

# Package ‘IFC’

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**Title** Tools for Imaging Flow Cytometry

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**BugReports** <https://github.com/gitdemont/IFC/issues>

**Description** Contains several tools to treat imaging flow cytometry data from 'ImageStream®' and 'FlowSight®' cytometers ('Amnis®', part of 'Luminex®'). Provides an easy and simple way to read and write .fcs, .rif, .cif and .daf files. Information such as masks, features, regions and populations set within these files can be retrieved for each single cell. In addition, raw data such as images stored can also be accessed. Users, may hopefully increase their productivity thanks to dedicated functions to extract, visualize, manipulate and export 'IFC' data. Toy data example can be installed through the 'IFCdata' package of approximately 32 MB, which is available in a 'drat' repository <<https://gitdemont.github.io/IFCdata/>>. See file 'COPYRIGHTS' and file 'AUTHORS' for a list of copyright holders and authors.

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**Depends** R (>= 3.4.0)

**Imports** Rcpp (>= 0.10.0), xml2, png, tiff, jpeg, utils, grid,  
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visNetwork

**Suggests** IFCdata, shiny, reticulate

**LinkingTo** Rcpp

**Additional\_repositories** <https://gitdemont.github.io/IFCdata/>

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IFC-package

*Tools for Imaging Flow Cytometry*

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## Description

Contains several tools to treat Imaging Flow Cytometry data from ImageStream(R) and FlowSight(R) cytometers (Amnis(R), part of Luminex(R)). Provides an easy and simple way to read or write .fcs, .rif, .cif and .daf files. Information such as masks, features, regions and populations set within these files can be retrieved for each single cell. In addition, raw data such as images stored can also be accessed. Users, may hopefully increase their productivity thanks to dedicated functions to extract, visualize, manipulate and export IFC data.

## Details

The IFC package provides several categories of functions:

- to read / write / export / visualize:

[readIFC](#), [writeIFC](#), [ExtractFromDAF](#), [ExportToDAF](#), [data\\_to\\_DAF](#), [ExtractFromXIF](#), [ExportToXIF](#), [ExtractFromFCS](#), [ExportToFCS](#), [ExportToBATCH](#), [BatchReport](#), [ExportToReport](#), [ExportToGallery](#), [ExportToNumpy](#), [DisplayGallery](#), [ExtractImages\\_toBase64](#), [ExtractImages\\_toFile](#), [ExtractImages\\_toMatrix](#), [ExtractMasks\\_toMatrix](#), [objectExtract](#), [popsNetwork](#), [plotGraph](#), [paletteIFC](#), [autoplot](#)

- to transform features values

[smoothLinLog](#), [inv\\_smoothLinLog](#)

- to deeply extract information from files:

[getInfo](#), [getOffsets](#), [getIFD](#), [getFullTag](#), [getAborted](#)

- dedicated to populations:

[popsCopy](#), [popsGetObjectsIds](#), [popsNetwork](#), [popsRename](#)

- for adding / removing features, regions, populations:  
[data\\_add\\_features](#), [data\\_add\\_regions](#), [data\\_add\\_pops](#), [data\\_rm\\_features](#), [data\\_rm\\_regions](#),  
[data\\_rm\\_pops](#)
- to allow several coercion:  
[buildBatch](#), [buildFeature](#), [buildGraph](#), [buildPopulation](#), [buildRegion](#)

### Author(s)

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autoplot

*Automatic Parameters Detection for IFC Graphs*

---

### Description

Function intended to generate IFC graphs with minimal inputs from users.  
 It is essentially based on automatic detection of graphical parameters thanks to 'shown\_pops' argument.

### Usage

```
autoplot(
  obj,
  shown_pops = NULL,
  subset = NULL,
  x = NULL,
  x_trans = NULL,
  y = NULL,
  y_trans = NULL,
  type = NULL,
  smoothingfactor = NULL,
  normalize = NULL,
  bin,
  viewport = "ideas",
  precision = c("light", "full")[1],
  color_mode = c("white", "black")[1],
  draw = TRUE,
  ...
)
```

### Arguments

obj	an 'IFC_data' object extracted by <code>ExtractFromDAF(extract_features = TRUE)</code> or <code>ExtractFromXIF(extract_features = TRUE)</code> .
shown_pops	one or several populations present in 'obj'. Default is NULL. If provided, <code>autoplot</code> will try to display these populations. See details when not provided.

`autoplot` will try to determine x and y and their transformations based on 'shown\_pops' parameter. If all populations provided in 'shown\_pops' are siblings, region(s) from which 'shown\_pops' were defined will be displayed.

In case 'shown\_pops' are not siblings, they will be treated as populations and a graph will be generating with an overlay of these populations. Order of this overlay is given by order of 'shown\_pops'.

Finally, changing any of the following arguments (x, x\_trans, y, y\_trans, type) to something else than the one detected from 'shown\_pops' will prevent from displaying region(s) and 'shown\_pops' populations will be displayed as overlay. However, please consider that if original type is 'histogram' changing x\_trans transformation will have no impact on this.

subset	a population present in 'obj'. Default is NULL. Background population that will be used to generate graph. This argument will not be used when graph is an histogram. If this argument is filled with a different population than what can be determined thanks to 'shown_pops', Then 'shown_pops' will be treated as overlay. However, 'shown_pops' argument can still be used to determine x, y axis and their transformation
x	feature for x-axis. Default is NULL. When empty, <code>autoplot</code> will try to determine it automatically from 'shown_pops' argument. If provided, x feature has to be a name from 'obj' features. Note that providing x feature : - takes precedence on automatic x-axis detection. - will reset x-axis transformation to "P" except if 'x_trans' is filled.
x_trans	parameter for x-axis transformation. Default is NULL. If not provided, transformation will be determined thanks to 'shown_pops'. It takes precedence when provided and if provided it has to be either "P" or coercible to a positive numeric. "P" will leave x-axis as is but a positive numeric will be passed has hyper argument of <code>smoothLinLog</code> to transform x-axis.
y	feature for y-axis. Default is NULL. When empty, <code>autoplot</code> will try to determine it automatically from 'shown_pops' argument. If provided, y feature has to be a name from obj features. Note that providing y feature - takes precedence on automatic y-axis detection. - will reset y-axis transformation to "P" except if 'y_trans' is filled.
y_trans	parameter for y-axis transformation. Default is NULL. If not provided, transformation will be determined thanks to 'shown_pops'. It takes precedence when provided and and if provided it has to be either "P" or coercible to a positive numeric. "P" will leave y-axis as is but a positive numeric will be passed has hyper argument of <code>smoothLinLog</code> to transform y-axis. Note that it is irrelevant for "histogram".
type	type of plot. Default is NULL to allow <code>autoplot</code> to determine 'type' automatically. If provided it has to be either "histogram", "scatter", "density". Note that when "histogram" is choosen, 'subset' parameter will not be used. Note that "density" will be possible only when 'subset' will be automatically determined or filled with only one population. Note that when <code>autoplot</code> has determined, thanks to 'shown_pops' that original plot is an "histogram", "Object Number" will be used as y-axis by default when 'type' is forced to "scatter" or "density".

smoothingfactor	when type of graph is "histogram", whether to smooth it or not. Default is NULL. Should be an integer [0:20] Note that 0 means no smoothing and other values will produce smoothing
normalize	when type of graph is "histogram", whether to normalize it or not. Default is NULL. Should be a logical.
bin	number of bins when graph's type is "histogram" / number of equally spaced grid points for density. Default is missing to allow <code>autoplot</code> to determine it by itself.
viewport	Either "ideas", "data" or "max" defining limits used for the graph. Default is "ideas". -"ideas" will use same limits as the one defined in ideas. -"data" will use data to define limits. -"max" will use data and regions drawn to define limits.
precision	when graphs is a 2D scatter with population overlay, this argument controls amount of information displayed. Default is "light". -"light", the default, will only display points of same coordinates that are among the other layers. -"full" will display all the layers.
color_mode	Whether to extract colors from obj in white or black mode. Default is "white".
draw	whether to draw plot. Default is TRUE.
...	Other arguments to be passed.

### Details

when 'shown\_pops' are not provided, `autoplot` can't determine anything.

So, if not provided default values will be used:

-'subset' = "All"

-'x' = "Object Number"

-'x\_trans' = "P"

-'y' = "Object Number"

-'y\_trans' = "P"

-'type' = "histogram"

### Value

an **lattice** trellis object

### Description

Batch creates graphical an statistical report.

**Usage**

```
BatchReport(
  fileName,
  obj,
  selection,
  write_to,
  overwrite = FALSE,
  gating,
  main,
  byrow = FALSE,
  times = 5,
  color_mode = c("white", "black")[1],
  add_key = "panel",
  precision = c("light", "full")[1],
  trunc_labels = 38,
  trans = "asinh",
  bin,
  viewport = "ideas",
  backend = "lattice",
  display_progress = TRUE,
  ...
)
```

**Arguments**

fileName, obj	either one or the other. Path to file(s) to read from for 'fileName' or list of 'IFC_data' objects for obj.
selection	indices of desired graphs. It can be provided as an integer vector or as a matrix. In such case, the layout of the matrix will reflect the layout of the extracted graphs for each 'fileName' or 'obj'. NA value will result in an empty place. When missing, it will be determined by the whole layout of 1st 'fileName' or 'obj' with 'gating' applied when provided
write_to	pattern used to export file(s). Placeholders, like c("%d/%s_fromR.pdf", "%d/%s_fromR.csv"), will be substituted: -%d: with full path directory -%p: with first parent directory -%e: with extension (without leading .) -%s: with shortname (i.e. basename without extension). Exported file(s) extension(s) will be deduced from this pattern using either 1st 'fileName' or 'obj'. Note that has to be a .pdf and/or .csv.
overwrite	whether to overwrite file or not. Default is FALSE. Note that if TRUE, it will overwrite file. In addition a warning message will be sent.
gating	an 'IFC_gating' object as extracted by readGatingStrategy(). Default is missing. If not missing, each 'IFC_data' provided in 'obj' or read from 'fileName' will be passed to applyGatingStrategy() before creating the report.
main	the main title of the document. Default is missing.
byrow	whether to add selected graphs for each file by row or not. Default is FALSE.

times	number of files to add before starting a new row or column (depending on 'by-row').
color_mode	Whether to extract colors in white or black mode. Default is "white".
add_key	whether to draw a "global" key under title or in the first "panel" or "both". Default is "panel". Accepted values are either: FALSE, "panel", "global", "both" or c("panel", "global"). Note that it only applies when display is seen as overlaying populations.
precision	when graphs is a 2D scatter with population overlay, this argument controls amount of information displayed. Default is "light". -"light", the default, will only display points of same coordinates that are among the other layers. -"full" will display all the layers.
trunc_labels	maximum number of characters to display for labels. Default is 38.
trans	name of the transformation function for density graphs. If missing the default, the BasePop[[1]]\$densitytrans, if any, will be retrieved, otherwise "asinh" will be used.
bin	default number of bin used for histogram. Default is missing.
viewport	Either "ideas", "data" or "max" defining limits used for the graph. Default is "ideas". -"ideas" will use same limits as the one defined in ideas. -"data" will use data to define limits. -"max" will use data and regions drawn to define limits.
backend	backend used for drawing. Allowed are "lattice", "base", "raster". Default is "lattice". -"lattice" is the original one used in <b>IFC</b> using <b>lattice</b> , -"base" will produce the plot using <b>base</b> , -"raster" uses "base" for plotting but 2D graphs points will be produced as <a href="#">rasterImage</a> . This has the main advantage of being super fast allowing for plotting a huge amount of points while generating smaller objects (in bytes). However, plot quality is impacted with "raster" method and resizing can lead to unpleasant looking.
display_progress	whether to display a progress bar. Default is TRUE.
...	other parameters to be passed.

### Value

It invisibly returns full path of exported .pdf and/or .csv file(s).

---

 buildBatch

*Batch Builder*


---

## Description

Prepares XML node for [ExportToBATCH](#).

## Usage

```
buildBatch(
  files,
  compensation,
  analysis,
  default_batch_dir,
  config_file,
  name = "Batch1",
  use_acquisition = FALSE,
  suffix = "",
  allow_channels_dissimilarity = FALSE,
  overwrite = TRUE,
  segment_rif = "None",
  options
)
```

## Arguments

files	path of files to batch.
compensation	path to compensation file.
analysis	path to analysis file.
default_batch_dir	<p>directory where batches are stored.</p> <p>It can be found in IDEAS(R) software, under Options -&gt; Application Defaults -&gt; Directories -&gt; Default Batch Report Files Directory.</p> <p>If missing, the default, it will be deduced from IDEAS(R) config file, However, if it can't be deduced then tempdir(check = TRUE) from <b>base</b> will be used.</p> <p>This argument takes precedence over 'config_file' and filling 'default_batch_dir' prevents the use of 'config_file' argument.</p>
config_file	<p>path to IDEAS(R) config file.</p> <p>It may depends on IDEAS(R) software installation but one may use "C:/Users/%USER%/AppData/Roaming/Corporation/userconfig.xml".</p>
name	name of batch. Default is "Batch1".
use_acquisition	whether to use acquisition as analysis template. Default is FALSE.
suffix	suffix to add to files when batched. Default is "".

allow_channels_dissimilarity	whether to allow building batch when all files were not acquired with same channels. Default is FALSE.
overwrite	whether to overwrite files or not. Default is TRUE.
segment_rif	size of file segmentation. Default is "None", for no segmentation. Allowed are "None", "100", "1K", "5K", "10K", "50K", "100K".
options	A list of arguments to be passed. If missing, the default, options will be set to: -"Brightfield compensation"=TRUE, -"EDF deconvolution"=TRUE, -"Camera background"=TRUE, -"Spatial alignment"=TRUE. Allowed are TRUE or FALSE for all, excepted for 'Spatial alignment' which can also be path to .rif file.

**Value**

a list containing batch information:  
-xml, the xml object to be written,  
-batch\_dir, the directory where xml file is desired to be saved according to 'default\_batch\_dir' and 'config\_file'.

---

buildFeature	<i>IFC Feature Coercion</i>
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---

**Description**

Helper to build a list to allow feature export.

**Usage**

```
buildFeature(  
  name,  
  type = c("single", "combined", "computed")[1],  
  def = "Camera Line Number",  
  val = NULL,  
  ...  
)
```

**Arguments**

name	feature's name. If missing, it will be determined thanks to def.
type	feature's type. Default is "single". Allowed are "single", "combined", "computed".
def	definition of the feature. Default is "Camera Line Number".

val a coercible to numeric vector of feature values. Default is NULL.  
 Note that although not mandatory for `buildFeature` it has to be provided to allow feature export in `ExportToDAF` and `data_add_features`.

