

Package ‘savR’

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Type Package

Title Parse and analyze Illumina SAV files

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Description Parse Illumina Sequence Analysis Viewer (SAV) files, access data, and generate QC plots.

License AGPL-3

URL <https://github.com/bcalder/savR>

BugReports <https://github.com/bcalder/savR/issues>

Depends ggplot2

Imports methods, reshape2, scales, gridExtra, XML

Suggests Cairo, testthat

biocViews Sequencing

NeedsCompilation no

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savR-package	<i>Parse and analyze Illumina SAV files</i>
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Description

Parse Illumina Sequence Analysis Viewer files

Details

Package:	savR
Type:	Package
Version:	1.7.5
Date:	2015-07-28
License:	AGPL-3
LazyLoad:	yes

Parse Illumina Sequence Analysis Viewer (SAV) files, access data, and generate QC plots.

Author(s)

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References

For information about Illumina SAV, please refer to
http://supportres.illumina.com/documents/documentation/software_documentation/sav/sequencinganalysisviewer_userguide_15020619c.pdf
 For other implementations (and inspiration) please see
<http://search.cpan.org/dist/Bio-IlluminaSAV/Bio/IlluminaSAV.pm>
<https://bitbucket.org/invitae/illuminate>

buildReports	<i>Generate Illumina reports folder</i>
--------------	---

Description

Generate a folder of images that approximates the format of the folder that was superceded by InterOp. Requires the Cairo package.

Usage

```
buildReports(project, destination)

## S4 method for signature 'savProject,character'
buildReports(project,
  destination = "./savR-reports")

## S4 method for signature 'savProject,missing'
buildReports(project)
```

Arguments

project	SAV project
destination	path to save reports folder

Examples

```
## Not run:
example(savR)
buildReports(fc, "reports")

## End(Not run)
```

clusterQualityGtN	<i>Get the proportion of clusters over a specified quality threshold</i>
-------------------	--

Description

Return the ratio of clusters with a quality score less than or equal to a specified value (n) for the requested lanes and cycles.

Usage

```
clusterQualityGtN(project, lane, cycle, n)

## S4 method for signature 'savProject,integer,integer,integer'
clusterQualityGtN(project, lane,
  cycle, n = 30L)
```

Arguments

project	SAV project
lane	lane(s) number
cycle	cycle(s) number
n	quality threshold

Examples

```
## Not run:  
example(savR)  
clusterQualityGtN(fc, 1L, 25L, 30L)  
  
## End(Not run)
```

clusters	<i>Get number of clusters per lane</i>
----------	--

Description

Sum the total number of clusters for all tiles in the lane.

Usage

```
clusters(project, lane)  
  
## S4 method for signature 'savProject,integer'  
clusters(project, lane = 1L)
```

Arguments

project	SAV project
lane	lane(s) number

Examples

```
## Not run:  
example(savR)  
clusters(fc, 1L)  
  
## End(Not run)
```

correctedIntensities *Get Corrected Intensity data*

Description

Returns a data frame of corrected intensity data.

Usage

```
correctedIntensities(project)

## S4 method for signature 'savProject'
correctedIntensities(project)
```

Arguments

project SAV project

Details

lane: Lane number

tile: Tile ID

cycle: Cycle number

avg_intensity: Average intensity

avg_cor_[ACGT]: Average corrected intensity of channel A, C, G, or T

avg_cor_called_[ACGT]: Average corrected intensity for called clusters in channel A, C, G, or T

num_{none|[ACGT]}: Number of called bases for no-call, A, C, G, or T

sig_noise: Signal to noise ratio

Value

sorted data.frame of CI data.

Examples

```
example(savR)
colnames(correctedIntensities(fc))
```

cycles	<i>Get the total number of cycles</i>
--------	---------------------------------------

Description

Accessor to obtain the total number of cycles sequenced in an Illumina sequencing run.

Usage

```
cycles(project)
```

```
## S4 method for signature 'savProject'  
cycles(project)
```

Arguments

project SAV project

Value

total number of cycles in run, including all sequencing and index reads.

