Package ‘savR’

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Description Parse Illumina Sequence Analysis Viewer (SAV) files, access data, and generate QC plots.
License AGPL-3
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BugReports https://github.com/bcalder/savR/issues
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R topics documented:

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Parse and analyze Illumina SAV files

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**  
*Generate Illumina reports folder*

**Description**

Generate a folder of images that approximates the format of the folder that was superceded by InterOp.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

**Usage**

```r
buildReports(project, destination)
```

### S4 method for signature 'savProject,character'

```r
buildReports(project, destination = "./savR-reports")
```

### S4 method for signature 'savProject,missing'

```r
buildReports(project)
```

**Arguments**

- `project`  
  - SAV project
- `destination`  
  - path to save reports folder

**Examples**

```r
## Not run:
example(savR)
betweenReports(fc, "reports")
## End(Not run)
```

---

**clusterQualityGtN**  
*Get the proportion of clusters over a specified quality threshold*

**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**

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

### S4 method for signature 'savProject,integer,integer,integer'

```r
clusterQualityGtN(project, lane, cycle, n = 30L)
```
clusters

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                                      Get number of clusters per lane

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**

```r
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**

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

Get the total number of cycles

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
e.example(savR)
cycles(fc)

directions

Get the number of sequence reads

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
e.example(savR)
directions(fc)
errorMetrics

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

Description

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

Usage

extractionMetrics(project)

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

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  Get flowcell layout

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
- `surfacetcount`: Number of surfaces
- `swathcount`: Number of imaging swaths
- `tilecount`: Number of tiles per swath
- `sectionperlane`: Number of sections per lane (NextSeq)
- `laneperssection`: Number of lanes per section (NextSeq)
- `tilenamingconvention`: 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**

```r
location(project)
```

## S4 method for signature 'savProject'

```r
location(project)
```
pfClusters

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
plotFWHM

Examples

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

## End(Not run)
```

---

**plotFWHM**  
*Generate FWHM plots*

**Description**

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

**Usage**

```r
plotFWHM(project, cycle, base)
```

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

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

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

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

**Arguments**

- **project**  
  SAV project

- **cycle**  
  sequence cycle

- **base**  
  nucleotide base (ACGT)

---

**plotIntensity**  
*Plot flowcell intensity by base and cycle*

**Description**

Draws a representation of a flowcell, showing the average corrected called intensity values.
plotQGT30

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 >= 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

Generate a heatmap of qualities

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

Get Quality Metrics data

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

eexample(savR)
colnames(qualityMetrics(fc))

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

eexample(savR)
reads(fc)
run

Get the Run ID

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
Corrected Intensity formatter

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**

```r
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: \((200 + (N - 1) \times 2)\)
- prephasing for read N: \((201 + (N - 1) \times 2)\)
- 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](https://bitbucket.org/invitae/illuminate)

**Examples**

```r
e.example(savR)
colnames(tileMetrics(fc))
```
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