... Other arguments to be passed.

**Value**

a list containing all feature information.

---

buildGraph	<i>IFC Graph Coercion</i>
------------	---------------------------

---

**Description**

Helper to build a list to allow graph export.

**Usage**

```
buildGraph(
  type = c("histogram", "scatter", "density")[3],
  xlocation = 0,
  ylocation = 0,
  f1 = "Object Number",
  f2 = "Object Number",
  scaletype = 1,
  xmin = -1,
  xmax = 1,
  ymin = 0,
  ymax = 1,
  title = paste0(unlist(lapply(BasePop, FUN = function(x) x$name)), collapse = ", "),
  xlabel = f1,
  ylabel = f2,
  axislabelsfontsize = 10,
  axistickmarklabelsfontsize = 10,
  graphtitlefontsize = 12,
  regionlabelsfontsize = 10,
  bincount = 0,
  freq = c("T", "F")[1],
  histogramsmoothingfactor = 0,
  xlogrange = "P",
  ylogrange = "P",
  maxpoints = +Inf,
  stats = c("true", "false")[2],
  xsize = c(320, 480, 640)[1],
  ysize = xsize + ifelse(stats == "true", splitterdistance, 0),
  splitterdistance = 120,
  xstats = "Count|%Gated|Mean",
```

```

    ystats = xstats,
    order,
    xstatsorder,
    Legend,
    BasePop = list(list()),
    GraphRegion = list(list()),
    ShownPop = list(list()),
    ...
)

```

### Arguments

type	Graph's type. Either "histogram", "scatter" or "density". Default is "density".
xlocation	Integer. Graph's x location. Default is 0.
ylocation	Integer. Graph's x location. Default is 0.
f1	Character. Graph x axis parameter. Default is "Object Number".
f2	Character. Graph y axis parameter. Default is "Object Number". Only used when 'type' is not "histogram".
scaletype	Integer. Graph scale. Either 0 (auto), 1 (manual). Default is 1.
xmin	Double. Graph's xmin. Default -1.
xmax	Double. Graph's xmax. Default 1.
ymin	Double. Graph's xmin. Default 0.
ymax	Double. Graph's xmax. Default 1.
title	Character. Graph title label. Default will use names of BasePop collapse with ', '.
xlabel	Character. Graph x axis label.
ylabel	Character. Graph y axis label.
axislabelsfonsize	Integer. Axis label font size. Default is 10. Allowed are: 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 26, 28. Checked but not yet implemented.
axistickmarklabelsfonsize	Integer. Axis tick font size. Default is 10. Allowed are: 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 26, 28. Checked but not yet implemented.
graphtitlefonsize	Integer. Axis title font size. Default is 12. Allowed are: 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 26, 28. Checked but not yet implemented.
regionlabelsfonsize	Integer. Axis region font size. Default is 10. Allowed are: 8, 9, 10, 11, 12, 14, 16, 18, 20, 22, 24, 26, 28. Checked but not yet implemented.

bincount	Integer. Histogram bin count. Default is 0. Allowed are: 0, 8, 16, 32, 64, 128, 256, 512, 1024.
freq	Character. Histogram with frequency normalization of not. Default is "T", allowed are "T" or "F".
histogramsmoothingfactor	Integer. Histogram smoothing factor. Allowed are [0-20]. Only partly implemented, default is 0 for no smoothing other values will produce same smoothing.
xlogrange	determines transformation instruction for x-axis. Default is "P" for no transformation.
ylogrange	determines transformation instruction for y-axis. Default is "P" for no transformation.
maxpoints	determines the maximum number of points to display. Default is +Inf to display all points. If provided, values from ]0,1] will be used as a proportion of the total number of points to show. While values values superior to 1 will be interpreted as the maximal number of points to show. It only applies to 2D graphs. When 'type' is "histogram", +Inf will be used whatever the value provided as input.
stats	Character. Either "true" or "false" to display stats. Default is "false".
xsize	Integer. Graph's x size. Default is 320 for small. Regular are: 320 (small), 480 (medium), 640 (big). Checked but not yet implemented.
ysize	Integer. Graph's y size. Default is 'ysize' + 'splitterdistance' when 'stats' is set to "true". Checked but not yet implemented.
splitterdistance	Integer. Default is 120. Checked but not yet implemented.
xstats	Character. x stats to be computed. Default is 'Count %Gated Mean'. It has to be a filled with the concatenation of 'Count', '%Total', '%Gated', '%Plotted', 'Objects/mL', 'Mean', 'Median', 'Std. Dev.', 'MAD', 'CV', 'Minimum', 'Maximum', 'Geo. Mean', 'Mode', 'Variance' and/or 'NaN', collapse with ' '. Checked but not yet implemented.
ystats	Character. y stats to be computed. Should be identical to 'xstats'. Default is xstats. Checked but not yet implemented.
order	Character. Order to display populations. When 'type' is "density" it will be BasePop[[1]]\$name. When 'type' is "histogram" or "density" 'ShownPop' are not allowed Otherwise, it will use each of 'GraphRegion', 'BasePop' and 'ShownPop' names, collapse with ' '. Checked but not yet implemented.
xstatsorder	Character. Order of stat rows. It will use each of 'GraphRegion' names & each of 'BasePop' names, reverted and collapse with ' '. Checked but not yet implemented.
Legend	Default is list(list(onoff='false',x='0',y='0',width='96',height='128')). Not yet implemented.
BasePop	Default is list(list()). See details.
GraphRegion	Default is list(list()). Only allowed member are sub-list(s) with only one character component named 'name'.

ShownPop	Default is list(list()). Only allowed member are sub-list(s) with only one character component named 'name'.
...	Other arguments to be passed.

### Details

Many parameters are not used or are only partly implemented, but most are checked in order to be compatible for further export.

For 'BasePop', if left as is "All" will be used as default.

This parameter will be built / checked according to 'type' argument.

'BasePop' has to be a list of list(s) and each sub-list should can contain several elements, but only "name" is mandatory.

The sublist members are:

- "name", "linestyle", "fill",

and only when 'type' is "density"

- "densitybincount", "densitymin", "densitymax",

- "densitycolors", "densitycolorslightmode", "densitycolorsdarkmode",

- "densitylevel", "densitytrans".

Each sub-list will be created automatically with the following default values (except if explicitly provided):

-linestyle="Solid",

-fill="true",

-densitybincount="128",densitymin="0",densitymax="0",

-densitycolors="-167769611-134478861-2561-232961-655361",

-densitycolorslightmode="-167769611-134478861-2561-232961-655361",

-densitycolorsdarkmode="-167769611-134478861-2561-232961-655361",

-densitylevel="",

\*when provided it has to be in a format of "fill[true,false]||lines[true,false]||nlevels[integer>1]||lowest[numeric[0-1]]" \*describing how the levelplot should be drawn.

\*Besides, 'densitrans' will not be used. -densitytrans="asinh"

\*it can take a function to be applied to the 2D local densities

\*or a name of a feature within 'IFC\_data' object to draw a gradient against this feature

Note that when 'type' is "density", 'BasePop' should be of length one.

and fill will be overwritten to "true".

### Value

a list containing all graph information.

---

buildPopulation

*IFC Population Coercion*

---

### Description

Helper to build a list to allow population export.

**Usage**

```

buildPopulation(
  name,
  type,
  base = "All",
  color,
  lightModeColor,
  style,
  region,
  fx,
  fy,
  definition,
  obj,
  ...
)

```

**Arguments**

name	name of the population.
type	type of population. Either "B", "C", "G" or "T" for Base, Combined, Graphical or Tagged, respectively. If missing, the default, 'type' will be deduced from other parameters. If 'name' is "All" type will be "B". Otherwise, if 'fx' is given type will be "G". Otherwise, "T", if 'definition' is missing but not 'obj' or "C" if 'definition' is not missing.
base	which population is based on. It will be base="All", for 'type' "T" and "C" and base="", for 'type' "B". It is only needed when type = "G".
color	color of the population. See <a href="#">paletteIFC</a> for allowed colors. If not provided, it will be sampled.
lightModeColor	lightModeColor of the population. See <a href="#">paletteIFC</a> for allowed colors. If not provided, it will be sampled.
style	style of the population. Either 20, 4, 3, 1, 5, 0, 2, 18, 15, 17, respectively for: "Simple Dot", "Cross", "Plus", "Empty Circle", "Empty Diamond", "Empty Square", "Empty Triangle", "Solid Diamond", "Solid Square", "Solid Triangle".
region	Only if type="G". Name of the region defining the population.
fx	Only needed if type="G". Name of the x-feature defining the population.
fy	Only needed if type="G" and only if region is defined in 2D. Name of the y-feature defining the population.
definition	Only needed if type="C". Parameters defining the population.
obj	Only needed if type="T". Either a: -Logical vector of same length as "All" population indicating if a cell belongs to the population or not. -Integer vector of indices of cells that belongs to the population. Note that first object is 0.
...	Other arguments to be passed.

**Value**

a list containing all population information.

---

buildRegion	<i>IFC Region Coercion</i>
-------------	----------------------------

---

**Description**

Helper to build a list to allow region export.

**Usage**

```
buildRegion(
  type,
  label,
  cx,
  cy,
  color,
  lightcolor,
  ismarker = "false",
  doesnotoverride = "false",
  xlogrange,
  ylogrange,
  x,
  y,
  ...
)
```

**Arguments**

type	Region's type. Either "line", "rect", "poly" or "oval".
label	label of the region.
cx	x label's position. If not provided x center will be used.
cy	y label's position. If not provided y center will be used.
color	color of the region. See <a href="#">paletteIFC</a> for allowed colors.
lightcolor	lightcolor of the region. See <a href="#">paletteIFC</a> for allowed colors.
ismarker	Default is 'false'. Allowed are 'true' or 'false'. Used for compatibility with amnis file but role remains unknown.
doesnotoverride	Default is 'false'. Allowed are 'true' or 'false'. Used for compatibility with amnis file but role remains unknown.
xlogrange	determines transformation instruction for x-axis. Default is "P" for no transformation.

ylogrange	determines transformation instruction for y-axis. Default is "P" for no transformation.
x	vector of x vertices values.
y	vector of y vertices values.
...	Other arguments to be passed.

**Value**

a list containing all region information.

---

checksumIFC	<i>IFC Files Checksum</i>
-------------	---------------------------

---

**Description**

This function returns RIF/CIF checksum. Checksum is the sum of img IFDs (Image Field Directory) offsets of objects 0, 1, 2, 3 and 4.

**Usage**

```
checksumIFC(fileName, ...)
```

**Arguments**

fileName	path to file.
...	arguments to pass to <a href="#">checksumDAF</a> or <a href="#">checksumXIF</a> .

**Details**

if fileName is a DAF file, then CIF checksum is computed from images values found in DAF.

**Value**

an integer corresponding to IFC file checksum.

---

data\_add\_features      *Add Feature to IFC\_data Object*

---

### Description

Adds features to an already existing 'IFC\_data' object.

### Usage

```
data_add_features(obj, features, ...)
```

### Arguments

obj	an 'IFC_data' object extracted by ExtractFromDAF(extract_features = TRUE) or ExtractFromXIF(extract_features = TRUE).
features	a list of features to add to obj. Each element of this list will be coerced by <a href="#">buildFeature</a> .
...	Other arguments to be passed.

### Details

A warning will be thrown if a provided feature is already existing in obj. In such a case this feature will not be added to obj. If any input feature is not well defined and can't be created then an error will occur.

### Value

an IFC\_data object with features added.

### Examples

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  daf <- ExtractFromDAF(fileName = file_daf)
  ## copy 1st feature found in daf
  feat_def <- daf$features_def[[1]]
  if(length(feat_def) != 0) {
    feat_def_copy <- feat_def
    ## modify name and value of copied features
    feat_def_copy$name <- "copied_feature"
    feat <- daf$features[, feat_def$name]
    feat_copy <- feat
    feat_copy <- feat_copy * 10
    ## create new object with this new feature
    dafnew <- data_add_features(obj = daf, features = list(c(feat_def_copy, list(val = feat_copy))))
  }
} else {
```

```

    message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                    'https://gitdemont.github.io/IFCdata/',
                    'to install extra files required to run this example.'))
}

```

---

data\_add\_graphs      *Add Graphs to IFC\_data Object*

---

### Description

Adds graphs to an already existing 'IFC\_data' object.

### Usage

```
data_add_graphs(obj, graphs, adjust_graph = TRUE, ...)
```

### Arguments

obj	an 'IFC_data' object extracted by <code>ExtractFromDAF(extract_features = TRUE)</code> or <code>ExtractFromXIF(extract_features = TRUE)</code> .
graphs	a list of graph(s) to add to obj. Each element of this list will be coerced by <code>buildGraph</code> .
adjust_graph	whether to try to adjust graph(s) when possible. Default is TRUE. -TRUE, graph(s) will be kept if possible using only regions, pops it depends that can be found in 'obj', -FALSE, graph(s) will be kept only if all features, regions, pops it refers to are found in 'obj', -NA, is not allowed and will throw an error.
...	Other arguments to be passed.

### Value

an IFC\_data object with graphs added.

---

data\_add\_pops      *Add Population to IFC\_data Object*

---

### Description

Adds populations to an already existing 'IFC\_data' object.

**Usage**

```
data_add_pops(
  obj,
  pops,
  pnt_in_poly_algorithm = 1,
  pnt_in_poly_epsilon = 1e-12,
  display_progress = TRUE,
  ...
)
```

**Arguments**

**obj** an 'IFC\_data' object extracted by `ExtractFromDAF(extract_features = TRUE)` or `ExtractFromXIF(extract_features = TRUE)`.

**pops** a list of population(s) to add to 'obj'. Each element of this list will be coerced by `buildPopulation`.

**pnt\_in\_poly\_algorithm** algorithm used to determine if object belongs to a polygon region or not. Default is 1. Note that for the moment only 1(Trigonometry) is available.

**pnt\_in\_poly\_epsilon** epsilon to determine if object belongs to a polygon region or not. It only applies when algorithm is 1. Default is 1e-12.

**display\_progress** whether to display a progress bar. Default is TRUE.

**...** Other arguments to be passed.

**Details**

A warning will be thrown if a provided population is already existing in 'obj'. In such a case this population will not be added to 'obj'. If any input population is not well defined and can't be created then an error will occur.

**Value**

an IFC\_data object with pops added.

**Source**

For `pnt_in_poly_algorithm`, `Trigonometry`, is an adaptation of Jeremy VanDerWal's code <https://github.com/jjvanderwal/SDMTools>

**Examples**

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  daf <- ExtractFromDAF(fileName = file_daf)
```

```

## copy 1st population from existing daf
pop <- daf$pops[[1]]
if(length(pop) != 0) {
  pop_copy <- pop
  ## modify name, obj and type of copied population
  pop_copy$name <- paste0(pop_copy$name, "_copy")
  pop_copy$obj <- (which(pop_copy$obj)-1)[1]
  pop_copy$type <- "T"
  ## create new object with this new population
  dafnew <- data_add_pops(obj = daf, pops = list(pop_copy))
}
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}

```

---

data_add_regions	<i>Add Region to IFC_data Object</i>
------------------	--------------------------------------

---

### Description

Adds regions to an already existing 'IFC\_data' object.

