Package 'basecallQC'

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Type Package

Title Working with Illumina Basecalling and Demultiplexing input and output files

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Description
The basecallQC package provides tools to work with Illumina bcl2Fastq (versions >= 2.1.7) software.Prior to basecalling and demultiplexing using the bcl2Fastq software, basecallQC functions allow the user to update Illumina sample sheets from versions <= 1.8.9 to >= 2.1.7 standards, clean sample sheets of common problems such as invalid sample names and IDs, create read and index basemasks and the bcl2Fastq command. Following the generation of basecalled and demultiplexed data, the basecallQC packages allows the user to generate HTML tables, plots and a self contained report of summary metrics from Illumina XML output files.

LazyData TRUE

biocViews Sequencing, Infrastructure, DataImport, QualityControl

License GPL (>= 3)

Depends R (>= 3.4), stats, utils, methods, rmarkdown, knitr, prettydoc, yaml

Imports ggplot2, stringr, XML, raster, dplyr, data.table, tidyr, magrittr, DT, lazyeval, ShortRead

Suggests testthat, BiocStyle

VignetteBuilder knitr

SystemRequirements bcl2Fastq (versions >= 2.1.7)

Collate processIlluminaSamplesheets_Functions.R processXMLs_Functions.R allClasses.R allMethods.R processExternalFormats_Functions.R plots.R reporting.R tables.R FastQCShortRead_Functions.R processInterOps_Functions.R

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R topics documented:

`baseCallMetrics` *Gather basecalling metrics from a Run (using Run's ConversionStats.xml file).*

Description

Gather basecalling metrics from a Run (using Run's ConversionStats.xml file).

Usage

```
baseCallMetrics(bcl2fastqparams)
```

Arguments

`bcl2fastqparams`	A BCL2FastQparams object as created by BCL2FastQparams() constructor.

Value

A list of length two containing the full basecalling metrics from a Run (using Run's ConversionStats.xml file). Contains an unsummarised data.frame and basecalling metrics summarised to Sample, Lane, Sample by lane, and Sample by Lane and Tile.

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
convMetrics <- baseCallMetrics(bcl2fastqparams)
```

`basecallQC-class` *The basecallQC object and constructor.*

Description

Object and method to handle Illumina basecalling/demultiplexing inputs and output files. Provides sample sheet cleanup, basecall command and summary QC statistics for basecalling/demultiplexing.

The basecallQC object and constructor.

Usage

```
basecallQC(bcl2fastqparams, RunMetaData = NULL, sampleSheet = NULL,
  doFQMetric = FALSE)
```

Arguments

`bcl2fastqparams`	A BCL2FastQparams object as created by BCL2FastQparams() constructor.
`RunMetaData`	Any run metadata to attach (data.frame)
`sampleSheet`	A sample sheet for Illumina basecalling using bcl2Fastq (See vignette for more details).
`doFQMetric`	TRUE or FALSE. Perform ShortRead FastQ quality assessment using ShortRead's qa and report function

Details

The basecallQC object contains slots BCL2FastQparams, cleanedSampleSheet, baseMasks, BCLCommand, baseCallMetrics, demultiplexMetrics and fqQCmetrics.

- "BCL2FastQparams" A BCL2FastQparams object
- "cleanedSampleSheet" A data.frame containing the cleaned sample sheet for Illumina basecalling using bcl2Fastq versions >= 2.1.7
- "baseMasks" A data.frame containing basecall masks per lane for use with bcl2Fastq versions >= 2.1.7. Basemasks in data.frame for reads and indexes as well as the total basemasks for each lane.
- "BCLCommand" A character string containing the command to be used for basecalling using bcl2Fastq (versions >= 2.1.7).
- "baseCallMetrics" A list containing the full basecalling metrics from ConversionStats.xml. Contains an unsummarised data.frame and basecalling metrics summarised to Sample, Lane, Sample by lane, and Sample by Lane and Tile

- "demultiplexMetrics" A list containing the full demultiplexing metrics from DemultiplexingStats.xml. Contains an unsummarised data.frame and demultiplexing metrics filtered to per Sample metrics
- "fqQCmetrics" A list containing a data.frame of read counts and links to ShortRead QA reports and a ShortRead QA object containing quality information for generated fastQs.

Value

basecallQC a basecallQC object (See details for more information)

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
```

