Package ‘savR’
March 29, 2017

Type   Package
Title  Parse and analyze Illumina SAV files
Version 1.12.0
Date   2015-07-28
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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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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
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Generate a folder of images that approximates the format of the folder that was superceded by InterOp.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

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

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

clusterQualityGtN(project, lane, cycle, n)

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

Arguments

- **project**: SAV project
- **lane**: lane(s) number
- **cycle**: cycle(s) number
- **n**: quality threshold

Examples

```r
## 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

```r
clusters(project, lane)
```

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

Arguments

- **project**: SAV project
- **lane**: lane(s) number

Examples

```r
## 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

*Get the total number of cycles*

**Description**

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

**Usage**

```r
cycles(project)
```

```r
## 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**

```r
eexample(savR)
cycles(fc)
```

directions

*Get the number of sequence reads*

**Description**

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

**Usage**

```r
directions(project)
```

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

**Arguments**

- `project` SAV project

**Value**

number of reads

**Examples**

```r
eexample(savR)
directions(fc)```
Description

Error metrics for lane, tile, and cycle.

Usage

```r
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

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

Description

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

Usage

```r
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))

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

eexample(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)
- 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
location(project)

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

Arguments
project SAV project

Value
normalized path to Illumina run data.

Examples
eexample(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

### 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)
```

**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

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(savProject)

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

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

```r
savR(object)
```  
```r
## S4 method for signature 'character'
savR(object)
```  
```r
## S4 method for signature 'missing'
savR()
```  

Arguments

- `object`  
  String Path to Flowcell data

Examples

```r
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)
```

```r
## 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
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