### Usage

```
data_add_regions(obj, regions, ...)
```

### Arguments

obj	an 'IFC_data' object extracted by <code>ExtractFromDAF(extract_features = TRUE)</code> or <code>ExtractFromXIF(extract_features = TRUE)</code> .
regions	a list of region(s) to add to obj. Each element of this list will be coerced by <a href="#">buildRegion</a> .
...	Other arguments to be passed.

### Details

A warning will be thrown if a provided region is already existing in 'obj'. In such a case this region will not be added to 'obj'. If any input population is not well defined and can't be created then an error will occur.

### Value

an IFC\_data object with regions added.

## Examples

```

if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  daf <- ExtractFromDAF(fileName = file_daf)
  ## copy 1st region found in daf
  reg <- daf$regions[[1]]
  if(length(reg) != 0) {
    reg_copy <- reg
    ## modify region label and x boundaries
    reg_copy$label <- paste0(reg_copy$label, "_copy")
    reg_copy$x <- reg_copy$x*0.9
    ## create new object with this new region
    dafnew <- data_add_regions(obj = daf, regions = list(reg_copy))
  }
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}

```

---

data\_rm\_features

*Remove Features from an IFC\_data Object*

---

## Description

Removes regions from an already existing 'IFC\_data' object.

## Usage

```
data_rm_features(obj, features, list_only = TRUE, adjust_graph = TRUE, ...)
```

## Arguments

obj	an 'IFC_data' object extracted by ExtractFromDAF(extract_features = TRUE) or ExtractFromXIF(extract_features = TRUE).
features	a character vector of features names to remove within 'obj'. Note that "Object Number" is not allowed and will be excluded from 'features' if present.
list_only	whether to return a list of elements that will be impacted by the removal. Default is TRUE. If FALSE then modified object will be returned.
adjust_graph	whether to try to adjust graph(s) when possible. Default is TRUE. -TRUE, graph(s) will be kept if possible using only regions, pops it depends that can be found in 'obj', -FALSE, graph(s) will be kept only if all features, regions, pops it refers to are found in 'obj', -NA, graph(s) will be removed no matter if features, regions, pops it refers to are found in 'obj'.
...	Other arguments to be passed.

**Value**

an 'IFC\_data' object or a list of elements impacted by removal depending on 'list\_only' parameter.

---

data_rm_graphs	<i>Remove Graph from an IFC_data Object</i>
----------------	---

---

**Description**

Removes graphs from an already existing 'IFC\_data' object.

**Usage**

```
data_rm_graphs(obj, graphs, list_only = TRUE, adjust_graph = TRUE, ...)
```

**Arguments**

obj	an 'IFC_data' object extracted by ExtractFromDAF(extract_features = TRUE) or ExtractFromXIF(extract_features = TRUE).
graphs	an integer vector of graph(s) to remove within 'obj'.
list_only	whether to return a list of elements that will be impacted by the removal. Default is TRUE. If FALSE then modified object will be returned.
adjust_graph	whether to try to adjust graph(s) when possible. Default is TRUE. -TRUE, graph(s) will be kept if possible using only regions, pops it depends that can be found in 'obj', -FALSE, graph(s) will be kept only if all features, regions, pops it refers to are found in 'obj', -NA, graph(s) will be removed no matter if features, regions, pops it refers to are found in 'obj'.
...	Other arguments to be passed.

**Value**

an 'IFC\_data' object or a list of elements impacted by removal depending on 'list\_only' parameter.

---

data\_rm\_pops                      *Remove Population from an IFC\_data Object*

---

### Description

Removes populations from an already existing 'IFC\_data' object.

### Usage

```
data_rm_pops(obj, pops, list_only = TRUE, adjust_graph = TRUE, ...)
```

### Arguments

obj	an 'IFC_data' object extracted by ExtractFromDAF(extract_features = TRUE) or ExtractFromXIF(extract_features = TRUE).
pops	a character vector of population names to remove within 'obj'. Note that "All" and "" are not allowed and will be excluded from 'pops' if present.
list_only	whether to return a list of elements that will be impacted by the removal. Default is TRUE. If FALSE then modified object will be returned.
adjust_graph	whether to try to adjust graph(s) when possible. Default is TRUE. -TRUE, graph(s) will be kept if possible using only regions, pops it depends that can be found in 'obj', -FALSE, graph(s) will be kept only if all features, regions, pops it refers to are found in 'obj', -NA, graph(s) will be removed no matter if features, regions, pops it refers to are found in 'obj'.
...	Other arguments to be passed.

### Value

an 'IFC\_data' object or a list of elements impacted by removal depending on 'list\_only' parameter.

---

data\_rm\_regions                      *Remove Region from an IFC\_data Object*

---

### Description

Removes regions from an already existing 'IFC\_data' object.

### Usage

```
data_rm_regions(obj, regions, list_only = TRUE, adjust_graph = TRUE, ...)
```

**Arguments**

obj	an 'IFC_data' object extracted by ExtractFromDAF(extract_features = TRUE) or ExtractFromXIF(extract_features = TRUE).
regions	a character vector of regions names to remove within 'obj'.
list_only	whether to return a list of elements that will be impacted by the removal. Default is TRUE. If FALSE then modified object will be returned.
adjust_graph	whether to try to adjust graph(s) when possible. Default is TRUE. -TRUE, graph(s) will be kept if possible using only regions, pops it depends that can be found in 'obj', -FALSE, graph(s) will be kept only if all features, regions, pops it refers to are found in 'obj', -NA, graph(s) will be removed no matter if features, regions, pops it refers to are found in 'obj'.
...	Other arguments to be passed.

**Value**

an 'IFC\_data' object or a list of elements impacted by removal depending on 'list\_only' parameter.

---

 data\_to\_DAF

*DAF File Writer*


---

**Description**

Writes an 'IFC\_data' object to a daf file

**Usage**

```
data_to_DAF(
  obj,
  write_to,
  viewing_pop = "All",
  overwrite = FALSE,
  binary = TRUE,
  endianness = .Platform$endian,
  display_progress = TRUE,
  verbose = FALSE,
  fullname = TRUE,
  cifdir = dirname(obj$fileName),
  ntry = +Inf,
  ...
)
```

**Arguments**

obj	an 'IFC_data' object extracted with features extracted.
write_to	<p>pattern used to export file. Placeholders, like "%d/%s_fromR.%e", will be substituted:</p> <ul style="list-style-type: none"> <li>-%d: with full path directory of 'obj\$fileName'</li> <li>-%p: with first parent directory of 'obj\$fileName'</li> <li>-%e: with extension of 'obj\$fileName' (without leading .)</li> <li>-%s: with shortname from 'obj\$fileName' (i.e. basename without extension).</li> </ul> <p>Exported file extension will be deduced from this pattern. Note that it has to be a .daf.</p>
viewing_pop	Character String. Allow user to change displayed population. Default is 'All'.
overwrite	<p>whether to overwrite file or not. Default is FALSE. Note that if TRUE, it will overwrite exported file if path of 'obj\$fileName' and deduced from 'write_to' arguments are different. Otherwise, you will get an error saying that overwriting source file is not allowed.</p> <p>Note also that an original file, i.e. generated by IDEAS(R) or INSPIRE(R), will never be overwritten. Otherwise, you will get an error saying that overwriting original file is not allowed.</p>
binary	<p>whether to write object to file in binary mode or not. Default is TRUE.</p> <p>Note that it can represent a convenient way to make file written in binary mode back-compatible with former version of IDEAS software.</p> <p>!\\ However unexpected behaviour may happen if features, regions, pops, ... are depending on masks (e.g. AdaptiveErode, Component, LevelSet, Watershed) introduced in newer version of IDEAS software.</p> <p>!\\ Important please note that conversion from binary to non-binary and back to binary may create some rounding adjustment resulting in some features/image values changes.</p> <p>Finally, if data originate from FCS, 'binary' will be forced to FALSE.</p>
endianness	<p>The endian-ness ("big" or "little") of the target system for the file. Default is .Platform\$endian.</p> <p>Endianness describes the bytes order of data stored within the files. This parameter may not be modified.</p>
display_progress	whether to display a progress bar. Default is TRUE.
verbose	whether to display information (use for debugging purpose). Default is FALSE.
fullname	whether to export daf file with full name of its corresponding cif, if found. Default is TRUE. If cif can't be found, daf file will be exported with the original cif file name.
cifdir	the path of the directory to initially look to cif file. Default is dirname(obj\$fileName). Only apply when 'fullname' is set to TRUE.
ntry	number of times <code>data_to_DAF</code> will be allowed to find corresponding cif file. Default is +Inf. Only apply when 'fullname' is set to TRUE.
...	other arguments to be passed.

**Value**

It invisibly returns full path of exported file.

**Examples**

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  tmp <- tempdir(check = TRUE)
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  daf <- ExtractFromDAF(fileName = file_daf)
  ## add a new population to daf
  dafnew <- data_add_pops(daf, list(buildPopulation(name = "test", type = "T", obj = 0)))
  ## export obj to file using binary mode
  data_to_DAF(obj = dafnew, write_to = paste0(tmp, "\\test_bin.daf"),
             overwrite = TRUE, binary = TRUE)
  ## exporting to non binary mode
  data_to_DAF(obj = dafnew, write_to = paste0(tmp, "\\test_notbin.daf"),
             overwrite = TRUE, binary = FALSE)
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                 'https://gitdemont.github.io/IFCdata/',
                 'to install extra files required to run this example.'))
}
```

---

DisplayGallery

*Gallery Display*

---

**Description**

Displays gallery of 'IFC\_img' / 'IFC\_msk' objects

**Usage**

```
DisplayGallery(
  ...,
  objects,
  offsets,
  image_type = "img",
  layout,
  name = "DisplayGallery",
  caption = FALSE,
  pageLength = 10L,
  pdf_pageSize = "A2",
  pdf_pageOrientation = "landscape",
  pdf_image_dpi = 96,
  extract_max = 10,
  sampling = FALSE,
  display_progress = TRUE,
```

```

    mode = c("rgb", "gray")[1]
)

```

## Arguments

...	arguments to be passed to <a href="#">objectExtract</a> with the exception of 'ifd' and 'bypass'(=TRUE). If 'param' is provided 'export'("base64") and the above parameters will be overwritten. If 'offsets' are not provided extra arguments can also be passed with ... to <a href="#">getOffsets</a> . />\If not any of 'fileName', 'info' and 'param' can be found in ... then attr(offsets, "fileName_image") will be used as 'fileName' input parameter to pass to <a href="#">objectParam</a> .
objects	integer vector, IDEAS objects ids numbers to use. This argument is not mandatory, if missing, the default, all objects will be used.
offsets	object of class 'IFC_offset'. This argument is not mandatory but it may allow to save time for repeated image export on same file.
image_type	image_type of desired offsets. Either "img" or "msk". Default is "img".
layout	a character vector of [acquired channels + 'composite' images] members to export. Default is missing to export everything. Note that members can be missing to be removed from final display. Note that members not found will be automatically removed and a warning will be thrown.
name	id of the datatable container. Default is DisplayGallery.
caption	whether to display caption name or not. Default is FALSE.
pageLength	integer, number of objects to display per page. Default is 10.
pdf_pageSize	string, page dimension when exporting to pdf. Default is "A2".
pdf_pageOrientation	string, page orientation when exporting to pdf. Default is "landscape". Allowed are "landscape" or "portrait".
pdf_image_dpi	integer, desired image resolution. Default is 96, for full resolution.
extract_max	maximum number of objects to extract. Default is 10. Use +Inf to extract all.
sampling	whether to sample objects or not. Default is FALSE.
display_progress	whether to display a progress bar. Default is TRUE.
mode	( <a href="#">objectParam</a> argument) color mode export. Either "rgb" or "gray". Default is "rgb".

## Details

arguments of [objectExtract](#) will be deduced from [DisplayGallery](#) input arguments.  
Please note that PDF export link will be available if 'write\_to' will not result in a "bmp".  
Please note that exporting to "tiff" may depend on browser capabilities.  
Please note that a warning may be sent if gallery to display contains large amount of data. This is due to use of `datatable()` from **DT**.

Warning message:

In instance\$preRenderHook(instance) :

It seems your data is too big for client-side DataTables. You may consider server-side processing:

<http://rstudio.github.io/DT/server.html>

For these reasons, it may be better to use "png" extension to display images.

### Value

it invisibly returns a list whose members are:

-data, data for DT::datatable(),

-args, associated arguments to pass to DT::datatable().

### Examples

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a cif file
  file_cif <- system.file("extdata", "example.cif", package = "IFCdata")
  cif <- ExtractFromXIF(fileName = file_cif)
  info <- getInfo(fileName = file_cif, from = "analysis")
  ## randomly show at most 10 "img" objects from file
  DisplayGallery(info = info, image_type = "img", extract_max = 10,
                sampling = TRUE, write_to = "example.png")
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

---

ExportToBATCH

*Batch File Writer*

---

### Description

Writes an XML file to batch files

### Usage

```
ExportToBATCH(batch)
```

### Arguments

batch                    list of batch nodes as created by [buildBatch](#).

### Value

It invisibly returns full path of xml batch file.

ExportToDAF

*DAF File Writer***Description**

Writes a new DAF file based on another one and exports new region(s), pop(s), feature(s), graph(s) and / or mask(s).

**Usage**

