

# Package ‘IncucyteDRC’

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**Type** Package

**Title** Dose Response Curves from Incucyte Proliferation Assays

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**Description** Package to import data generated by the Incucyte Zoom from Essen Bio-sciences and use this to fit dose response curves using the drc package.

**URL** <https://github.com/chapmandu2/IncucyteDRC>

**BugReports** <https://github.com/chapmandu2/IncucyteDRC/issues>

**License** GPL-2

**LazyData** TRUE

**Imports** cowplot, dplyr, drc, DT, ggplot2, magrittr, shiny, tidyr, XML

**RoxygenNote** 5.0.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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## R topics documented:

IncucyteDRC-package . . . . .	2
calculateCutTimeForGrowthCurve . . . . .	3
calculateCutTimeForIDRCSet . . . . .	4
calculateDRCDData . . . . .	5
calculateEC50 . . . . .	6
exportDRCDDataToDataFrame . . . . .	6
exportDRCDDataToDotmatics . . . . .	7

exportDRCDDataToPRISM . . . . .	8
exportEC50Data . . . . .	9
fitDoseResponseCurve . . . . .	10
fitGrowthCurvesGrouped . . . . .	11
fitGrowthCurvesIndividual . . . . .	11
importIncucyteData . . . . .	12
importPlatemap . . . . .	13
importPlatemapXML . . . . .	14
makeIncucyteDRCSet . . . . .	14
plotDoseResponseCurve . . . . .	15
plotIncucyteDRCSet . . . . .	16
plotPlatemap . . . . .	17
populateIncucyteDRCSetMetadata . . . . .	17
print.IncucyteDRCPlateData . . . . .	18
print.IncucyteDRCSet . . . . .	18
print.IncucyteDRCSetList . . . . .	19
shinyVisApp . . . . .	20
shinyVisServer . . . . .	20
shinyVisUI . . . . .	21
splitIncucyteDRCPlateData . . . . .	21

## Index 23

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IncucyteDRC-package     *Dose Response Curves from Incucyte Proliferation Assays*

---

### Description

To open the vignette type `vignette("Overview")`

The IncucyteDRC package provides a workflow for users of the Incucyte Zoom live cell imaging system from Essen Biosciences who want to carry out a dose response analysis on their data. For example, you may have grown cells in a 96-well plate that have been treated with a range of concentrations of several different small molecule inhibitors. Although the Incucyte Zoom software allows you to conveniently visualise these data, exporting the data to a form that can then be readily analysed in PRISM is convoluted. The IncucyteDRC package contains functions to make this process easier, as well as a graphical user interface.

For full details, please read the accompanying paper for the package on F1000R: Chapman et al 2016

If you want to see the package in action before deciding whether or not you want to install it, there is a [YouTube video](#).

### Author(s)

Phil Chapman <phil.chapman@cruk.manchester.ac.uk>

### References

See F1000R article

---

```
calculateCutTimeForGrowthCurve  
    calculateCutTimeForGrowthCurve
```

---

## Description

For a given growth curve model, calculates the appropriate cut time for a specific number of doublings

## Usage

```
calculateCutTimeForGrowthCurve(gcm, baseline_time = 24, no_doublings = 4,  
    max_val = 80)
```

## Arguments

gcm	Growth curve model
baseline_time	The timepoint which forms the baseline for calculating number of doublings
no_doublings	The number of doublings required
max_val	The maximum allowable growth curve value

## Value

list object containing a single row data frame with the results and a plotted representation

## Examples

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')  
test_pm <- importPlatemapXML(pm_file)  
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')  
test_data <- importIncucyteData(data_file, metric='pc')  
  
test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')  
  
print(test_list)  
  
test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])  
plotIncucyteDRCSet(test_idrc_set, grouped=TRUE)  
test_idrc_set$fitted_models_grouped  
test_gcm <- test_idrc_set$fitted_models_grouped$gc_model[[1]]  
test_gcm  
calculateCutTimeForGrowthCurve(test_gcm, baseline_time=24, no_doublings=4, max_val=80)
```

---

`calculateCutTimeForIDRCSet`*calculateCutTimeForIDRCSet*

---

**Description**

Uses the control growth curves in an IncucyteDRCSet to calculate the appropriate cut time for a specific number of doublings

**Usage**