Examples

```
example(savR)  
cycles(fc)
```

directions	<i>Get the number of sequence reads</i>
------------	---

Description

Returns the number of sequencing reads (excluding index reads).

Usage

```
directions(project)
```

```
## S4 method for signature 'savProject'  
directions(project)
```

Arguments

project SAV project

Value

number of reads

Examples

```
example(savR)  
directions(fc)
```

errorMetrics	<i>Get Error Metrics</i>
--------------	--------------------------

Description

Error metrics for lane, tile, and cycle.

Usage

```
errorMetrics(project)

## S4 method for signature 'savProject'
errorMetrics(project)
```

Arguments

project SAV project

Details

lane: Lane number
tile: Tile ID
cycle: Cycle number
errorrate: Error rate
nPerfect: number of perfect reads
n[1-4]Error: Number of reads with 1, 2, 3 and 4 errors

Value

sorted data.frame of Error metrics

Examples

```
example(savR)
colnames(extractionMetrics(fc))
```

extractionMetrics	<i>Get Extraction Metrics</i>
-------------------	-------------------------------

Description

Extraction (intensity and FWHM) metrics for lane, tile, and cycle.

Usage

```
extractionMetrics(project)

## S4 method for signature 'savProject'
extractionMetrics(project)
```

Arguments

project SAV project

Details

lane: Lane number

tile: Tile ID

cycle: Cycle number

FWHM_[ACGT]: Full width at half maximum for A, C, G, or T

int_[ACGT]: Intensity of channel A, C, G, or T

datestamp: Time/date stamp

Value

sorted data.frame of Extraction metrics

Examples

```
example(savR)
colnames(extractionMetrics(fc))
```

flowcellLayout	<i>Get flowcell layout</i>
----------------	----------------------------

Description

Accessor to obtain information about the characteristics of the flowcell from an Illumina sequencing run.

Usage

```
flowcellLayout(project)

## S4 method for signature 'savProject'
flowcellLayout(project)
```

Arguments

project SAV project

Value

[illuminaFlowCellLayout-class](#) object

Examples

```
example(savR)
flowcellLayout(fc)
```

```
illuminaFlowCellLayout-class
    Layout of an Illumina flowcell
```

Description

Class representation of the features of an Illumina flow cell.

Slots

lanecount: Number of lanes on the flowcell
 surfacecount: Number of surfaces
 swathcount: Number of imaging swaths
 tilecount: Number of tiles per swath
 sectionperlane: Number of sections per lane (NextSeq)
 lanepersession: Number of lanes per section (NextSeq)
 tilenamingsconvention: Description of deviation from original formatting layout

```
illuminaRead-class    Illumina read
```

Description

Class representation of the features of an Illumina sequencing read.

Slots

number: the index of this read in sequencing
 cycles: number of cycles in this read
 index: logical representing whether or not this read is an index read

```
location    Get Flowcell folder location
```

Description

Accessor to obtain the path to data for a particular SAV project.

Usage

```
location(project)

## S4 method for signature 'savProject'
location(project)
```

Arguments

project SAV project

Value

normalized path to Illumina run data.

Examples

```
example(savR)
location(fc)
```

pfBoxplot *PF Boxplot*

Description

Generate a boxplot of the numbers of clusters and the number of Illumina pass-filter clusters per tile and lane

Usage

```
pfBoxplot(project)

## S4 method for signature 'savProject'
pfBoxplot(project)
```

Arguments

project SAV project

pfClusters *Get number of PF clusters per lane*

Description

Sum the total pass filter number of clusters for all tiles in the lane.

Usage

```
pfClusters(project, lane)

## S4 method for signature 'savProject,integer'
pfClusters(project, lane = 1L)
```

Arguments

project SAV project
lane lane(s) number

Examples

```
## Not run:
example(savR)
pfClusters(fc, 1L)

## End(Not run)
```

plotFWHM	<i>Generate FWHM plots</i>
----------	----------------------------

Description

Plots the average full width of clusters at half maximum (FWHM) of each tile for a given cycle and base.

