

# 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

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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)**

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Generate a folder of images that approximates the format of the folder that was superceded by InterOp.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

*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**

```
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)  
 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)
```

**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 <a href="#">savProject-class</a> 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 preceding 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	<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

*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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