```
calculateCutTimeForIDRCSet(idrc_set, baseline_time = 24, no_doublings = 4,  
  max_val = 80)
```

**Arguments**

<code>idrc_set</code>	IncucyteDRCSet object
<code>baseline_time</code>	The timepoint which forms the baseline for calculating number of doublings
<code>no_doublings</code>	The number of doublings required
<code>max_val</code>	The maximum allowable growth curve value

**Value**

IncucyteDRCSet object

**Examples**

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')  
test_pm <- importPlatemapXML(pm_file)  
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')  
test_data <- importIncucyteData(data_file, metric='pc')  
  
test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')  
  
print(test_list)  
  
test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])  
plotIncucyteDRCSet(test_idrc_set, grouped=TRUE)  
test_idrc_set <- calculateCutTimeForIDRCSet(test_idrc_set)  
plotIncucyteDRCSet(test_idrc_set, grouped=TRUE)  
print(test_idrc_set$cut_plot)
```

---

calculateDRCDData	<i>calculateDRCDData</i>
-------------------	--------------------------

---

### Description

For a given cut time, calculate values from the growth curves in a IncucyteDRCSet object

### Usage

```
calculateDRCDData(idrc_set, cut_time = NULL)
```

### Arguments

<code>idrc_set</code>	IncucyteDRCSet object
<code>cut_time</code>	Desired cut time. If NULL will use the <code>cut_time</code> in the IncucyteDRCSet object (if set)

### Value

IncucyteDRCSet object

### Examples

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)

test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])
test_idrc_set <- fitGrowthCurvesIndividual(test_idrc_set)
plotIncucyteDRCSet(test_idrc_set, grouped=FALSE)
plotIncucyteDRCSet(test_idrc_set, grouped=TRUE)
test_idrc_set <- calculateDRCDData(test_idrc_set, cut_time=100)
print(test_idrc_set)
test_idrc_set$drc_data
plotIncucyteDRCSet(test_idrc_set)
```

---

calculateEC50	<i>calculateEC50</i>
---------------	----------------------

---

**Description**

Calculates the EC50s for the dose response curves in an IncucyteDRCSet object

**Usage**

```
calculateEC50(idrc_set)
```

**Arguments**

idrc\_set      IncucyteDRCSet object

**Value**

IncucyteDRCSet object

**Examples**

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)

test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])
test_idrc_set <- fitGrowthCurvesIndividual(test_idrc_set)
test_idrc_set <- calculateDRCDData(test_idrc_set, cut_time=100)
test_idrc_set <- fitDoseResponseCurve(test_idrc_set)
test_idrc_set <- calculateEC50(test_idrc_set)
exportEC50Data(test_idrc_set)
```

---

exportDRCDDataToDataFrame	<i>exportDRCDDataToDataFrame</i>
---------------------------	----------------------------------

---

**Description**

Exports data into a standard data frame format for an IncucyteDRCSet

**Usage**

```
exportDRCDDataToDataFrame(idrc_set, include_control = FALSE,
  add_metadata = FALSE)
```

**Arguments**

```
idrc_set      IncucyteDRCSets object
include_control Whether to include control sample as zero conc control
add_metadata  Whether or not to merge IncucyteDRCSets metadata into the output
```

**Value**

IncucyteDRCSets object

**Examples**

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)

test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])
test_idrc_set <- fitGrowthCurvesIndividual(test_idrc_set)
test_idrc_set <- calculateDRCData(test_idrc_set, cut_time=100)
exportDRCDDataToDataFrame(test_idrc_set)
exportDRCDDataToDataFrame(test_idrc_set, include_control=TRUE)
exportDRCDDataToDataFrame(test_idrc_set, include_control=TRUE, add_metadata=TRUE)
```

---

