(int,cycles=seq(1,dim(int)[3],by=1),theta=matrix(rep(c(0.8806
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 length(cycles)*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 consecutives cycles.

TileNormalize estimates the local trend by loess fitting of the model int ~ x+y and substracts 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 sum(entropy[n,5+k+1:l])<=IThresholds[l] where l=MinimumTagLength. If such a sub-vector exists, it is then extended in both direction until the total entropy exceeds the threshold: sum(results[n,5+k1:k2])>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

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 then 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 convergencce, 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 DNAStringSet 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
```

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",
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 DNAStringSet 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*length(tag)-total_entropy(tag))/nb_cycles),
- 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 visualy 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)
```

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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