```
ExportToDAF(
  fileName,
  write_to,
  pops = list(),
  regions = list(),
  features = list(),
  graphs = list(),
  masks = list(),
  viewing_pop = "All",
  endianness = .Platform$endian,
  verbose = FALSE,
  overwrite = FALSE,
  fullname = TRUE,
  cifdir = dirname(fileName),
  ntry = +Inf,
  ...
)
```

**Arguments**

fileName	path of file to read data from.
write_to	pattern used to export file. Placeholders, like "%d/%s_fromR.%e", will be substituted: -%d: with full path directory of 'fileName' -%p: with first parent directory of 'fileName' -%e: with extension of 'fileName' (without leading .) -%s: with shortname from 'fileName' (i.e. basename without extension). Exported file extension will be deduced from this pattern. Note that has to be a .daf.
pops	list of population(s) to export. Will be coerced to exportable format by buildPopulation.
regions	list of region(s) to export. Will be coerced to exportable format by buildRegion.
features	list of feature(s) to export.
graphs	list of graph(s) to export. Not yet implemented.
masks	list of mask(s) to export. Not yet implemented.

viewing_pop	Character String. Allow user to change displayed population. Default is 'All'.
endianness	The endian-ness ("big" or "little") of the target system for the file. Default is <code>.Platform\$endian</code> . Endianness describes the bytes order of data stored within the files. This parameter may not be modified.
verbose	whether to display information (use for debugging purpose). Default is FALSE.
overwrite	whether to overwrite file or not. Default is FALSE. Note that if TRUE, it will overwrite exported file if path of 'fileName' and deduced from 'write_to' arguments are different. Otherwise, you will get an error saying that overwriting source file is not allowed. Note also that an original file, i.e. generated by IDEAS(R) or INSPIRE(R), will never be overwritten. Otherwise, you will get an error saying that overwriting original file is not allowed.
fullname	whether to export daf file with full name of its corresponding cif, if found. Default is TRUE. If cif can't be found, daf file will be exported with the original cif file name.
cifdir	the path of the directory to initially look to cif file. Default is <code>dirname(fileName)</code> . Only apply when 'fullname' is set to TRUE.
ntry	number of times <code>ExportToDAF</code> will be allowed to find corresponding cif file. Default is <code>+Inf</code> . Only apply when 'fullname' is set to TRUE.
...	other arguments to be passed.

### Value

It invisibly returns full path of exported file.

### Examples

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  tmp <- tempdir(check = TRUE)
  ## create a tagged population named test with 1st object
  pop <- buildPopulation(name = "test", type = "T", obj = 0)
  ExportToDAF(file_daf, write_to = paste0(tmp, "\\test.daf"),
              overwrite = TRUE, pops = list(pop))
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

ExportToFCS

*FCS File Writer***Description**

Writes an 'IFC\_data' object to a Flow Cytometry Standard (FCS) file.

**Usage**

```
ExportToFCS(
  obj,
  write_to,
  overwrite = FALSE,
  delimiter = "/",
  cytometer = "Image Stream",
  ...
)
```

**Arguments**

obj	an 'IFC_data' object extracted with features extracted.
write_to	pattern used to export file. Placeholders, like "%d/%s_fromR.%e", will be substituted: -%d: with full path directory of 'obj\$fileName' -%p: with first parent directory of 'obj\$fileName' -%e: with extension of 'obj\$fileName' (without leading .) -%s: with shortname from 'obj\$fileName' (i.e. basename without extension). Exported file extension will be deduced from this pattern. Note that it has to be a .fcs.
overwrite	whether to overwrite file or not. Default is FALSE. Note that if TRUE, it will overwrite exported file if path of 'fileName' and deduced from 'write_to' arguments are different. Otherwise, you will get an error saying that overwriting source file is not allowed. Note also that an original file will never be overwritten.
delimiter	an ASCII character to separate the FCS keyword-value pairs. Default is : "/".
cytometer	string, if provided it will be used to fill \$CYT keyword. However, when missing \$CYT will be filled with obj\$description\$FCS\$instrument if found, or "Image Stream" otherwise.
...	other arguments to be passed. keyword-value pairs can be passed here.

**Value**

invisibly returns full path of exported file.

---

ExportToGallery	<i>Gallery Export</i>
-----------------	-----------------------

---

### Description

Exports gallery of 'IFC\_img' / 'IFC\_msk' objects

### Usage

```
ExportToGallery(
    ...,
    objects,
    offsets,
    image_type = "img",
    layout,
    export = c("file", "matrix", "base64")[2],
    write_to,
    base64_id = FALSE,
    base64_att = "",
    overwrite = FALSE,
    main = "",
    add_channels = TRUE,
    add_ids = 1,
    add_lines = 2,
    bg_color = "grey20",
    dpi = 300,
    scale = list(),
    extract_max = 10,
    sampling = FALSE,
    display_progress = TRUE
)
```

### Arguments

...	arguments to be passed to <a href="#">objectExtract</a> with the exception of 'ifd' and 'bypass'(=TRUE). If 'param' is provided 'mode'(="rgb") and the above parameters will be overwritten. If 'offsets' are not provided extra arguments can also be passed with ... <a href="#">getOffsets</a> . /!\ If not any of 'fileName', 'info' and 'param' can be found in ... then attr(offsets, "fileName_image") will be used as 'fileName' input parameter to pass to <a href="#">objectParam</a> .
objects	integer vector, IDEAS objects ids numbers to use. This argument is not mandatory, if missing, the default, all objects will be used.
offsets	object of class 'IFC_offset'. This argument is not mandatory but it may allow to save time for repeated image export on same file.
image_type	image_type of desired offsets. Either "img" or "msk". Default is "img".

layout	a character vector of [acquired channels + 'composite' images] members to export. Default is missing to export everything. Note that members can be missing to be removed from final gallery export. Note that members not found will be automatically removed and a warning will be thrown.
export	export format. Either "file", "matrix", "base64". Default is "matrix".
write_to	used when 'export' is "file" or "base64" to compute respectively filename or base64 id attribute. Exported type will be deduced from this pattern. Allowed export are '.bmp', '.jpg', '.jpeg', '.png', '.tif', '.tiff'. Note that '.bmp' are faster but not compressed producing bigger data. Placeholders, if found, will be substituted: -%d: with full path directory -%p: with first parent directory -%e: with extension (without leading .) -%s: with shortname (i.e. basename without extension) -%o: with objects (at most 10, will be collapse with "_", if more than one). -%c: with channel_id (will be collapse with "_", if more than one, composite in any will be bracketed). A good trick is to use: -%d/%s_gallery_Obj[%o]_Ch[%c].tiff", when 'export' is "file" -%s_gallery.bmp", when 'export' is "base64". Note that if missing and 'export' is not "file", 'write_to' will be set to "%s_gallery.bmp".
base64_id	whether to add id attribute to base64 exported object. Default is TRUE. Only applied when 'export' is "base64".
base64_att	attributes to add to base64 exported object. Default is "". Only applied when export is "base64". For example, use "class=draggable". Note that id (if base64_id is TRUE) and width and height are already used.
overwrite	whether to overwrite file or not. Default is FALSE.
main	main title that will be displayed on top center of the image. If too large it will be clipped.
add_channels	whether to add channels names. Default is TRUE.
add_ids	integer, indice of column to mark objects ids number. Default is 1. If add_ids < 1, no ids are added.
add_lines	integer, size of separating lines between objects. Default is 1. If add_lines < 1, no separating lines are added.
bg_color	background color for main, channels and separating lines. Default is "grey20".
dpi	integer, the resolution of the image in DPI (dots per inch). Default is 300. Please note that whatever this parameter is final resolution will be 96 dpi. However image will be scaled according this parameter and magnification factor will be equal to this parameter divided by 96.
scale	a named list whose members are 'size', 'style', 'color', 'xoff', 'yoff'. Default is list() to draw no scale. Otherwise, -'size' positive integer. Scale's bar size in micro-meter. Default is '7'. This parameter can't be lesser than 6px nor higher than image width + scale text. -'style' a character string. Scale's bar style, either "dash" or "line". Default is "dash". -'color' a character string. color of the scale. Default is "white".

-'xoff' positive integer. x offset in image to draw scale, starting from bottom left corner.  
 -'yoff' positive integer. y offset in image to draw scale, starting from bottom left corner.

extract\_max      maximum number of objects to extract. Default is 10. Use +Inf to extract all.  
 sampling          whether to sample objects or not. Default is FALSE.  
 display\_progress      whether to display a progress bar. Default is TRUE.

### Details

arguments of `objectExtract` will be deduced from `ExportToGallery` input arguments. TRICK: for exporting only ONE 'objects', set 'add\_channels' = FALSE, 'add\_ids' >= 1, 'force\_width' = FALSE, 'dpi' = 96; this allows generating image with its original size incrusted with its id number.

### Value

Depending on 'export':  
 -"matrix", a rgb array,  
 -"base64", a data-uri string,  
 -"file", an invisible vector of ids corresponding to the objects exported.

---

 ExportToNumpy

*Numpy Export*


---

### Description

Exports IFC objects to numpy array [objects,height,width,channels]

### Usage

```
ExportToNumpy(
  ...,
  objects,
  offsets,
  image_type = "img",
  size = c(64, 64),
  force_width = FALSE,
  display_progress = TRUE,
  python = Sys.getenv("RETICULATE_PYTHON"),
  dtype = c("uint8", "int16", "uint16", "double")[3],
  mode = c("raw", "gray")[1],
  export = c("file", "matrix")[2],
  write_to,
  overwrite = FALSE
)
```

**Arguments**

...	arguments to be passed to <a href="#">objectExtract</a> with the exception of 'ifd' and 'bypass'(=TRUE). If 'param' is provided the above parameters will be overwritten. If 'offsets' are not provided extra arguments can also be passed with ... <a href="#">getOffsets</a> . />\ If not any of 'fileName', 'info' and 'param' can be found in ... then attr(offsets, "fileName_image") will be used as 'fileName' input parameter to pass to <a href="#">objectParam</a> .
objects	integer vector, IDEAS objects ids numbers to use. This argument is not mandatory, if missing, the default, all objects will be used.
offsets	object of class 'IFC_offset'. This argument is not mandatory but it may allow to save time for repeated image export on same file.
image_type	image_type of desired offsets. Either "img" or "msk". Default is "img".
size	a length 2 integer vector of final dimensions of the image, height 1st and width 2nd. Default is c(64,64).
force_width	whether to use information in 'info' to fill size. Default is FALSE. When set to TRUE, width of 'size' argument will be overwritten.
display_progress	whether to display a progress bar. Default is TRUE.
python	path to python. Default is Sys.getenv("RETICULATE_PYTHON"). Note that this numpy should be available in this python to be able to export to numpy array file, otherwise 'export' will be forced to "matrix".
dtype	desired array's data-type. Default is "double". Allowed are "uint8", "int16", "uint16" or "double". If 'mode' is "raw", this parameter will be forced to "int16".
mode	( <a href="#">objectParam</a> argument) color mode export. Either "raw", "gray". Default is "raw".
export	export format. Either "file", "matrix". Default is "matrix". Note that you will need 'reticulate' package installed to be able to export to numpy array file, otherwise 'export' will be forced to "matrix".
write_to	used when 'export' is "file" to compute respectively filename. Exported type will be deduced from this pattern. Allowed export are '.npy'. Placeholders, if found, will be substituted: -%d: with full path directory -%p: with first parent directory -%e: with extension of (without leading .) -%s: with shortname (i.e. basename without extension) -%o: with objects (at most 10, will be collapse with "_", if more than one). -%c: with channel_id (will be collapse with "_", if more than one, composite in any will be bracketed). A good trick is to use: -%d/%s_Obj[%o]_Ch[%c].npy", when 'export' is "file"
overwrite	whether to overwrite file or not. Default is FALSE.

**Details**

arguments of [objectExtract](#) will be deduced from [ExportToNumpy](#) input arguments.  
Please note that size parameter has to be supplied and could not be set to (0,) when 'object' length

is not equal to one

`ExportToNumpy` requires `reticulate` package, python and numpy installed to create npy file.

If one of these is missing, 'export' will be set to "matrix".

### Value

Depending on 'export':

- "matrix", an array whose dimensions are [object, height, width, channel].

- "file", it invisibly returns path of .npy exported file.

---

ExportToReport

*Graphical and Statistic Report Generation*

---

### Description

Generates report from 'IFC\_data' object.

### Usage

```
ExportToReport(
  obj,
  selection,
  write_to,
  overwrite = FALSE,
  onepage = TRUE,
  color_mode = c("white", "black")[1],
  add_key = "panel",
  precision = c("light", "full")[1],
  trunc_labels = 38,
  trans = "asinh",
  bin,
  viewport = "ideas",
  backend = "lattice",
  display_progress = TRUE,
  ...
)
```

### Arguments

`obj` an 'IFC\_data' object extracted with features extracted.

`selection` indices of desired graphs. It can be provided as an integer vector or as a matrix. In such case, the layout of the matrix will reflect the layout of the extracted graphs.

NA value will result in an empty place.

Otherwise, when 'selection' is provided as a vector not identical to `seq_along(obj$graphs)`, 'onepage' parameter will be set to FALSE.

Note that indices are read from left to right, from top to bottom. Default is missing for extracting all graphs.

write_to	<p>pattern used to export file(s). Placeholders, like c("%d/%s_fromR.pdf", "%d/%s_fromR.csv"), will be substituted:</p> <ul style="list-style-type: none"> <li>-%d: with full path directory of 'obj\$fileName'</li> <li>-%p: with first parent directory of 'obj\$fileName'</li> <li>-%e: with extension of 'obj\$fileName' (without leading .)</li> <li>-%s: with shortname from 'obj\$fileName' (i.e. basename without extension).</li> </ul> <p>Exported file(s) extension(s) will be deduced from this pattern. Note that has to be a .pdf and/or .csv.</p>
overwrite	whether to overwrite file or not. Default is FALSE. Note that if TRUE, it will overwrite file. In addition a warning message will be sent.
onepage	whether to generate a pdf with all graphs on one page or not. Default is TRUE.
color_mode	Whether to extract colors from obj in white or black mode. Default is "white".
add_key	<p>whether to draw a "global" key under title or in the first "panel" or "both". Default is "panel".</p> <p>Accepted values are either: FALSE, "panel", "global", "both" or c("panel", "global").</p> <p>Note that it only applies when display is seen as overlaying populations.</p>
precision	<p>when graphs is a 2D scatter with population overlay, this argument controls amount of information displayed. Default is "light".</p> <ul style="list-style-type: none"> <li>-"light", the default, will only display points of same coordinates that are among the other layers.</li> <li>-"full" will display all the layers.</li> </ul>
trunc_labels	maximum number of characters to display for labels. Default is 38.
trans	name of the transformation function for density graphs. If missing the default, the BasePop[[1]]\$densitytrans, if any, will be retrieved, otherwise "asinh" will be used.
bin	default number of bin used for histogram. Default is missing.
viewport	<p>Either "ideas", "data" or "max" defining limits used for the graph. Default is "ideas".</p> <ul style="list-style-type: none"> <li>-"ideas" will use same limits as the one defined in ideas.</li> <li>-"data" will use data to define limits.</li> <li>-"max" will use data and regions drawn to define limits.</li> </ul>
backend	<p>backend used for drawing. Allowed are "lattice", "base", "raster". Default is "lattice".</p> <ul style="list-style-type: none"> <li>-"lattice" is the original one used in <b>IFC</b> using <b>lattice</b>,</li> <li>-"base" will produce the plot using <b>base</b>,</li> <li>-"raster" uses "base" for plotting but 2D graphs points will be produced as <a href="#">rasterImage</a>.</li> </ul> <p>This has the main advantage of being super fast allowing for plotting a huge amount of points while generating smaller objects (in bytes). However, plot quality is impacted with "raster" method and resizing can lead to unpleasant looking.</p>
display_progress	whether to display a progress bar. Default is TRUE.
...	other parameters to be passed.

**Details**

depending on 'write\_to', function will create .pdf and/or .csv file(s) report with according to graphs found in 'obj'.

- csv file if created will contain "Min.", "1st Qu.", "Median", "Mean", "3rd Qu.", "Max." for each graph found for x and y (if not histogram) for drawn populations and regions.

- pdf file if created will contain graphs and to a certain extent some stats "Min.", "Median", "Mean", "Max." (no more than 7 rows).

Note that only graphs will be exported (no images, features values, population stats, ...) in the same layout they were created and without sizing.

**Value**

It invisibly returns full path of exported .pdf and/or .csv file(s).

**Examples**

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  tmp <- tempdir(check = TRUE)
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  daf <- ExtractFromDAF(fileName = file_daf, extract_images = FALSE,
    extract_offsets = FALSE, display_progress = FALSE)
  L = length(daf$graphs)
  if(L > 0) {
    ## randomly export at most 5 graphs from daf
    sel = sample(1:L, min(5, L))
    ExportToReport(obj = daf, selection = sel,
      write_to = paste0(tmp, "\\test.pdf"), overwrite = TRUE)
  }
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
    'https://gitdemont.github.io/IFCdata/',
    'to install extra files required to run this example.'))
}
```

---

 ExportToXIF

*RIF/CIF File Writer*


---

**Description**

Subsets or merges RIF or CIF files.