```
exportDRCDDataToDotmatics
```

```
exportDRCDDataToDotmatics
```

---

**Description**

Exports data in Dotmatics format for an IncucyteDRCSets or IncucyteDRCSetsList object that represents a full plate of data. The platemap must be provided as an IncucyteDRCPlatemap object and should correspond to the data contained in the IncucyteDRCSets or IncucyteDRCSetsList object.

**Usage**

```
exportDRCDDataToDotmatics(idrc_set_list, platemap)
```

**Arguments**

idrc\_set\_list    IncucyteDRCSetsList object  
 platemap        IncucyteDRCPatemap object from importPlatemap or importPlatemapXML

**Value**

list object with samplelist and data elements

**Examples**

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_drc <- splitIncucyteDRCPatemapData(test_pm, test_data, group_columns='growthcondition')
test_drc <- lapply(test_drc, fitGrowthCurvesIndividual)
test_drc <- lapply(test_drc, fitGrowthCurvesGrouped)
test_drc <- lapply(test_drc, calculateDRCDData, cut_time=100)
print(test_drc)
print(test_drc[[2]])
exportDRCDDataToDotmatics(test_drc, test_pm)
exportDRCDDataToDotmatics(test_drc[[2]], test_pm)
```

---

exportDRCDDataToPRISM    *exportDRCDDataToPRISM*

---

**Description**

Exports data in PRISM format for an IncucyteDRCSets

**Usage**

```
exportDRCDDataToPRISM(idrc_set, include_control = FALSE,
  add_metadata = FALSE)
```

**Arguments**

idrc\_set        IncucyteDRCSets object  
 include\_control  
               Whether to include control sample as zero conc control  
 add\_metadata    Whether or not to merge IncucyteDRCSets metadata into the output

**Value**

IncucyteDRCSets object



**Examples**

```

pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)

test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])
test_idrc_set <- fitGrowthCurvesIndividual(test_idrc_set)
test_idrc_set <- calculateDRCData(test_idrc_set, cut_time=100)
exportDRCDataToPRISM(test_idrc_set)
exportDRCDataToPRISM(test_idrc_set, include_control=TRUE)
exportDRCDataToPRISM(test_idrc_set, include_control=TRUE, add_metadata=TRUE)

```

---

exportEC50Data

*exportEC50Data*


---

**Description**

Exports EC50 data into a standard data frame format from the dose response fit for an Incucyte-DRCSet object

**Usage**

```
exportEC50Data(idrc_set, add_metadata = FALSE)
```

**Arguments**

idrc\_set            IncucyteDRCSet object  
add\_metadata        Whether or not to merge IncucyteDRCSet metadata into the output

**Value**

IncucyteDRCSet object

**Examples**

```

pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)

```

```

test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])
test_idrc_set <- fitGrowthCurvesIndividual(test_idrc_set)
test_idrc_set <- calculateDRCDData(test_idrc_set, cut_time=100)
test_idrc_set <- fitDoseResponseCurve(test_idrc_set)
test_idrc_set <- calculateEC50(test_idrc_set)
exportEC50Data(test_idrc_set)

```

---

fitDoseResponseCurve *fitDoseResponseCurve*

---

### Description

Fits the dose response curve using drc for an IncucyteDRCSet object

### Usage

```
fitDoseResponseCurve(idrc_set, include_control = FALSE)
```

### Arguments

idrc_set	IncucyteDRCSet object
include_control	Whether to include control sample as zero conc control

### Value

IncucyteDRCSet object

### Examples

```

pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)

test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])
test_idrc_set <- fitGrowthCurvesIndividual(test_idrc_set)
test_idrc_set <- calculateDRCDData(test_idrc_set, cut_time=100)
test_idrc_set <- fitDoseResponseCurve(test_idrc_set)
test_idrc_set <- calculateEC50(test_idrc_set)
exportEC50Data(test_idrc_set)

```

---

```
fitGrowthCurvesGrouped  
    fitGrowthCurvesGrouped
```

---

**Description**

Function to fit loess function to the growth curve data in an IncucyteDRCSet object