`BCL2FastQparams-class` *The Parameters for BCL2FastQparams object.*

Description

Parameter class and accessors for use with basecallQC

Parameter class and accessors

Usage

```
BCL2FastQparams(runXML = NULL, config = NULL, runDir = NULL,
  outDir = NULL, verbose = TRUE)
```

Arguments

`runXML`	file path to runParameters.xml ,if not specified looks in top level of run directory.
`config`	file path to config.ini ,if not specified looks in top level of run directory.
`runDir`	file path to run directory.
`outDir`	file path to out directory.
`verbose`	TRUE or FALSE. Messages on or off. Warnings/errors persist

Details

The BCL2FastQparams object contains slots RunDir, OutDir and RunParameters

- "RunDir" Character string specifying the top level Run directory
- "OutDir" Character string specifying the output directory
- "RunParameters" A data.frame containing the information from runParameters.xml (See vignette for more details).

Value

A BCL2FastQparams object (See details).

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)
```

`createBasemasks` *Function to create basemasks for basecalling from Illumina samplesheet (for bcl2Fastq versions >= 2.1.7).*

Description

Parses the Illumina sample sheet for versions >= 2.1.7 and creates basemasks.

Usage

```
createBasemasks(cleanedSampleSheet, param)
```

Arguments

`cleanedSampleSheet`	Data.frame of cleaned samplesheet for Illumina basecalling using bcl2Fastq versions >= 2.1.7 (see vignette for more details)
`param`	A BCL2FastQparams object

Value

A data.frame containing basecall masks per lane for reads and indexes as well as per lane complete basemasks.

Author(s)

Thomas Carroll and Marian Dore

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)

cleanedSampleSheet <- validateBCLSheet(sampleSheet,param=bcl2fastqparams)
basemasks <- createBasemasks(cleanedSampleSheet,param=bcl2fastqparams)
```

`createBCLcommand` *Function to create command for Illumina basecalling/demultiplexing using bcl2fastq versions >= 2.1.7.*

Description

Creates the command to be used for basecalling/demultiplexing with bcl2fastq versions >= 2.1.7

Usage

```
createBCLcommand(bcl2fastqparams, cleanedSampleSheet, baseMasks)
```

Arguments

`bcl2fastqparams`	A BCL2FastQparams object.
`cleanedSampleSheet`	Data.frame of cleaned samplesheet for Illumina basecalling/demultiplexing using bcl2fastq versions >= 2.1.7 (see vignette for more details)
`baseMasks`	A data.frame of basemasks as created by createBasemasks() function

Value

A character vector containing the command for Illumina basecalling using bcl2fastq versions >= 2.1.7

Author(s)

Thomas Carroll and Marian Dore

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)

cleanedSampleSheet <- validateBCLSheet(sampleSheet,param=bcl2fastqparams)
baseMasks <- createBasemasks(cleanedSampleSheet,param=bcl2fastqparams)
toSubmit <- createBCLcommand(bcl2fastqparams,cleanedSampleSheet,baseMasks)
```

`demultiplexMetrics` *Gather demultiplexing metrics from a Run (using Run's DemultiplexingStats.xml file).*

Description

Gather demultiplexing metrics from a Run (using Run's DemultiplexingStats.xml file).

Usage

```
demultiplexMetrics(bcl2fastqparams)
```

Arguments

`bcl2fastqparams`	A BCL2FastQparams object as created by BCL2FastQparams() constructor.

Value

A list of length two containing the full demultiplexing metrics from a Run (using Run's DemultiplexingStats.xml file). Contains an unsummarised data.frame and demultiplexing metrics filtered to per Sample metrics

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
demuxMetrics <- demultiplexMetrics(bcl2fastqparams)
```

`demuxBarplot` *Barplot of Illumina demultiplexing statistics.*

Description

Produces a barplot of demultiplexing statistics of reads with perfect/mismatched barcode.