Usage

```
plotFWHM(project, cycle, base)

## S4 method for signature 'savProject,integer,character'
plotFWHM(project, cycle = 1L,
  base = c("A", "C", "G", "T"))

## S4 method for signature 'savProject,missing,missing'
plotFWHM(project)

## S4 method for signature 'savProject,integer,missing'
plotFWHM(project, cycle)

## S4 method for signature 'savProject,missing,character'
plotFWHM(project, base)
```

Arguments

project	SAV project
cycle	sequence cycle
base	nucleotide base (ACGT)

plotIntensity	<i>Plot flowcell intensity by base and cycle</i>
---------------	--

Description

Draws a representation of a flowcell, showing the average corrected called intensity values.

Usage

```

plotIntensity(project, cycle, base)

## S4 method for signature 'savProject,integer,character'
plotIntensity(project, cycle = 1L,
  base = c("A", "C", "G", "T"))

## S4 method for signature 'savProject,missing,missing'
plotIntensity(project)

## S4 method for signature 'savProject,integer,missing'
plotIntensity(project, cycle)

## S4 method for signature 'savProject,missing,character'
plotIntensity(project, base)

```

Arguments

project	A savProject-class object
cycle	integer cycle number
base	character for nucleotide

plotQGT30

Plot Quality > 30 for a flowcell

Description

Generate a plot for a given cycle of the percentage of clusters in each tile that are \geq Q30.

Usage

```

plotQGT30(project, cycle)

## S4 method for signature 'savProject,integer'
plotQGT30(project, cycle = 1L)

## S4 method for signature 'savProject,missing'
plotQGT30(project)

```

Arguments

project	SAV project
cycle	sequence cycle

qualityHeatmap	<i>Generate a heatmap of qualities</i>
----------------	--

Description

Plots a heatmap of quality vs cycle for a given lane for 1 or more sequence reads. Read qualities include sequence + index.

Usage

```
qualityHeatmap(project, lane, read, collapse)

## S4 method for signature 'savProject,integer,integer,logical'
qualityHeatmap(project, lane,
  read, collapse = T)

## S4 method for signature 'savProject,numeric,numeric,missing'
qualityHeatmap(project, lane,
  read)
```

Arguments

project	SAV project
lane	integer lane specification
read	integer vector of sequence reads to include (not including index reads)
collapse	whether or not to collapse index reads into the preceeding read (# reads = directions), default TRUE

qualityMetrics	<i>Get Quality Metrics data</i>
----------------	---------------------------------

Description

Quality metric by lane, tile and cycle.

Usage

```
qualityMetrics(project)

## S4 method for signature 'savProject'
qualityMetrics(project)
```

Arguments

project	SAV project
---------	-------------

Details

lane: Lane number

tile: Tile ID

cycle: Cycle number

Q1-Q50: Number of clusters with quality of indicated column

Value

sorted data.frame of quality data

Examples

```
example(savR)
colnames(qualityMetrics(fc))
```

reads

Get reads

Description

Accessor to obtain information about the reads of a particular Illumina sequencing run.

Usage

```
reads(project)
```

```
## S4 method for signature 'savProject'
reads(project)
```

Arguments

project SAV project

Value

List of [illuminaRead-class](#) objects

Examples

```
example(savR)
reads(fc)
```

run	<i>Get the Run ID</i>
-----	-----------------------

Description

Accessor to obtain the string identifier of an Illumina sequencing run.

Usage

```
run(project)

## S4 method for signature 'savProject'
run(project)
```

Arguments

project SAV project

Value

parsed Illumina run id

Examples

```
example(savR)
run(fc)
```

savCorrectedIntensityFormat-class
<i>Corrected Intensity formatter</i>

Description

Lane, tile, cycle, average intensity, corrected intensities (ACGT), average corrected called intensities (ACGT), number of no-calls, number of (ACGT) calls, and signal to noise ratio.