**Usage**

```
fitGrowthCurvesGrouped(idrc_set)
```

**Arguments**

idrc\_set          IncucyteDRCSet object

**Value**

IncucyteDRCSet object

**Examples**

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')  
test_pm <- importPlatemapXML(pm_file)  
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')  
test_data <- importIncucyteData(data_file, metric='pc')  
  
test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')  
  
print(test_list)  
  
test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])
```

---

```
fitGrowthCurvesIndividual  
    fitGrowthCurvesIndividual
```

---

**Description**

Function to fit splines to the growth curve data in an IncucyteDRCSet object

**Usage**

```
fitGrowthCurvesIndividual(idrc_set)
```

**Arguments**

`idrc_set`            IncucyteDRCSet object

**Value**

IncucyteDRCSet object

**Examples**

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)

test_idrc_set <- fitGrowthCurvesIndividual(test_list[[2]])
```

---

`importIncucyteData`      *importIncucyteData*

---

**Description**

Imports data exported from Incucyte Zoom software- NEED MORE DOCUMENTATION HERE ABOUT HOW TO DO EXPORT!!

**Usage**

```
importIncucyteData(filepath, metric = "pc", plateid = basename(filepath))
```

**Arguments**

`filepath`            Path to a data file generated by the Incucyte Zoom software

`metric`             Metric must be either `pc` (percent confluence) or `ca` (confluence area). Default is `pc`.

`plateid`            An identifier for the plate. If set to `NULL` then filename used as default

**Value**

IncucyteDRCPlateData object

## Examples

```
#dataset 1
data_file1 <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data1 <- importIncucyteData(data_file1, metric='pc')
test_data1
head(test_data1$data)

#dataset 2
data_file2 <- system.file(file='extdata/example_data2.txt', package='IncucyteDRC')
test_data2 <- importIncucyteData(data_file2, metric='pc')
```

---

importPlatemap	<i>importPlatemap</i>
----------------	-----------------------

---

## Description

Imports a platemap configuration from a tab delimited file or dataframe.

## Usage

```
importPlatemap(input, control_cpd = "DMSO")
```

## Arguments

input	Either a path to a text file or a data frame
control_cpd	Specify the compound to use as baseline. Defaults to DMSO

## Value

IncucyteDRCPlateMap object

## Examples

```
pm_file <- system.file(file='extdata/example_platemap.txt', package='IncucyteDRC')
test_pm <- importPlatemap(pm_file)
head(test_pm)
test_pm_df <- importPlatemap(as.data.frame(test_pm))
head(test_pm_df)
```

importPlatemapXML      *importPlatemapXML*

---

### Description

Imports .Platemap XML files from Incucyte Zoom software and extracts information in the Compound, GrowthCondition and CellType fields.

### Usage

```
importPlatemapXML(filepath, control_cpd = "DMSO")
```

### Arguments

filepath            Path to a .Platemap XML file generated by the Incucyte Zoom software  
control\_cpd        Specify the compound to use as baseline. Defaults to DMSO

### Value

data frame

### Examples

```
#example data 1  
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')  
test_pm <- importPlatemapXML(pm_file)  
head(test_pm)  
  
#example data 2  
pm_file2 <- system.file(file='extdata/example2.PlateMap', package='IncucyteDRC')  
test_pm2 <- importPlatemapXML(pm_file2)  
head(test_pm2)
```

---

makeIncucyteDRCSet      *makeIncucyteDRCSet*

---

### Description

Function to construct an IncucyteDRCSet object. Contains data for just those wells that are from the same cell line background - ie cell line, passage number, cell number etc are all the same. Give that the same cell line background is used, the control wells are common to all wells regardless of different compounds or concentrations of compound.

### Usage

```
makeIncucyteDRCSet(platemap, platedata, cut_time = NULL, metadata = NULL,  
                  pm_warn = TRUE)
```

**Arguments**

platemap	Platemap dataframe containing information for just those wells required
platedata	IncucyteDRCPlateData object that will be filtered according to the wells present in the platemap
cut_time	The time at which to extract the data for the dose response curve. Default is NULL.
metadata	A single row data frame containing any information specific to this IncucyteDRCSet object.
pm_warn	Boolean to control platemap check warnings. Default is TRUE.

