

# Package ‘savR’

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**Type** Package

**Title** Parse and analyze Illumina SAV files

**Version** 1.34.0

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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

**git\_url** <https://git.bioconductor.org/packages/savR>

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

---

## 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)**

R. Brent Calder <brent.calder@einstein.yu.edu>

**References**

For information about Illumina SAV, please refer to  
[http://supportres.illumina.com/documents/documentation/software\\_documentation/sav/sequencinganalysisviewer\\_userguide\\_15020619c.pdf](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Generate a folder of images that approximates the format of the folder that was superceded by InterOp.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))
```

---

|                     |                                       |
|---------------------|---------------------------------------|
| <code>cycles</code> | <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)

`lanepersection`: 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 | <i>Get Flowcell folder location</i> |
|----------|-------------------------------------|

---

**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 | <i>PF Boxplot</i> |
|-----------|-------------------|

---

**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 | <i>Get number of PF clusters per lane</i> |
|------------|-------------------------------------------|

---

**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 <a href="#">savProject-class</a> object |
| cycle   | integer cycle number                      |
| base    | character for nucleotide                  |

---

|           |                                            |
|-----------|--------------------------------------------|
| plotQGT30 | <i>Plot Quality &gt; 30 for a flowcell</i> |
|-----------|--------------------------------------------|

---

### 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 | <i>Get reads</i> |
|-------|------------------|

---

**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 | <i>Structure for holding parsed InterOp headers and data</i> |
|---------------|--------------------------------------------------------------|

---

**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 | <i>Base class for formatters</i> |
|-----------------|----------------------------------|

---

**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 | <i>SAV project class</i> |
|------------------|--------------------------|

---

**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 | <i>Build a SAV project</i> |
|------|----------------------------|

---

**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 | <i>Tile Metrics formatter</i> |
|---------------------|-------------------------------|

---

**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 | <i>Get Tile Metrics</i> |
|-------------|-------------------------|

---

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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