Usage

```
## S4 method for signature 'baseCallQC'
demuxBarplot(object,groupBy)

## S4 method for signature 'basecallQC'
demuxBarplot(object = "basecallQC",
  groupBy = c("Lane"))

## S4 method for signature 'list'
demuxBarplot(object = "basecallQC", groupBy = c("Lane"))
```

Arguments

`object`	A basecallQC object or list from call to demultiplexMetrics()
`groupBy`	Character vector of how data is grouped for plotting. Should be either "Project","Sample" or "Lane".

Value

A ggplot2 object.

Author(s)

Thomas Carroll and Marian Dore

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
plot <- demuxBarplot(bclQC)
```

`demuxBoxplot` *Boxplot of Illumina demultiplexing statistics.*

Description

Produces a boxplot of demultiplexing statistics of reads with perfect/mismatched barcode.

Usage

```
## S4 method for signature 'baseCallQC'
demuxBoxplot(object,groupBy)

## S4 method for signature 'basecallQC'
demuxBoxplot(object = "basecallQC",
  groupBy = c("Lane"))

## S4 method for signature 'list'
demuxBoxplot(object = "basecallQC", groupBy = c("Lane"))
```

Arguments

`object`	A basecallQC object or list from call to demultiplexMetrics()
`groupBy`	Character vector of how data is grouped for plotting. Should be either "Project","Sample" or "Lane".

Value

A ggplot2 object.

Author(s)

Thomas Carroll and Marian Dore

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
plot <- demuxBoxplot(bclQC)
```

`indexlengths` *Index lengths*

Description

Index lengths as defined by runParameters.xml

Usage

```
## S4 method for signature 'BCL2FastQparams'
indexlengths(object)

## S4 method for signature 'BCL2FastQparams'
indexlengths(object = "BCL2FastQparams")
```

Arguments

`object`	A BCL2FastQparams object

Value

Index lengths as defined runParameters.xml.

Author(s)

Thomas Carroll

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)
indexlength <- indexlengths(bcl2fastqparams)
```

`interOpsReport` *Function to parse InterOps files and generate summary reports*

Description

Parses the InterOps binary files produced by Illumina's Real Time Analysis sofware and used by Illumina's SAV sofware. InterOp binary files contain information on phasing/prephsing, yield,read numbers and basecalling quality score distributions per cycle. This interOpsReport functions parses and summarises the InterOps files, TileMetrics.bin and QMetrics.bin, and the Stats directory XML files, ConversionStats.xml and DemultiplexingStats.xml.

Usage

```
interOpsReport(bcl2fastqparams, verbose = TRUE)
```

Arguments

`bcl2fastqparams`	A BCL2FastQparams object.
`verbose`	TRUE or FALSE . TRUE reports progress through file parsing.

Details

The interOpsReport function returns a list of machine and run information, basecalling quality information and demultiplexing information. The three named elements are descibed below.

- "machineReport" A data.frame containing information machine and software parameters
- "sequencingReport" A data.frame of mean cluster density, percentage clusters passing filter, phasing and prephasing percentages, number of reads total/passing filter and percent of reads with mean quality score > Q30 grouped by lane and read
- "demuxReport" A data.frame of demultiplexing results containing yield, number of reads, percentage of reads with quality scores greater than >Q30 and the percent of total reads per lane. Results are summarised per lane for samples, underdetermined indexes and all indexes (identifed and unidentified).

Value

A named list of length 3 containing machine and run information, basecalling quality information and demultiplexing information.

Author(s)

Thomas Carroll.

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)

# myRes_BCAGJ8ANXX <- interOpsReport(bcl2fastqparams,verbose=TRUE)
```

`makeFQTable` *Generate an HTML table linking to per sample summary fastq QC statistics from ShortRead*

Description

Creates an HTML table linking to per sample summary fastq QC statistics from ShortRead

Usage

```
makeFQTable(object, output = "static")
```

Arguments

`object`	A basecall QC object as returned from basecallQC function
`output`	Whether the report contains frozen or sortable tables. Options are "static" and "html"

Value

A HTML table for reporting fastq QC results from ShortRead. Table contains read counts and links to ShortRead QA reports per sample.