**Usage**

```
ExportToXIF(
  fileName,
  write_to,
  objects,
```

```

offsets,
fast = TRUE,
extract_features = FALSE,
endianness = .Platform$endian,
verbose = FALSE,
verbosity = 1,
overwrite = FALSE,
display_progress = TRUE,
add_tracking = TRUE,
...
)

```

### Arguments

fileName	path(s) of file(s) to subset or merge. If multiple files are provided they will be merged. Otherwise, if only one file is input it will be subsetted. All files have to be either '.rif' or '.cif' files. All files should have same channels.
write_to	<p>pattern used to export file. Placeholders, like "%d/%s_fromR.%e", will be substituted:</p> <ul style="list-style-type: none"> <li>-%d: with full path directory of first element of 'fileName'</li> <li>-%p: with first parent directory of first element of 'fileName'</li> <li>-%e: with extension of first element of 'fileName' (without leading .)</li> <li>-%s: with shortname from of first element of 'fileName' (i.e. basename without extension).</li> </ul> <p>Exported file extension will be deduced from this pattern. It has to be the same as 'fileName', i.e. .cif or .rif.</p>
objects	integer vector, IDEAS objects ids numbers to use. If missing, the default, all objects will be used. Only apply for subsetting.
offsets	<p>object of class 'IFC_offset'. If missing, the default, offsets will be extracted from 'fileName'.</p> <p>This param is not mandatory but it may allow to save time for repeated XIF export on same file. Only apply for subsetting.</p>
fast	<p>whether to fast extract 'objects' or not. Default is TRUE. Meaning that 'objects' will be extracting expecting that objects are stored in ascending order.</p> <p>Note that a warning will be sent if an 'object' is found at an unexpected order. In such a case you may need to rerun function with 'fast' = FALSE. If set to FALSE, all object_ids will be scanned from 'fileName' to ensure extraction of desired 'objects'.</p> <p><b>IMPORTANT:</b> whatever this argument is, features are extracted assuming an ascending order of storage in file.</p> <p>Only apply for subsetting.</p>
extract_features	<p>whether to try to extract features. Default is FALSE. <b>IMPORTANT:</b> it is not clear if how features are stored and which objects they rely to when input file is already a merge or a subset. For this reason it should be carefully checked. Note that features extraction is not implemented for merging.</p>
endianness	the endian-ness ("big" or "little") of the target system for the file. Default is .Platform\$endian.

	Endianness describes the bytes order of data stored within the files. This parameter may not be modified.
verbose	whether to display information (use for debugging purpose). Default is FALSE.
verbosity	quantity of information displayed when verbose is TRUE; 1: normal, 2: rich. Default is 1.
overwrite	whether to overwrite file or not. Default is FALSE. Note that if TRUE, it will overwrite exported file if path(s) of file(s) in 'fileName' and deduced from 'write_to' arguments are different. Otherwise, you will get an error saying that overwriting source file is not allowed. Note also that an original file, i.e. generated by IDEAS(R) or INSPIRE(R), will never be overwritten. Otherwise, you will get an error saying that overwriting original file is not allowed.
display_progress	whether to display a progress bar. Default is TRUE.
add_tracking	whether to register files' paths and objects' ids in the exported file. Default is TRUE.
...	other arguments to be passed.

### Details

when 'extract\_features' is set TRUE, only features stored in binary format will be extracted if found. If the input 'fileName' is a merged of several files then features will be extracted from these files. If these files can't be found, Warning(s) will be thrown and input 'fileName' will be extracted without features values.

### Value

It invisibly returns full path of exported file.

### Examples

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  tmp <- tempdir(check = TRUE)
  ## use a cif file, but you can also subset rif
  file_cif <- system.file("extdata", "example.cif", package = "IFCdata")
  ## subset objects 0,1 and 4 from file
  exported <- ExportToXIF(fileName = file_cif, write_to = paste0(tmp, "\\test.cif"),
    overwrite = TRUE, objects = c(0,1,4))
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
    'https://gitdemont.github.io/IFCdata/',
    'to install extra files required to run this example.'))
}
```

**Description**

Extracts data from DAF Files.

**Usage**

```
ExtractFromDAF(
    fileName,
    extract_features = TRUE,
    extract_images = TRUE,
    extract_offsets = TRUE,
    extract_stats = TRUE,
    endianness = .Platform$endian,
    pnt_in_poly_algorithm = 1,
    pnt_in_poly_epsilon = 1e-12,
    display_progress = TRUE,
    ...
)
```

**Arguments**

fileName	path to file.
extract_features	whether to extract features (and graphs, pops and regions) from file. Default is TRUE.
extract_images	whether to extract images information from file. Default is TRUE.
extract_offsets	whether to extract IFDs offsets from corresponding. Default is TRUE. See <a href="#">getOffsets</a> for further details.
extract_stats	whether to extract population statistics. Default is TRUE.
endianness	The endian-ness ("big" or "little") of the target system for the file. Default is .Platform\$endian. Endianness describes the bytes order of data stored within the files. This parameter may not be modified.
pnt_in_poly_algorithm	algorithm used to determine if object belongs to a polygon region or not. Default is 1. Note that for the moment only 1(Trigonometry) is available.
pnt_in_poly_epsilon	epsilon to determine if object belongs to a polygon region or not. It only applies when algorithm is 1. Default is 1e-12.
display_progress	whether to display a progress bar. Default is TRUE.
...	Other arguments to be passed.

**Details**

When `extract_features` is TRUE it allows features, graphs, pops, regions to be extracted.  
 If `extract_features` is TRUE, `extract_stats` will be automatically forced to TRUE.  
 If `extract_stats` is TRUE, `extract_features` will be automatically forced to TRUE.  
 If `extract_offsets` is TRUE, `extract_images` will be automatically forced to TRUE.  
 If `extract_images` is TRUE, information about images will be extracted.

**Value**

A named list of class 'IFC\_data', whose members are:

- description, a list of descriptive information,
- fileName, path of fileName input,
- fileName\_image, path of .cif image fileName is referring to,
- features, a data.frame of features,
- features\_def, a describing how features are defined,
- graphs, a list of graphical elements found,
- pops, a list describing populations found,
- regions, a list describing how regions are defined,
- images, a data.frame describing information about images,
- offsets, an integer vector of images and masks IFDs offsets,
- stats, a data.frame describing populations count and percentage to parent and total population,
- checksum, checksum of .cif image fileName is referring to computed from images values found in current daf.

**Source**

For `pnt_in_poly_algorithm`, Trigonometry, is an adaptation of Jeremy VanDerWal's code <https://github.com/jjvanderwal/SDMTools>

**Examples**

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  daf <- ExtractFromDAF(fileName = file_daf)
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

---

 ExtractFromFCS

*FCS File Reader*


---

**Description**

Extracts data from Flow Cytometry Standard (FCS) Files.

**Usage**

```
ExtractFromFCS(fileName, ...)
```

**Arguments**

fileName	path(s) of file(s). If multiple files are provided they will be merged and populations will be created to identify each single file within returned 'IFC_data' object.
...	other arguments to be passed to readFCS function, with the exception of 'options\$text_only'.

**Value**

A named list of class 'IFC\_data', whose members are:

- description, a list of descriptive information,
- Merged\_fcs, character vector of path of files used to create fcs, if input was a merged,
- Keywords, a named-list of keywords values, only keywords from 1st 'fcs' segment will be retrieved
- fileName, path of fileName input,
- fileName\_image, path of .cif image fileName is referring to,
- features, a data.frame of features,
- features\_def, a describing how features are defined,
- graphs, a list of graphical elements found,
- pops, a list describing populations found,
- regions, a list describing how regions are defined,
- images, a data.frame describing information about images,
- offsets, an integer vector of images and masks IFDs offsets,
- stats, a data.frame describing populations count and percentage to parent and total population,
- checksum, a checksum integer.

**Source**

Data File Standard for Flow Cytometry, version FCS 3.1 from Spidlen J. et al. available at doi: [10.1002/cyto.a.20825](https://doi.org/10.1002/cyto.a.20825).

---

 ExtractFromXIF

*RIF/CIF File Reader*


---

**Description**

Extracts data from RIF or CIF Files.

**Usage**

```
ExtractFromXIF(
  fileName,
  extract_features = TRUE,
  extract_images = FALSE,
```

```

extract_offsets = FALSE,
extract_stats = TRUE,
pnt_in_poly_algorithm = 1,
pnt_in_poly_epsilon = 1e-12,
force_default = TRUE,
verbose = FALSE,
verbosity = 1,
display_progress = TRUE,
fast = TRUE,
recursive = FALSE,
...
)

```

### Arguments

fileName	path to file.
extract_features	whether to extract features from file. Default is TRUE. If TRUE, <a href="#">ExtractFromXIF</a> will try to export features. If it fails a message will be sent. Otherwise, graphs, pops and regions will be also extracted.
extract_images	whether to extract images information from file. Default is FALSE.
extract_offsets	whether to extract IFDs offsets from corresponding. Default is FALSE. See <a href="#">getOffsets</a> for further details.
extract_stats	whether to extract population statistics. Default is TRUE.
pnt_in_poly_algorithm	algorithm used to determine if object belongs to a polygon region or not. Default is 1. Note that for the moment only 1(Trigonometry) is available.
pnt_in_poly_epsilon	epsilon to determine if object belongs to a polygon region or not. It only applies when algorithm is 1. Default is 1e-12.
force_default	when display information can't be retrieved whether to use default values. Default is TRUE.
verbose	whether to display information (use for debugging purpose). Default is FALSE.
verbosity	quantity of information displayed when verbose is TRUE; 1: normal, 2: rich. Default is 1.
display_progress	whether to display a progress bar. Default is TRUE.
fast	whether to fast 'extract_offsets' or not. Default is TRUE. Meaning that offsets will be extracting expecting that raw object are stored in ascending order. if extract_images is FALSE, a message will be thrown since extraction method does not ensure correct mapping between objects and offsets. if extract_images is TRUE, a warning will be sent if an object is found at an unexpected order.

recursive        whether to recursively apply `ExtractFromXIF` on files defining input `fileName` when it is a merged. Default is `FALSE`.

...                Other arguments to be passed.

### Details

If `extract_stats` is `TRUE`, `extract_features` will be automatically forced to `TRUE`.

If `extract_images` is `TRUE`, `extract_offsets` will be automatically forced to `TRUE`.

If `extract_offsets` is `TRUE`, offsets of images and masks IFDs will be extracted.

If `extract_images` is `TRUE`, information about images will be extracted.

If the input `fileName` is a merged of several files and `recursive` is set to `TRUE`, then `ExtractFromXIF` will be applied recursively on these files.

!/\ Note that features extraction is mandatory to correctly extract graphs, pops, regions and statistics values.

### Value

A named list of class `'IFC_data'`, whose members are:

- description, a list of descriptive information,
- fileName, path of `fileName` input,
- fileName\_image, same as `fileName`,
- features, a `data.frame` of features,
- features\_def, a describing how features are defined,
- graphs, a list of graphical elements found,
- pops, a list describing populations found,
- regions, a list describing how regions are defined,
- images, a `data.frame` describing information about images,
- offsets, an integer vector of images and masks IFDs offsets,
- stats, a `data.frame` describing populations count and percentage to parent and total population,
- checksum, current file checksum.

If `fileName` is a merged of several files returned object will be of class `'IFC_data'` and `'Merged'`. If `recursive` is set to `"TRUE"`, `ExtractFromXIF` will be applied recursively on files defining the merged. and the returned object will be a list of the above-mentioned list for each of these files.

### Source

For `pnt_in_poly_algorithm`, Trigonometry, is an adaptation of Jeremy VanDerWal's code <https://github.com/jjvanderwal/SDMTools>

### Examples

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a cif file, but you can also read rif
  file_cif <- system.file("extdata", "example.cif", package = "IFCdata")
  cif <- ExtractFromXIF(fileName = file_cif)
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

```
}

```

---

```
ExtractImages_toBase64
```

*Shortcut for Batch Images Extraction to Base64*

---

### Description

Function to shortcut extraction, normalization and eventually colorization of images to matrix ! excludes mask.

### Usage

```
ExtractImages_toBase64(
  ...,
  objects,
  offsets,
  display_progress = TRUE,
  mode = c("rgb", "gray")[1]
)
```

### Arguments

...	arguments to be passed to <a href="#">objectExtract</a> with the exception of 'ifd' and 'bypass'(=TRUE). If 'param' is provided 'export'("base64") and 'mode' will be overwritten. If 'offsets' are not provided extra arguments can also be passed with ... <a href="#">getOffsets</a> . /!\ If not any of 'fileName', 'info' and 'param' can be found in ... then attr(offsets, "fileName_image") will be used as 'fileName' input parameter to pass to <a href="#">objectParam</a> .
objects	integer vector, IDEAS objects ids numbers to use. This argument is not mandatory, if missing, the default, all objects will be used.
offsets	object of class 'IFC_offset'. This argument is not mandatory but it may allow to save time for repeated image export on same file.
display_progress	whether to display a progress bar. Default is TRUE.
mode	( <a href="#">objectParam</a> argument) color mode export. Either "rgb", "gray". Default is "rgb".

### Details

arguments of [objectExtract](#) will be deduced from [ExtractImages\\_toBase64](#) input arguments.

### Value

A list of base64 encoded images corresponding to objects extracted.

---

ExtractImages\_toFile *Shortcut for Batch Images Extraction to Files*

---

## Description

Function to shortcut extraction, normalization and eventually colorization of images to matrix ! excludes mask.

## Usage