**Value**

IncucyteDRCSet object

**Examples**

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_pm_filtered <- dplyr::filter(test_pm,
                                samptype %in% c('C', 'S') & growthcondition == '8 x 10e4/mL')
test_set <- makeIncucyteDRCSet(test_pm_filtered, test_data)

print(test_set)
```

---

plotDoseResponseCurve *plotDoseResponseCurve*

---

**Description**

Plots the dose response curve for a given sample id from an IncucyteDRCSet object

**Usage**

```
plotDoseResponseCurve(idrc_set, sampleid, native = FALSE)
```

**Arguments**

idrc_set	IncucyteDRCSet object
sampleid	The sample id to plot
native	deprecated

**Value**

a ggplot2 object (if native is FALSE) or NULL but draws to open graphics object (if native is TRUE)

**Examples**

```

pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)

test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])
test_idrc_set <- fitGrowthCurvesIndividual(test_idrc_set)
test_idrc_set <- calculateDRCData(test_idrc_set, cut_time=100)
test_idrc_set <- fitDoseResponseCurve(test_idrc_set)
test_idrc_set <- calculateEC50(test_idrc_set)
plotDoseResponseCurve(test_idrc_set, 'PDD00017273', native=FALSE)

```

---

`plotIncucyteDRCSet`      *plotIncucyteDRCSet*

---

**Description**

Plot the growth curve data from an `IncucyteDRCSet` object

**Usage**

```
plotIncucyteDRCSet(idrc_set, grouped = FALSE)
```

**Arguments**

<code>idrc_set</code>	IncucyteDRCSet object
<code>grouped</code>	Boolean - whether the curves should be grouped or not.

**Value**

ggplot object

**Examples**

```

pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)

test_idrc_set <- fitGrowthCurvesGrouped(test_list[[2]])

```



```
test_idrc_set <- fitGrowthCurvesIndividual(test_idrc_set)
plotIncucyteDRCSet(test_idrc_set, grouped=FALSE)
plotIncucyteDRCSet(test_idrc_set, grouped=TRUE)
```

---

plotPlatemap	<i>plotPlatemap</i>
--------------	---------------------

---

### Description

Visualisation of an Incucyte platemap

### Usage

```
plotPlatemap(pm)
```

### Arguments

`pm` Platemap data frame generated by either `importPlatemap` or `importPlatemapXML` functions.

### Value

ggplot object

### Examples

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
plotPlatemap(test_pm)

library(magrittr)
pm_file2 <- system.file(file='extdata/example2.PlateMap', package='IncucyteDRC')
importPlatemapXML(pm_file2) %>% plotPlatemap()
```

---

populateIncucyteDRCSetMetadata	<i>populateIncucyteDRCSetMetadata</i>
--------------------------------	---------------------------------------

---

### Description

Function to populate the metadata slot of an `IncucyteDRCSet` object. Not exported, used as part of the `splitIncucyteDRCPlateData` function.

### Usage

```
populateIncucyteDRCSetMetadata(idrc_set, group_columns)
```

**Arguments**

`idrc_set` IncucyteDRCSet object  
`group_columns` Vector of columns that are present in the data frame to generate the groups.

**Value**

IncucyteDRCSet object

---

`print.IncucyteDRCPlateData`  
*print.IncucyteDRCPlateData*

---

**Description**

Prints information on an IncucyteDRCPlateData object

**Usage**

```
## S3 method for class 'IncucyteDRCPlateData'
print(x, ...)
```

**Arguments**

`x` IncucyteDRCPlateData object  
`...` Additional arguments

**Examples**

```
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')
print(test_data)
```

---

`print.IncucyteDRCSet` *print.IncucyteDRCSet*

---

**Description**

Prints information on an IncucyteDRCSet object

**Usage**

```
## S3 method for class 'IncucyteDRCSet'
print(x, ...)
```

### Arguments

x	IncucyteDRCSet object
...	Additional arguments

### Examples

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')
test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')
class(test_list)
class(test_list[[2]])
print(test_list[[2]])
```

---