Author(s)

Thomas Carroll

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
#makeFQTable(bclQC,output="static")
```

`passFilterBar` *Barplot of Illumina basecalling statistics for reads passing filter.*

Description

Produces a barplot of Illumina basecalling statistics for reads passing filter.

Usage

```
## S4 method for signature 'baseCallQC'
passFilterBar(object,groupBy,metricToPlot)

## S4 method for signature 'basecallQC'
passFilterBar(object = "basecallQC",
  groupBy = c("Lane"), metricToPlot = "Yield")

## S4 method for signature 'list'
passFilterBar(object = "basecallQC", groupBy = c("Lane"),
  metricToPlot = "Yield")
```

Arguments

`object`	A basecallQC object or list from call to baseCallMetrics()
`groupBy`	Character vector of how data is grouped for plotting. Should be either "Project","Sample","Lane","Til
`metricToPlot`	Character vector defining which metric will be displayed in plot. Should be either "Yield","Yield30","QualityScoreSum" or "ClusterCount".

Value

A ggplot2 object.

Author(s)

Thomas Carroll and Marian Dore

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
plot <- passFilterBar(bclQC)
```

`passFilterBoxplot` *Boxplot of Illumina basecalling statistics for reads passing filter.*

Description

Produces a boxplot of basecalling statistics for reads passing filter.

Usage

```
## S4 method for signature 'baseCallQC'
passFilterBoxplot(object,groupBy,metricToPlot)

## S4 method for signature 'basecallQC'
passFilterBoxplot(object = "basecallQC",
  groupBy = c("Lane"), metricToPlot = "Yield")

## S4 method for signature 'list'
passFilterBoxplot(object = "basecallQC",
  groupBy = c("Lane"), metricToPlot = "Yield")
```

Arguments

`object`	A basecallQC object or list from call to baseCallMetrics()
`groupBy`	Character vector of how data is grouped for plotting. Should be either "Project","Sample","Lane","Til
`metricToPlot`	Character vector defining which metric will be displayed in plot. Should be either "Yield","Yield30","QualityScoreSum" or "ClusterCount".

Value

A ggplot2 object.

Author(s)

Thomas Carroll and Marian Dore

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
plot <- passFilterBoxplot(bclQC,groupBy = "Sample")
```

`passFilterTilePlot` *Tile plot of Illumina basecalling statistics for reads passing filter.*

Description

Produces a plot of metric per Tile for basecalling statistics of reads passing/failing filter.

Usage

```
## S4 method for signature 'baseCallQC'
passFilterTilePlot(object,metricToPlot)

## S4 method for signature 'basecallQC'
passFilterTilePlot(object = "basecallQC",
  metricToPlot = "Yield")

## S4 method for signature 'list'
passFilterTilePlot(object = "basecallQC",
  metricToPlot = "Yield")
```

Arguments

`object`	A basecallQC object or list from call to baseCallMetrics()
`metricToPlot`	Character vector defining which metric will be displayed in plot. Should be either "Yield","Yield30","QualityScoreSum" or "ClusterCount".

Value

A ggplot2 object.

Author(s)

Thomas Carroll and Marian Dore

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
plot <- passFilterTilePlot(bclQC,metricToPlot="Yield")
```

`readlengths` *Read lengths*

Description

Read lengths as defined by runParameters.xml

Usage

```
## S4 method for signature 'BCL2FastQparams'
readlengths(object)

## S4 method for signature 'BCL2FastQparams'
readlengths(object = "BCL2FastQparams")
```

Arguments

`object`	A BCL2FastQparams object

Value

Read lengths as defined runParamaeters.xml

Author(s)

Thomas Carroll

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)
readlength <- readlengths(bcl2fastqparams)
```

`reportBCL` *Generate basecallQC report*

Description

Creates a summary report from basecalling and demultiplexing metrics.

Usage