```
ExtractImages_toFile(
    ...,
    objects,
    offsets,
    display_progress = TRUE,
    mode = c("rgb", "gray")[1],
    write_to
)
```

## Arguments

...	arguments to be passed to <a href="#">objectExtract</a> with the exception of 'ifd' and 'bypass'(=TRUE). If 'param' is provided 'export'(="file"), 'write_to' and 'mode' will be overwritten. If 'offsets' are not provided extra arguments can also be passed with ... <a href="#">getOffsets</a> . /!\ If not any of 'fileName', 'info' and 'param' can be found in ... then attr(offsets, "fileName_image") will be used as 'fileName' input parameter to pass to <a href="#">objectParam</a> .
objects	integer vector, IDEAS objects ids numbers to use. This argument is not mandatory, if missing, the default, all objects will be used.
offsets	object of class 'IFC_offset'. This argument is not mandatory but it may allow to save time for repeated image export on same file.
display_progress	whether to display a progress bar. Default is TRUE.
mode	( <a href="#">objectParam</a> argument) color mode export. Either "rgb", "gray" . Default is "rgb".
write_to	( <a href="#">objectParam</a> argument) used to compute exported file name. Exported "file" extension will be deduced from this pattern. Allowed export are '.bmp', '.jpg', '.jpeg', '.png', '.tif', '.tiff'. Note that '.bmp' are faster but not compressed producing bigger data. Placeholders, if found, will be substituted: -%d: with full path directory -%p: with first parent directory -%e: with extension (without leading .) -%s: with shortname (i.e. basename without extension)

-%o: with object\_id  
 -%c: with channel\_id  
 A good trick is to use "%d/%s/%s\_%o\_%c.tiff".

### Details

arguments of `objectExtract` will be deduced from `ExtractImages_toFile` input arguments.

### Value

It invisibly returns a list of exported file path of corresponding to objects extracted.

---

ExtractImages\_toMatrix

*Shortcut for Batch Images Extraction to Matrices/Arrays*

---

### Description

Function to shortcut extraction, normalization and eventually colorization of images to matrix ! excludes mask.

### Usage

`ExtractImages_toMatrix(..., objects, offsets, display_progress = TRUE)`

### Arguments

...	arguments to be passed to <code>objectExtract</code> with the exception of 'ifd' and 'bypass' (=TRUE). If 'param' is provided 'export' (= "matrix") will be overwritten. If 'offsets' are not provided extra arguments can also be passed with ... <code>getOffsets</code> . /!\ If not any of 'fileName', 'info' and 'param' can be found in ... then <code>attr(offsets, "fileName_image")</code> will be used as 'fileName' input parameter to pass to <code>objectParam</code> .
objects	integer vector, IDEAS objects ids numbers to use. This argument is not mandatory, if missing, the default, all objects will be used.
offsets	object of class 'IFC_offset'. This argument is not mandatory but it may allow to save time for repeated image export on same file.
display_progress	whether to display a progress bar. Default is TRUE.

### Details

arguments of `objectExtract` will be deduced from `ExtractImages_toMatrix` input arguments.

### Value

A list of matrices/arrays of images corresponding to objects extracted.

---

ExtractMasks\_toMatrix *Shortcut for Batch Masks Extraction to Matrices/Arrays*

---

### Description

Function to shortcut extraction, normalization and eventually colorization of masks to matrix ! excludes image.

### Usage

```
ExtractMasks_toMatrix(..., objects, offsets, display_progress = TRUE)
```

### Arguments

...	arguments to be passed to <a href="#">objectExtract</a> with the exception of 'ifd' and 'by-pass'(=TRUE). If 'param' is provided 'export'("matrix") will be overwritten. If 'offsets' are not provided extra arguments can also be passed with ... <a href="#">getOffsets</a> . />\ If not any of 'fileName', 'info' and 'param' can be found in ... then attr(offsets, "fileName_image") will be used as 'fileName' input parameter to pass to <a href="#">objectParam</a> .
objects	integer vector, IDEAS objects ids numbers to use. This argument is not mandatory, if missing, the default, all objects will be used.
offsets	object of class 'IFC_offset'. This argument is not mandatory but it may allow to save time for repeated image export on same file.
display_progress	whether to display a progress bar. Default is TRUE.

### Details

arguments of [objectExtract](#) will be deduced from [ExtractMasks\\_toMatrix](#) input arguments.

### Value

A list of matrices/arrays of masks corresponding to objects extracted.

---

gen\_altnames

*Alternative Names Generator*

---

### Description

Generates unique non matching alternative names

**Usage**

```
gen_altnames(
  x,
  n = 10,
  forbidden = character(),
  random_seed = list(seed = 252, "Mersenne-Twister", "Inversion", "Rounding")
)
```

**Arguments**

x	a character vector.
n	number of characters of the desired returned name. Default is 10.
forbidden	forbidden character vector. Default is character().
random_seed	a list of elements to pass to <a href="#">set.seed</a> or a single value, interpreted as an integer, or NULL. Default is list(seed = 0xFC, "Mersenne-Twister", "Inversion", "Rounding"). Note that NA_integer_ or list(seed = NA_integer_) can be used to not call <a href="#">set.seed</a> at all. Note also that the default is chosen because it is compatible with old R version.

**Details**

'forbidden' should not encompass all possible returned value otherwise the function will never end.

**Value**

a character vector.

---

 getAborted

*Aborted Batch Files Retrieval*


---

**Description**

Try to retrieve files whose processing failed during batch. This is a very beta version

**Usage**

```
getAborted(aborted, default_batch_dir, config_file)
```

**Arguments**

aborted	path to file containing aborted information. If missing, the default, a dialog box will be displayed to choose this file. Note, that if provided 'default_batch_dir' and 'config_file' will not be used.
---------	---

default\_batch\_dir

directory where batches are stored.

It can be found in IDEAS(R) software, under Options -> Application Defaults -> Directories -> Default Batch Report Files Directory. If missing, the default, it will be deduced from IDEAS(R) config file, However, if it can't be deduced then current working directory will be used.

This argument takes precedence over 'config\_file' and filling 'default\_batch\_dir' prevents the use of 'config\_file' argument.

config\_file

path to IDEAS(R) config file.

It may depends on IDEAS(R) software installation but one may use "C:/Users/%USER%/AppData/Roaming/Corporation/userconfig.xml".

### Value

a list of 4 elements:

-not\_existing: a list of files paths that caused failure because they were not found during batch,

-not\_handled: a list of failed files and the retrieved error message.

-failed\_found: a list of failed files and their unique corresponding paths,

-failed\_match: a list of failed files and their all paths that could match.

---

getFullTag

*Image Field Directory Full Tag Retrieval*

---

### Description

Retrieves full tag value from IFDs (Image Field Directory) extracted by [getIFD](#).

### Usage

```
getFullTag(IFD, which = 1, tag = "256", raw = FALSE)
```

### Arguments

IFD an object of class 'IFC\_ifd\_list' extracted by [getIFD](#).

which scalar, integer (index) or the name of 'IFD' sub-element to extract 'tag' from. Default is 1 to extract 'tag' from the first member of 'IFD'.

tag scalar, integer (index) or the name of the IFD[[which]] of the desired 'tag'.

raw whether to return tag as a raw vector. Default is FALSE.

### Details

It may be usefull to extract all information contained in a specific 'tag' since [getIFD](#) is designed to be run with argument trunc\_bytes so as to only extract essential bytes to run faster and save memory. Nonetheless, thanks to [getFullTag](#) users will still be able to get full extraction of specific tag.

### Value

the full value of the corresponding IFD tag.

**Source**

TIFF 6.0 specifications archived from web <https://web.archive.org/web/20211209104854/https://www.adobe.io/open/standards/TIFF.html>

---

 getIFD

*RIF/CIF Image Field Directories Extraction*


---

**Description**

Extracts IFDs (Image File Directory) in RIF or CIF files.

IFDs contain information about images or masks of objects stored within XIF files.

The first IFD is special in that it does not contain image or mask information but general information about the file.

Users are highly encouraged to read TIFF specifications to have a better understanding about what IFDs are.

**Usage**

```
getIFD(
  fileName,
  offsets = "first",
  trunc_bytes = 12,
  force_trunc = FALSE,
  verbose = FALSE,
  verbosity = 1,
  display_progress = FALSE,
  bypass = FALSE,
  ...
)
```

**Arguments**

fileName	path to file.
offsets	either "all", "first" or an object of class 'IFC_offset'. Default is "first".
trunc_bytes	a positive integer maximal number of individual scalar to extract BYTE/ASCII/SBYTE/UNDEFINED for TAGS (1, 2, 6 or 7). Default is 12. However, if less is found, less is returned in map. Note that, if 0 is provided, it will be automatically set to 1.
force_trunc	whether to force truncation for all TAGS types. Default is FALSE. If TRUE, 'trunc_bytes' will be used for TAGS (3, 4, 5, 8, 9, 10, 11 and 12) to extract desired number of individual scalar corresponding to each types.
verbose	whether to display information (use for debugging purpose). Default is FALSE.
verbosity	quantity of information displayed when verbose is TRUE; 1: normal, 2: rich. Default is 1.

display_progress	whether to display a progress bar. Default is FALSE.
bypass	whether to bypass checks on 'trunc_bytes', 'force_trunc', 'verbose', 'verbosity' and 'display_progress'. Default is FALSE.
...	other arguments to be passed.

## Details

Function will return IFDs (image, mask or first) from the file using provided offsets argument. IFDs contain several tags that can be viewed as descriptive meta-information of raw data stored within RIF or CIF file. For more details see TIFF specifications. If 'offsets' == "first" only first IFD will be returned. If 'offsets' == "all" all images and masks IFDs will be returned but not "first" one. Be aware that errors may occur if offsets are not extracted with [getOffsets](#) or [subsetOffsets](#).

## Value

A list of named lists, each containing:

- tags, a named list whose names are tags found, where each tag is a list of tag, typ, siz, val, byt, len, off, map information.
- infos, a named list containing essential information about IFDs, IMAGE\_LENGTH, IMAGE\_WIDTH, OBJECT\_ID, COMPRESSION, TYPE, STRIP\_OFFSETS, STRIP\_BYTE\_COUNTS, BG\_MEAN, BG\_STD
- curr\_IFD\_offset, the position of current IFD offset
- next\_IFD\_offset, the position of next IFD offset

## Source

TIFF 6.0 specifications archived from web <https://web.archive.org/web/20211209104854/https://www.adobe.io/open/standards/TIFF.html>

## Examples

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a cif file
  file_cif <- system.file("extdata", "example.cif", package = "IFCdata")
  ## read 1st IFD
  IFD_first <- getIFD(fileName = file_cif, offsets = "first")
  ## show information contained in 1st IFD
  print(sapply(IFD_first[[1]]$tags, FUN=function(x) x))
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

---

getInfo *IFC File Information Extraction*

---

**Description**

Retrieves rich information from RIF, CIF and DAF files.

**Usage**

```
getInfo(  
  fileName,  
  from = c("acquisition", "analysis")[2],  
  verbose = FALSE,  
  verbosity = 1,  
  warn = TRUE,  
  force_default = TRUE,  
  cifdir = dirname(fileName),  
  ntry = +Inf,  
  ...  
)
```

**Arguments**

fileName	path to file..
from	whether to extract information from 'acquisition' or 'analysis'. Default is 'analysis'.
verbose	whether to display information (use for debugging purpose). Default is FALSE.
verbosity	quantity of information print to console when verbose is TRUE; 1: normal, 2: rich. Default is 1.
warn	whether to send warning message when trying to read 'analysis' information from a 'rif' file. Default is TRUE.
force_default	when display information can't be retrieved whether to use default values. Default is TRUE.
cifdir	the path of the directory to initially look to cif file. Default is dirname(fileName). Only apply when 'fileName' is a .daf file.
ntry	number of times <code>getInfo</code> will be allowed to find corresponding cif file. Default is +Inf. Only apply when 'fileName' is a .daf file. If cif can't be found, but 'ntry' is reached, then an error will be thrown.
...	other arguments to be passed.

**Value**

a list of information (open .daf file in a text editor for more details) about input fileName of class 'IFC\_info' and 'acquisition' or 'analysis', whose members are:  
-objcount, number of object in file,

- date, date of file creation,
- instrument, instrument identification,
- sw\_raw, version of software for raw data,
- sw\_processed, version of software for processed data,
- channelwidth, default channel width in pixel,
- in\_use, channels used,
- brightfield, whether brightfield is applied on channels and its intensity,
- illumination, laser illumination parameters,
- collectionmode, the collection mode,
- magnification, magnification used,
- coremode, the core mode,
- evmode, the high gain mode,
- CrossTalkMatrix, compensation matrix applied,
- ChannelPresets, channel preset,
- ImageDisplaySettings, image display settings,
- Images, information about colors, range and channels,
- masks, masks defined,
- ViewingModes, modes of visualization,
- checksum, checksum computed,
- Merged\_rif, character vector of path of files used to create rif, if input file was a merged,
- Merged\_cif, character vector of path of files used to create cif, if input file was a merged,
- XIF\_test, integer defining XIF type,
- checksum, integer corresponding to file checksum,
- fileName, path of fileName input,
- fileName\_image, path of fileName\_image.

### Examples

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  info <- getInfo(fileName = file_daf, from = "analysis")
  ## show some information
  print(info$Images)
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

---

getOffsets

*RIF/CIF File Image Field Directories Offsets Extraction*

---

### Description

Extracts offsets of the IFDs (Image Field Directories) within a XIF file. Users are highly encouraged to read TIFF specifications to have a better understanding about what offsets and IFDs are.

**Usage**