```
print.IncucyteDRCSetList
      print.IncucyteDRCSetList
```

---

### Description

Prints information on an IncucyteDRCSetList object

### Usage

```
## S3 method for class 'IncucyteDRCSetList'
print(x, ...)
```

### Arguments

x	IncucyteDRCSet object
...	Additional arguments

### Examples

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')
test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')
class(test_list)
print(test_list)
```

---

shinyVisApp	<i>Shiny Visualisation App</i>
-------------	--------------------------------

---

**Description**

Provides an interactive web app for the running the IncucyteDRC workflow

**Usage**

```
shinyVisApp()
```

**Value**

Launches an interactive Shiny application

---

shinyVisServer	<i>Shiny Visualisation Server</i>
----------------	-----------------------------------

---

**Description**

Creates a shiny server for the interactive web app for the running the IncucyteDRC workflow

**Usage**

```
shinyVisServer(input, output)
```

**Arguments**

input	Shiny input list
output	Shiny output list

**Value**

A shiny server

---

`shinyVisUI`*Shiny Visualisation UI*

---

**Description**

Creates a shiny UI for the interactive web app for the running the IncucyteDRC workflow

**Usage**

```
shinyVisUI()
```

**Value**

A shiny UI

---

`splitIncucyteDRCPlateData`*splitIncucyteDRCPlateData*

---

**Description**

Function to construct a list of IncucyteDRCSet objects from a IncucyteDRCPlateData object.

**Usage**

```
splitIncucyteDRCPlateData(platemap, platedata, group_columns, cut_time = NULL)
```

**Arguments**

<code>platemap</code>	Platemap dataframe of the form generated by <code>importPlatemapXML</code>
<code>platedata</code>	IncucyteDRCPlateData object to be split
<code>group_columns</code>	Vector of columns that are present in the data frame to generate the groups.
<code>cut_time</code>	The time at which to extract the data for the dose response curve. Default is NULL.

**Value**

list of IncucyteDRCSet objects

**Examples**

```
pm_file <- system.file(file='extdata/example.PlateMap', package='IncucyteDRC')
test_pm <- importPlatemapXML(pm_file)
data_file <- system.file(file='extdata/example_data.txt', package='IncucyteDRC')
test_data <- importIncucyteData(data_file, metric='pc')

test_list <- splitIncucyteDRCPlateData(test_pm, test_data, group_columns='growthcondition')

print(test_list)
```

# Index

[calculateCutTimeForGrowthCurve](#), 3  
[calculateCutTimeForIDRCSet](#), 4  
[calculateDRCData](#), 5  
[calculateEC50](#), 6

[exportDRCDataToDataFrame](#), 6  
[exportDRCDataToDotmatics](#), 7  
[exportDRCDataToPRISM](#), 8  
[exportEC50Data](#), 9

[fitDoseResponseCurve](#), 10  
[fitGrowthCurvesGrouped](#), 11  
[fitGrowthCurvesIndividual](#), 11

[importIncucyteData](#), 12  
[importPlatemap](#), 13  
[importPlatemapXML](#), 14  
[IncucyteDRC \(IncucyteDRC-package\)](#), 2  
[IncucyteDRC-package](#), 2

[makeIncucyteDRCSet](#), 14

[plotDoseResponseCurve](#), 15  
[plotIncucyteDRCSet](#), 16  
[plotPlatemap](#), 17  
[populateIncucyteDRCSetMetadata](#), 17  
[print.IncucyteDRCPlateData](#), 18  
[print.IncucyteDRCSet](#), 18  
[print.IncucyteDRCSetList](#), 19

[shinyVisApp](#), 20  
[shinyVisServer](#), 20  
[shinyVisUI](#), 21  
[splitIncucyteDRCPlateData](#), 21