Slots

name: vector of column names
type: vector of data types of elements
lengths: vector of byte lengths for each element
order: vector of column names for sorting
version: integer version number

savData-class *Structure for holding parsed InterOp headers and data*

Description

Structure for holding parsed InterOp headers and data

Slots

header: list of parsed header values

data: data.frame of parsed values

savErrorFormat-class *Error Metrics formatter*

Description

Lane, tile, cycle, errorrate, nPerfect, n1Error, n2Error, n3Error, n4Error.

Slots

name: vector of column names

type: vector of data types of elements

lengths: vector of byte lengths for each element

order: vector of column names for sorting

version: integer version number

savExtractionFormat-class
 Extraction Metrics formatter

Description

Lane, tile, cycle, FWHM (ACGT), intensity (ACGT), datestamp, timestamp. Datestamp and timestamp are munged at the moment because R does not have native support for 32-bit unsigned integers and I have not implemented a solution.

Slots

name: vector of column names

type: vector of data types of elements

lengths: vector of byte lengths for each element

order: vector of column names for sorting

version: integer version number

savFormat-class *Base class for formatters*

Description

Defines the necessary slots to create parse different binary files using the same generic parser.

Slots

name: vector of column names
type: vector of data types of elements
lengths: vector of byte lengths for each element
order: vector of column names for sorting
version: integer version number
default: logical default format ()

savProject-class *SAV project class*

Description

Represents a flowcell, metadata and parsed SAV information

Slots

location: Full path to flowcell directory
reads: List of [illuminaRead-class](#)
layout: [illuminaFlowCellLayout-class](#)
runid: Run ID
number: Run number
flowcell: Flowcell ID
instrument: Instrument ID
date: Run date
cycles: Total number of cycles
directions: Total number of sequence runs (ends)
parsedData: SAV data

savQualityFormat-class

Quality Metrics formatter

Description

Lane, tile, cycle, Q1-Q50 counts

Slots

name: vector of column names

type: vector of data types of elements

lengths: vector of byte lengths for each element

order: vector of column names for sorting

version: integer version number

savQualityFormatV5-class

Quality Metrics formatter version 5

Description

Lane, tile, cycle, Q1-Q50 counts

Slots

name: vector of column names

type: vector of data types of elements

lengths: vector of byte lengths for each element

order: vector of column names for sorting

version: integer version number

savR

Build a SAV project

Description

Constructor to build a [savProject-class](#) object and populate it. A SAV project consists of binary files generated by an Illumina sequencing run and placed in a folder named "InterOp". This folder contains a number of ".bin" files that contain statistics about the run. Creating this object parses all of the files and makes the data available for analysis.

Usage

```
savR(object)

## S4 method for signature 'character'
savR(object)

## S4 method for signature 'missing'
savR()
```

Arguments

object String Path to Flowcell data

Examples

```
fc <- savR(system.file("extdata", "MiSeq", package="savR"))
fc
```

savTileFormat-class *Tile Metrics formatter*

Description

Lane, tile, code, value. Codes are:

Details

100	Cluster Density
101	PF Cluster Density
102	Number of clusters
103	Number of PF clusters
400	Control lane

Slots

name: vector of column names

type: vector of data types of elements

lengths: vector of byte lengths for each element

order: vector of column names for sorting

version: integer version number (header consists of version (1b), length (1b))

 tileMetrics

Get Tile Metrics

Description

Returns the Tile Metrics SAV data.

Usage

```
tileMetrics(project)
```

```
## S4 method for signature 'savProject'
tileMetrics(project)
```

Arguments

project SAV project

Details

Metrics for each tile are encoded in the following format:

cluster density:	100
PF cluster density:	101
number of clusters:	102
number of PF clusters:	103
phasing for read N:	$(200 + (N - 1) * 2)$
prephasing for read N:	$(201 + (N - 1) * 2)$
percent aligned for read N:	$(300 + N - 1)$
control lane:	400

lane: Lane number

tile: Tile ID

code: Code described above

value: Value for code key

Value

sorted data.frame of tile metrics

References

Codes for Tile Metrics were obtained from the Python Illuminate package:
<https://bitbucket.org/invitae/illuminate>

Examples

```
example(savR)
colnames(tileMetrics(fc))
```

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