```
getOffsets(fileName, fast = TRUE, display_progress = TRUE, verbose = FALSE)
```

**Arguments**

fileName	path to file.
fast	whether to fast extract objects or not. Default is TRUE. Meaning that offsets will be extracting expecting that objects are stored in ascending order. A message will be thrown since fast extraction method does not ensure correct mapping between objects and offsets. If set to FALSE, all object_ids will be scanned from 'fileName' to ensure extraction of desired offsets.
display_progress	whether to display a progress bar. Default is TRUE.
verbose	whether to display information (use for debugging purpose). Default is FALSE.

**Details**

Offsets are byte positions of IFDs found within RIF or CIF file. For more details see TIFF specifications.

**Value**

an integer vector of class 'IFC\_offset' of IFDs offsets found in XIF file.

**Source**

TIFF 6.0 specifications archived from web <https://web.archive.org/web/20211209104854/https://www.adobe.io/open/standards/TIFF.html>

**Examples**

```
if(requireNamespace("IFCdata", quietly = TRUE)) {  
  ## use a cif file  
  file_cif <- system.file("extdata", "example.cif", package = "IFCdata")  
  system.time(offsets_fast <- getOffsets(fileName = file_cif, fast = TRUE))  
  system.time(offsets_slow <- getOffsets(fileName = file_cif, fast = FALSE))  
  identical(offsets_fast, offsets_slow)  
} else {  
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',  
                  'https://gitdemont.github.io/IFCdata/',  
                  'to install extra files required to run this example.'))  
}
```

---

inv\_smoothLinLog      *Inverse Smooth LinLog Transformation*

---

### Description

Gets values back just to their original values before applying smoothLinLog.

### Usage

```
inv_smoothLinLog(x, hyper = 1000, base = 10, lin_comp = log(base))
```

### Arguments

x	A numeric vector.
hyper	value where transition between Lin/Log is applied.
base	base of Log scale.
lin_comp	value that is used to smooth transition between Lin/Log. Default is log(base).

### Value

the inverse smoothLinLog transformation of the input.

---

objectCleanse      *Object Cleanser*

---

### Description

Removes abnormalities (clipped/debris) from image.

### Usage

```
objectCleanse(mat, msk, add_noise = TRUE, random_seed = NULL, bg = 0, sd = 0)
```

### Arguments

mat	a numeric matrix (image).
msk	a numeric matrix (mask identifying abnormalities).
add_noise	if TRUE adds normal noise to background using rnorm(), from <b>Rcpp</b> . Default is TRUE.
random_seed	a list of elements to pass to <a href="#">set.seed</a> or a single value, interpreted as an integer, or NULL to be used when 'add_noise' is set to TRUE. Default is NULL. Note that NA_integer_ or list(seed = NA_integer_) can be used to not call <a href="#">set.seed</a> at all.
bg	mean value of the background added if add_noise is TRUE. Default is 0.
sd	standard deviation of the background added if add_noise is TRUE. Default is 0.

**Value**

According to `msk`, pixel values in `mat` are substituted by either `bg` [`add_noise == FALSE`] or `rnorm(n = prod(dim(mat)), mean=bg, sd=sd)` [`add_noise == TRUE`].

---

<code>objectDisplay</code>	<i>Object Display</i>
----------------------------	-----------------------

---

**Description**

This function is intended to display object extracted by [objectExtract](#).

**Usage**

```
objectDisplay(
  image,
  input_range = c(0, 4095),
  full_range = FALSE,
  force_range = FALSE,
  gamma = 1,
  color = "Green",
  dpi = 300
)
```

**Arguments**

<code>image</code>	An object extracted by <a href="#">objectExtract</a> of class 'IFC_img' or 'IFC_msk'. Note that a matrix with finite values can also be used.
<code>input_range</code>	a finite numeric vector of 2 values, sets the range of the input intensity values. Values exceeding this range are clipped. Default is 'c(0, 4095)'.
<code>full_range</code>	if 'full_range' is TRUE, then 'input_range' will be set to 'c(0, 4095)' and 'gamma' forced to 1. Default is FALSE.
<code>force_range</code>	if 'force_range' is TRUE, then 'input_range' will be adjusted to object range in [-4095, +inf] and 'gamma' forced to 1. Default is FALSE. Note that this parameter takes the precedence over 'input_range' and 'full_range'.
<code>gamma</code>	gamma correction. Default is 1, for no correction.
<code>color</code>	a color. Default is "Green".
<code>dpi</code>	display resolution. Default is 300.

**Details**

If input 'image' is of class 'IFC\_img' or 'IFC\_msk', then if 'input\_range', 'full\_range', 'force\_range', 'gamma' and / or 'color' parameters is/are missing, it/they will be extracted from 'image' attributes. If input 'image' is not of one of class 'IFC\_img' or 'IFC\_msk', then `force_range` will be forced to TRUE.

An error will be thrown if input image contains non finite values.

**Value**

it invisibly returns NULL

---

objectExtract

*Object Extraction*

---

**Description**

Extracts / Decompress objects stored in RIF or CIF Files.

**Usage**

```
objectExtract(ifd, param, verbose = FALSE, bypass = FALSE, ...)
```

**Arguments**

ifd	list of sub elements of IFD data information extracted by <code>getIFD</code> . This parameter can't be missing.
param	object of class 'IFC_param', containing extraction parameters defined by <code>objectParam</code> . This argument is not mandatory but it may allow to save time for repeated image export on same file. If this parameter is missing, <code>objectExtract</code> will use extra ... to pass arguments to <code>objectParam</code> to control object extraction. However, if 'param' is provided, '...' will be ignored.
verbose	whether to display information (use for debugging purpose). Default is FALSE.
bypass	whether to bypass checks on 'ifd' and 'param'. Default is FALSE.
...	other arguments to be passed to <code>objectParam</code> . If 'param' is not provided then '...' will be used to compute 'param'. /!\ If not any of 'fileName', 'info' can be found in '...' then <code>attr(ifd, "file-Name_image")</code> will be used as 'fileName' input parameter to pass to <code>objectParam</code> .

**Value**

A list (for every extracted objects) of list (for every exported channels) depending on "export" parameter:

- "matrix", a matrix when 'mode' is set to "raw" or "gray" OR an array when 'mode' == "rgb",
- "base64", a data-uri string,
- "file", an invisible file path corresponding to the location of exported file(s).

**Source**

For image decompression, Lee Kamentsky's code porting from <https://github.com/ome/bioformats/blob/4146b9a1797501f0fec7d6cfe69124959bff96ee/components/formats-bsd/src/loci/formats/in/FlowSightReader.java>  
cited in [https://linkinghub.elsevier.com/retrieve/pii/S1046-2023\(16\)30291-2](https://linkinghub.elsevier.com/retrieve/pii/S1046-2023(16)30291-2)

BSD implementations of Bio-Formats readers and writers

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## Examples

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a cif file
  file_cif <- system.file("extdata", "example.cif", package = "IFCdata")
  cif_offs <- getOffsets(fileName = file_cif, fast = TRUE)
  ## extract information
  info <- getInfo(fileName = file_cif, from = "analysis")
  ## retrieve number of objects stored
  nobj <- as.integer(info$objcount)
  ## randomly subset the offsets of at most 5 "img" objects
  sel = sample(0:(nobj-1), min(5, nobj))
  sub_offs <- subsetOffsets(cif_offs, objects = sel, image_type = "img")
  ## read IFDs from these "img" objects
  IFDs <- getIFD(fileName = file_cif, offsets = sub_offs)
  ## extract raw data of these "img" objects to matrix
  raw = objectExtract(ifd = IFDs, info = info, mode = "raw",
    export = "matrix")
  ## extract base64 "rgb" colored version of these "img" objects to base64
  b64 = objectExtract(ifd = IFDs, info = info, mode = "rgb",
    export = "base64", base64_id = TRUE,
    write_to = "example_%o_%c.png")
  ## use DisplayGallery to show the first "img" objects and play with ... extra parameters
  ## force_range, add_noise, selection, composite, see objectParam
```

```

DisplayGallery(info = info, offsets = cif_offs, objects = sel,
               base64_id = TRUE, write_to = "example_%o_%c.png",
               force_range = c(FALSE,TRUE,FALSE,TRUE), add_noise = FALSE,
               selection = c(1,2,4,6), composite = "1.7/4.3")
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                 'https://gitdemont.github.io/IFCdata/',
                 'to install extra files required to run this example.'))
}

```

---

objectParam

*Object Extraction Parameters Definition*


---

## Description

Defines 'IFC\_object' object extraction parameters.

## Usage

```

objectParam(
  ...,
  info,
  mode = c("rgb", "gray", "raw")[3],
  export = c("file", "matrix", "base64")[2],
  write_to,
  base64_id = FALSE,
  base64_att = "",
  overwrite = FALSE,
  composite = "",
  selection = "all",
  size = c(0, 0),
  force_width = TRUE,
  random_seed = NULL,
  removal = "none",
  add_noise = TRUE,
  full_range = FALSE,
  force_range = FALSE,
  spatial_correction = FALSE
)

```

## Arguments

...	arguments to be passed to <a href="#">getInfo</a> , only if 'info' is not provided.
info	object of class 'IFC_info', rich information extracted by <a href="#">getInfo</a> . This argument is not mandatory but it may allow to save time for repeated image export on same file. If missing, the default, 'info' will be extracted thanks to '...'.
mode	color mode export. Either "rgb", "gray" or "raw". Default is "raw". Note that "raw" is only possible when 'export' is "matrix".

export	format mode export. Either "file", "matrix", "base64". Default is "matrix".
write_to	used when export is "file" or "base64" to compute respectively exported file name or base64 id attribute. Exported "file" extension and "base64" MIME type will be deduced from this pattern. Allowed export are ".bmp", ".jpg", ".jpeg", ".png", ".tif", ".tiff". Note that '.bmp' are faster but not compressed producing bigger data. Placeholders, if found, will be substituted: -%d: with full path directory -%p: with first parent directory -%e: with extension (without leading .) -%s: with shortname (i.e. basename without extension) -%o: with object_id -%c: with channel_id A good trick is to use: -%d/%s/%s_%o_%c.tiff", when 'export' is "file" -%o_%c.bmp", when 'export' is "base64". Note that if missing and 'export' is not "file", 'write_to' will be set to "%o_%c.bmp".
base64_id	whether to add id attribute to base64 exported object. Default is FALSE. Only applied when export is "base64".
base64_att	attributes to add to base64 exported object. Default is "". Only applied when export is "base64". For example, use "class=draggable". Note that id (if base64_id is TRUE) and width and height are already used.
overwrite	only apply when 'export' is "file" whether to overwrite file or not. Default is FALSE.
composite	character vector of image composite. Default is "", for no image composite. Should be like "1.05/2.4/4.55" for a composition of 5 perc. of channel 1, 40 perc. of channel 2 and 50 perc. of channel 55. Note that channels should have been acquired and final image composition should be 100 perc., otherwise an error is thrown. Note that each composite will be appended after 'selection'.
selection	physical channels to extract. Note that this parameter will be ordered. Default is "all" to extract all acquired channels. Use "none" to only extract composite.
size	a length 2 integer vector of final dimensions of the image, height 1st and width 2nd. Default is c(0,0) for no change.
force_width	whether to use information in 'info' to fill size. Default is TRUE. When set to TRUE, width of 'size' argument will be overwritten.
random_seed	a list of elements to pass to <a href="#">set.seed</a> or a single value, interpreted as an integer, or NULL to be used when 'add_noise' is set to TRUE. Default is NULL. Note that NA_integer_ or list(seed = NA_integer_) can be used to not call <a href="#">set.seed</a> at all.
removal	removal method: Either "none", "raw", "clipped", "masked", "MC". -"none", to keep image as is -"raw", to keep image as is, it provides a convenient way to retrieve "raw" value for the mask.

	-"clipped", to remove clipped object from image. -"masked", to only keep masked object from image. -"MC", to only keep MC masked object from image. This parameter will be repeated with rep_len() from <b>base</b> for every physical channel that needs to be extracted according to 'selection' and 'composite' parameters.
add_noise	if TRUE adds normal noise to background using rnorm(), from <b>Rcpp</b> . Default is TRUE. Note that it is better to set it to FALSE when 'removal' is "masked" or "MC". Doing so will allow to place masked object in a zero filled background, otherwise background will still be filled with noise. This parameter will be repeated with rep_len() from <b>base</b> for every physical channel that needs to be extracted according to 'selection' and 'composite' parameters.
full_range	only apply when mode is not "raw", if full_range is TRUE, then [0,4095] range will be kept. Default is FALSE. It is like "raw" mode but allowing normalization to [0,1]. This parameter will be repeated with rep_len() from <b>base</b> for every physical channel that needs to be extracted according to 'selection' and 'composite' parameters.
force_range	only apply when mode is not "raw", if force_range is TRUE, then range will be adjusted to object range in [-4095, +inf] resulting in normalization. Default is FALSE. Note that this parameter takes the precedence over 'full_range'. This parameter will be repeated with rep_len() from <b>base</b> for every physical channel that needs to be extracted according to 'selection' and 'composite' parameters.
spatial_correction	only apply on RIF file, whether to apply spatial correction. Default is FALSE.

### Details

when a mask is detected, 'add\_noise', 'full\_range' and 'force\_range' are set to FALSE.

### Value

an object of class 'IFC\_param'.

---

paletteIFC

*R/IDEAS Color Palette Mapping*

---

### Description

Maps colors between IDEAS and R.

**Usage**

```
paletteIFC(
  x = c("", "palette", "palette_R", "to_light", "to_dark")[1],
  col = "White"
)
```

**Arguments**

`x` either "", "palette", "palette\_R", to\_light, to\_dark. Default is "".

`col` a compatible color to transform to color or lightModeColor. Default is "White".  
 if 'x' == to\_light, function will convert 'col' to lightModeColor.  
 if 'x' == to\_dark, function will convert 'col' to color.  
 if 'col' is not found or 'x' is anything else then a data.frame of compatible colors is returned.

**Value**

IFC palette of available colors.