```
## S4 method for signature 'basecallQC'
reportBCL(object,reportOut,reportOutDir,output,reportRMDfile,FQQC)

## S4 method for signature 'basecallQC'
reportBCL(object = "basecallQC",
  reportOut = "report.html", reportOutDir = getwd(), output = "static",
  reportRMDfile = NULL, FQQC = FALSE)
```

Arguments

`object`	A basecall QC object as returned from basecallQC() function
`reportOut`	Name of report file
`reportOutDir`	Directory for the report file
`output`	Whether the report contains frozen or sortable tables. Options are "static" and "html"
`reportRMDfile`	RMD to be used for reporting. (Default uses standard report template)
`FQQC`	TRUE or FALSE, whether to run ShortRead fastq QC on any fastQ in output directory.

Value

An HTML report is written to file.

Author(s)

Thomas Carroll

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
reportBCL(bclQC,"TestReport.html",output="html")
```

`summaryConvStatsTable` *Creates an HTML table of per sample summary statistics from basecalling results*

Description

Creates an HTML table of per sample summary statistics from basecalling results

Usage

```
## S4 method for signature 'baseCallQC'
summaryConvStatsTable(object)

## S4 method for signature 'basecallQC'
summaryConvStatsTable(object = "basecallQC",
  output = "static")

## S4 method for signature 'list'
summaryConvStatsTable(object = "basecallQC",
  output = "static")
```

Arguments

`object`	A basecallQC object or list from call to baseCallMetrics()
`output`	Whether the report contains frozen or sortable tables. Options are "static" and "html"

Value

An HTML table for reporting basecalling results.

Author(s)

Thomas Carroll

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
summaryDemuxTable(bclQC,output="static")
```

`summaryDemuxTable` *Generate an HTML table of per sample summary demultiplexing statistics*

Description

Generate an HTML table of per sample summary demultiplexing statistics

Usage

```
## S4 method for signature 'baseCallQC'
summaryDemuxTable(object)

## S4 method for signature 'basecallQC'
summaryDemuxTable(object = "basecallQC",
  output = "static")

## S4 method for signature 'list'
summaryDemuxTable(object = "basecallQC", output = "static")
```

Arguments

`object`	A basecallQC object or list from call to demultiplexMetrics()
`output`	Whether the report contains frozen or sortable tables. Options are "static" and "html"

Value

An HTML table for reporting demultiplexing results.

Author(s)

Thomas Carroll

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
```

```
outDir <- file.path(fileLocations,"Runs/161105_D00467_0205_AC9L0AANXX/C9L0AANXX/")
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),outDir,verbose=FALSE)
bclQC <- basecallQC(bcl2fastqparams,RunMetaData=NULL,sampleSheet)
summaryDemuxTable(bclQC,output="static")
```

`validateBCLSheet` *Illumina sample sheet cleaning and updating for bcl2Fastq versions >= 2.1.7*

Description

Parses an Illumina bcl2Fastq sample sheet to create a standardised/updated sample sheet for bcl2Fastq >= Version 2.1.7

Usage

```
validateBCLSheet(sampleSheet, param = bcl2fastqparams)
```

Arguments

`sampleSheet`	File location of a sample sheet for Illumina basecalling using bcl2Fastq (See vignette for more details).
`param`	A BCL2FastQparams object

Value

cleanedSampleSheet A data.frame containing the cleaned sample sheet for Illumina basecalling using bcl2Fastq versions >= 2.1.7.

Author(s)

Thomas Carroll and Marian Dore

Examples

```
fileLocations <- system.file("extdata",package="basecallQC")
runXML <- dir(fileLocations,pattern="runParameters.xml",full.names=TRUE)
config <- dir(fileLocations,pattern="config.ini",full.names=TRUE)
sampleSheet <- dir(fileLocations,pattern="*\\.csv",full.names=TRUE)
bcl2fastqparams <- BCL2FastQparams(runXML,config,runDir=getwd(),verbose=FALSE)
cleanedSampleSheet <- validateBCLSheet(sampleSheet,param=bcl2fastqparams)
```

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