---

 plotGraph

---

*Plot and Stats Computation for IFC Graph*


---

**Description**

Computes plot and stats from a IFC graph

**Usage**

```
plotGraph(
  obj,
  graph,
  draw = FALSE,
  stats_print = draw,
  color_mode = c("white", "black")[1],
  add_key = "panel",
  precision = c("light", "full")[1],
  trunc_labels = 38,
  trans = "asinh",
  bin,
  viewport = "ideas",
  backend = "lattice",
  ...
)
```

**Arguments**

obj	an 'IFC_data' object extracted with features extracted.
graph	a graph from 'obj' or a list that can be coerced by <code>buildGraph</code> .
draw	whether to draw plot or not. Default is FALSE.
stats_print	whether to print stats or not. Default is given by 'draw' argument.
color_mode	whether to extract colors from 'obj' in white or black mode. Default is "white".
add_key	whether to draw a "global" key under title or in the first "panel" or "both". Default is "panel". Accepted values are either: FALSE, "panel", "global", "both" or c("panel", "global"). Note that it only applies when display is seen as overlaying populations.
precision	when graphs is a 2D scatter with population overlay, this argument controls amount of information displayed. Default is "light". -"light", the default, will only display points of same coordinates that are among the other layers. -"full" will display all the layers.
trunc_labels	maximum number of characters to display for labels. Default is 38.
trans	the name of a transformation function for density graphs. If missing the default, the BasePop[[1]]\$densitytrans, if any, will be retrieved, otherwise "asinh" will be used.
bin	number of bin used for histogram / density. Default is missing.
viewport	either "ideas", "data" or "max" defining limits used for the graph. Default is "ideas". -"ideas" will use same limits as the one defined in ideas. -"data" will use data to define limits. -"max" will use data and regions drawn to define limits.
backend	backend used for drawing. Allowed are "lattice", "base", "raster", "raster-edge", "raster-hybrid". Default is "lattice". -"lattice" is the original one used in <b>IFC</b> using <b>lattice</b> , -"base" will produce the plot using <b>base</b> , -"raster" uses "base" for plotting but 2D graphs points will be produced as <code>rasterImage</code> . This has the main advantage of being super fast allowing for plotting a huge amount of points while generating smaller objects (in bytes). However, plot quality is impacted with "raster" method and resizing can lead to unpleasant looking. -"raster-edge" is the same as "raster" except that points outside of limits will be drawn onto the edge. -"raster-hybrid" uses "raster" for drawing on top of a first "raster-edge" pass to produce an hybrid display.
...	other arguments to be passed.

**Value**

it invisibly returns a list whose members are:

- stats, a table of statistics computed for the graph, if 'stats\_print' was TRUE,
- input, a list with input parameters.

---

popsCompute	<i>IFC_pops Computation</i>
-------------	-----------------------------

---

### Description

Function used to compute 'IFC\_pops' object  
It requires pops, regions and features.

### Usage

```
popsCompute(  
  pops,  
  regions,  
  features,  
  pnt_in_poly_algorithm = 1,  
  pnt_in_poly_epsilon = 1e-12,  
  display_progress = TRUE,  
  title_progress = "",  
  ...  
)
```

### Arguments

pops	list of populations that will be coerced by <a href="#">buildPopulation</a> .
regions	an object of class 'IFC_regions', list of regions.
features	an object of class 'IFC_features', data.frame of features.
pnt_in_poly_algorithm	algorithm used to determine if object belongs to a polygon region or not. Default is 1. Note that for the moment only 1(Trigonometry) is available.
pnt_in_poly_epsilon	epsilon to determine if object belongs to a polygon region or not. It only applies when algorithm is 1. Default is 1e-12.
display_progress	whether to display a progress bar. Default is TRUE.
title_progress	character string, giving the title of the progress bar. Default is "".
...	other arguments to be passed.

### Value

an object of class 'IFC\_pops'.

### Source

For pnt\_in\_poly\_algorithm, Trigonometry, is an adaptation of Jeremy VanDerWal's code <https://github.com/jjvanderwal/SDMTools>

popsCopy

*Copy Populations from One File to Another File***Description**

Copies populations from a DAF file into a copy of another DAF file. Only creates new file with copied population.

**Usage**

```
popsCopy(
  from,
  into,
  write_to,
  pops,
  use_regex = FALSE,
  overwrite = FALSE,
  append_name = TRUE,
  offset = 0,
  endianness = .Platform$endian,
  verbose = FALSE,
  ...
)
```

**Arguments**

from	path to file to copy populations from.
into	path to file that will be used as a template to copy population into. Caution, it is mandatory that 'into' contains 'from' starting at 'offset'.
write_to	pattern used to export file. Placeholders, like "%d/%s_fromR.%e", will be substituted: -%d: with full path directory of 'into' -%p: with first parent directory of 'into' -%e: with extension of 'into' (without leading .) -%s: with shortname from 'into' (i.e. basename without extension). Exported file extension will be deduced from this pattern. Note that it has to be a .daf.
pops	regular expression or vector of desired populations present in 'from'. If missing, the default, all populations found will be copied. If given but not found, a warning will be sent.
use_regex	whether to use regex to pick up population into 'from'. Default is FALSE.
overwrite	whether to overwrite existing file or not. Default is FALSE. Note that if TRUE, it will overwrite exported file if path of 'into' and deduced from 'write_to' arguments are different. Otherwise, you will get an error saying that overwriting source file is not allowed.

Note also that an original file, i.e. generated by IDEAS(R) or INSPIRE(R), will never be overwritten. Otherwise, you will get an error saying that overwriting original file is not allowed.

append_name	whether to append_name basename(from) to exported populations. Default is TRUE.
offset	Object number of 1st object of 'from' in 'into'. Default is 0.
endianness	The endian-ness ("big" or "little") of the target system for the file. Default is .Platform\$endian. Endianness describes the bytes order of data stored within the files. This parameter may not be modified.
verbose	whether to display information (use for debugging purpose). Default is FALSE.
...	Other arguments to be passed.

### Details

Populations are exported as tagged populations.

### Value

a new file is created containing exported populations.  
It invisibly returns full path of exported file.

---

popsGetObjectsIds      *IFC\_pops Object Numbers*

---

### Description

Retrieves objects ids belonging to a population.

### Usage

```
popsGetObjectsIds(obj, pop = "")
```

### Arguments

obj	an 'IFC_data' object extracted with features extracted.
pop	a population name from 'obj'. Default is "". If left as is or not found an error is thrown displaying all available population in 'obj'.

### Value

An integer vector is returned

**Examples**

```

if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  daf <- ExtractFromDAF(fileName = file_daf)
  obj <- popsGetObjectsIds(obj = daf, pop = names(daf$pops)[length(daf$pops)])
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}

```

---

popsNetwork

*IFC\_pops Network Display*


---

**Description**

Builds and displays populations network.

**Usage**

```

popsNetwork(
  obj,
  hierarchical = TRUE,
  color_mode = "white",
  highlight = NULL,
  seed = NULL,
  direction = "LR",
  weighted = TRUE,
  ...
)

```

**Arguments**

obj	an 'IFC_data' object extracted with features extracted.
hierarchical	whether to display network using a hierarchical layout or not. Default is TRUE.
color_mode	Whether to extract colors from 'obj' in "white" or "black" mode. Default is "white".
highlight	population to permanently highlight. If found in 'obj', this population will be displayed with its color. Default is NULL.
seed	If you provide a seed manually, the layout will be the same every time. Default is NULL.
direction	The direction of the hierarchical layout. Default is 'LR'. The available options are: 'UD', 'DU', 'LR', 'RL'. To simplify: up-down, down-up, left-right, right-left.
weighted	whether to scale population's node size according to count. Default is TRUE.
...	other argument to be passed.

**Value**

a **visNetwork** object.

**Examples**

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  daf <- ExtractFromDAF(fileName = file_daf)
  popsNetwork(obj = daf)
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

---

popsRename

*Populations Renaming*

---

**Description**

Renames populations in an 'IFC\_data' object

**Usage**

```
popsRename(
  obj,
  old_names = character(),
  new_names = character(),
  loops = 10L,
  verbose = TRUE,
  ...
)
```

**Arguments**

obj	an 'IFC_data'.
old_names	character vector of name(s) of population(s) to rename inside 'obj'. Default is character().
new_names	character vector of desired new population(s) name(s). Default is character().
loops	a positive integer specifying the maximum number of recursive loops before raising an error. Default is 10L.
verbose	whether to show a final message about the renaming. Default is TRUE.
...	other arguments to be passed.

**Value**

an object of class 'IFC\_data'.

readFCS

*FCS File Parser***Description**

Parse data from Flow Cytometry Standard (FCS) compliant files.

**Usage**

```
readFCS(
  fileName,
  options = list(header = list(start = list(at = 0, n = 6), space = list(at = 6, n =
    4), text_beg = list(at = 10, n = 8), text_end = list(at = 18, n = 8), data_beg =
    list(at = 26, n = 8), data_end = list(at = 34, n = 8)), apply_scale = TRUE, dataset =
    1, force_header = FALSE, text_only = FALSE, text_check = FALSE, text_empty = FALSE,
    text_trim = "none"),
  display_progress = TRUE,
  ...
)
```

**Arguments**

fileName	path to file.
options	list of options used to parse FCS file. It should contain (otherwise, it will be filled with the default values listed below): <ul style="list-style-type: none"> <li>- header, a list whose members define the "at" offset from header\$start\$at and the "n" number of bytes to extract:           <ul style="list-style-type: none"> <li>- start: where to start reading current FCS dataset. Default is list(at = 0, n = 6),</li> <li>- space: where to retrieve space. Default is list(at = 6, n = 4),</li> <li>- text_beg: where to retrieve file text segment beginning. Default is list(at = 10, n = 8),</li> <li>- text_end: where to retrieve file text segment end. Default is list(at = 18, n = 8),</li> <li>- data_beg: where to retrieve file data segment beginning. Default is list(at = 26, n = 8),</li> <li>- data_end: where to retrieve file data segment end. Default is list(at = 34, n = 8),</li> </ul> </li> <li>- apply_scale, whether to apply data scaling. It only applies when fcs file is stored as DATATYPE "I". Default is TRUE.</li> <li>- dataset, (coerced to) an ordered vector of unique indices of desired dataset(s) to extract. Default is 1 to extract only the first dataset, whereas NULL allows to extract all available datasets.</li> <li>- force_header, whether to force the use of header to determine the position of data segment. Default is FALSE, for using positions found in "\$BEGINDATA" and "\$ENDDATA" keywords.</li> <li>- text_only, whether to only extract text segment. Default is FALSE.</li> </ul>

- text\_check, whether to check text segment is compliant with FCS specifications. Default is FALSE.
- text\_empty, whether to allow empty values when parsing text segment. Default is FALSE.
- text\_trim, remove whitespace in keywords names. Default is "none". Allowed are "both", "left", "right" and "none".

display\_progress  
whether to display a progress bar. Default is TRUE.

... other arguments to be passed.

### Details

'options' may be tweaked according to file type, instrument and software used to generate it. Default 'options' should allow to read most files.  
'options' members with the exception of 'header' may be passed thanks to '...'

### Value

a list whose elements are lists for each dataset stored within the file.  
each sub-list contains:

- header, list of header information corresponding to 'options'
- delimiter, unique character used to separate keyword-value pairs
- text, list of keywords values,
- data, data.frame of values.

### Source

Data File Standard for Flow Cytometry, version FCS 3.1 from Spidlen J. et al. available at doi: [10.1002/cyto.a.20825](https://doi.org/10.1002/cyto.a.20825).

---

readIFC	<i>IFC Files Generic Reader</i>
---------	---------------------------------

---

### Description

Reads IFC data from IFC files no matter if they are FCS, DAF, RIF or CIF.

### Usage

```
readIFC(fileName, ...)
```

### Arguments

fileName path to file.  
... arguments to pass to [ExtractFromDAF](#) or [ExtractFromXIF](#) or [ExtractFromFCS](#).

**Details**

If input 'fileName' is a DAF file [ExtractFromDAF](#) will be used to read the file.

If it is a CIF or RIF file [readIFC](#) will use [ExtractFromXIF](#).

Finally, if 'fileName' is not a DAF, nor a CIF, nor a RIF file [readIFC](#) will use [ExtractFromFCS](#).

**Value**

an object of class 'IFC\_data'.

**Examples**

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a rif file, but you can also read daf or cif
  file_rif <- system.file("extdata", "example.rif", package = "IFCdata")
  rif <- readIFC(fileName = file_rif)
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

---

 smoothLinLog

*Smooth LinLog Transformation*


---

**Description**

Transforms values in lin-log

**Usage**

```
smoothLinLog(x, hyper = 1000, base = 10, lin_comp = log(base))
```

**Arguments**

x	A numeric vector.
hyper	value where transition between Lin/Log is applied.
base	base of Log scale.
lin_comp	value that is used to smooth transition between Lin/Log. Default is log(base).

**Value**

the smoothLinLog transformation of the input.

---

subsetOffsets	<i>IFC_offset Subsetting</i>
---------------	------------------------------

---

## Description

Subsets 'IFC\_offset'

## Usage

```
subsetOffsets(offsets, objects, image_type = c("img", "msk"))
```

## Arguments

offsets	object of class 'IFC_offset' to subset.
objects	integer vector, IDEAS objects ids numbers to extract.
image_type	image_type of desired offsets. Default is c("img", "msk"). Allowed are "img" and/or "msk".

## Value

a class 'IFC\_offset' integer vector or empty integer() if objects are outside of offsets.

## Examples

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  ## use a cif file
  file_cif <- system.file("extdata", "example.cif", package = "IFCdata")
  ## extract offsets
  offsets <- getOffsets(fileName = file_cif)
  ## subset offsets of the 4 first "img" objects
  sub_offs <- subsetOffsets(offsets = offsets, objects = 0:3, image_type = "img")
  ## show subsetted offsets' structure
  str(sub_offs)
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

writeIFC

*IFC Files Generic Writer***Description**

Writes IFC data to DAF and subsets or merges RIF/CIF Files.

**Usage**

```
writeIFC(fileName, ...)
```

**Arguments**

fileName	path to file.
...	arguments to pass to <a href="#">ExportToDAF</a> , <a href="#">ExportToXIF</a> , <a href="#">ExportToFCS</a> , or <a href="#">data_to_DAF</a> .

**Details**

If an 'IFC\_data' object is provided as 'fileName' or in '...' [ExportToFCS](#) or [data\\_to\\_DAF](#) will be used to export object. Otherwise, if 'fileName' is a DAF file [ExportToDAF](#) will be used to write file whereas if it is RIF or CIF file(s) [writeIFC](#) will use [ExportToXIF](#).

**Value**

it invisible returns the path of exported file.

**Examples**

```
if(requireNamespace("IFCdata", quietly = TRUE)) {
  tmp <- tempdir(check = TRUE)
  ## use a daf file
  file_daf <- system.file("extdata", "example.daf", package = "IFCdata")
  ## create a tagged population named test with 1st object
  pop <- buildPopulation(name = "test", type = "T", obj = 0)
  writeIFC(file_daf, write_to = paste0(tmp, "\\test_write.daf"),
           overwrite = TRUE, pops = list(pop))
  ## use a rif file, but you can also use a cif
  file_rif <- system.file("extdata", "example.rif", package = "IFCdata")
  writeIFC(fileName = file_rif, write_to = paste0(tmp, "\\test_write.rif"),
           overwrite = TRUE, objects = 0)
} else {
  message(sprintf('Please run `install.packages("IFCdata", repos = "%s", type = "source")` %s',
                  'https://gitdemont.github.io/IFCdata/',
                  'to install extra files required to run this example.'))
}
```

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