

Package: CyFj11 (via r-universe)

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Type Package

Title Parse FlowJo V11 Workspace Files and Export to FlowJo V10

Version 0.99.113

Description Provides functions to parse FlowJo v11 workspace files (.flowjo) and extract gating information, populations, and associated FCS files. Includes utilities for exporting data to FlowJo v10 workspace format. The package enables bidirectional data flow between FlowJo and R/Bioconductor, facilitating reproducible analysis workflows.

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Depends R (>= 4.5.0)

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BugReports <https://github.com/C3BI-pasteur-fr/CyFj11/issues>

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export_flowjo10_workspace
<i>Export GatingSet to FlowJo v10 Workspace</i>

Description

Export GatingSet to FlowJo v10 Workspace

Usage

```
export_flowjo10_workspace(  
  gating_set,  
  output_path,  
  workspace_name = NULL,  
  fcs_root = NULL,  
  overwrite = FALSE  
)
```

Arguments

gating_set	A GatingSet object to export. A named list of GatingSets, as returned by fj11_to_gatingset , is also accepted and merged with flowWorkspace::merge_list_to_gs() before export.
output_path	Path where the .xml file should be created
workspace_name	Optional name for the workspace
fcs_root	Optional base directory for FCS files. If provided, FCS files will be written there and URIs in the WSP will reference that location. If NULL, uses the actual paths found in the GatingSet.
overwrite	Logical. When fcs_root is supplied and FCS files already exist in that directory, FALSE (default) aborts with an error; TRUE silently replaces existing files.

Value

Logical indicating success

Examples

```
# Export a GatingSet to FlowJo v10 XML format
ws_path <- system.file("extdata", "min_test.flowjo", package = "CyFj11")
fcs_path <- system.file("extdata", package = "CyFj11")
ws <- read_flowjo11_workspace(ws_path)
gs <- fj11_to_gatingset(ws, group_name = 1, path = fcs_path)
out_file <- tempfile(fileext = ".xml")
export_flowjo10_workspace(gs, out_file)
file.exists(out_file)
```

fj11_to_gatingset	<i>Convert FlowJo v11 Workspace to GatingSet</i>
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Description

Parses a FlowJo v11 workspace and creates a GatingSet object with gating hierarchy, compensation, and transformations. Supports biexponential (Biex) transformations which are mapped to logicle transforms.

Usage

```
fj11_to_gatingset(
  fj11_workspace,
  group_name = NULL,
  subset = list(),
  execute = TRUE,
  path = NULL,
  cytoset = NULL,
  backend_dir = tempdir(),
  backend = c("h5", "tile"),
  include_gates = TRUE,
  compensation = NULL,
  additional.keys = "$TOT",
  additional.sampleID = FALSE,
  keywords = character(),
  keyword.ignore.case = FALSE,
  channel.ignore.case = FALSE,
  extend_val = 0,
  extend_to = -4000,
  leaf.bool = TRUE,
  include_empty_tree = FALSE,
  correct_faulty_gate = 0,
  transform = TRUE,
  use_transformed_coords = transform,
  max_search_depth = 5,
  stop_on_multiple = TRUE,
  mc.cores = 1,
```

```

    strip_comp_prefix = TRUE,
    sanitize_slashes = TRUE,
    ...
)

```

Arguments

fj11_workspace	List returned by read_flowjo11_workspace() containing the complete workspace structure
group_name	Character or numeric. Name or index of the sample group to import. If NULL, will list available groups interactively.
subset	Numeric vector, character vector of FCS filenames, or expression to filter samples. See Details.
execute	Logical. Should gates be executed immediately? Default TRUE. If FALSE, creates GatingSet structure without computing cell counts.
path	Character. Root directory to search for FCS files. Required if FCS files are not in workspace location.
cytoset	A cytoset object providing alternative data source (instead of FCS files). Useful for preprocessed data.
backend_dir	Directory for storing h5 backend data. Default is tempdir().
backend	Character. Storage backend, either "h5" or "tile". Default "h5".
include_gates	Logical. Should gates be imported? Default TRUE.
compensation	Compensation object, matrix, data.frame, or named list of these. Overrides workspace compensation. Names should match sample GUIDs.
additional.keys	Character vector of FCS keywords to include in sample GUID (concatenated with filename). Default is "\$TOT".
additional.sampleID	Logical. Include FlowJo sample ID in GUID? Default FALSE.
keywords	Character vector of keywords to extract as pData.
keyword.ignore.case	Logical. Case-insensitive keyword matching? Default FALSE.
channel.ignore.case	Logical. Case-insensitive channel matching? Default FALSE.
extend_val	Numeric. Threshold for extending gate coordinates. Default 0.
extend_to	Numeric. Value to extend gates to. Default -4000.
leaf.bool	Logical. Compute leaf boolean gates? Default TRUE.
include_empty_tree	Logical. Include samples without gates? Default FALSE.
correct_faulty_gate	Numerical, zero = don't correct, otherwise use this value as transformation max value and Try to correct faulty gates instead of erroring? Default TRUE.
transform	Logical. Apply transformations? Default TRUE.

```

use_transformed_coords
    Logical. Keep gate coordinates in FlowJo display (transformed) space rather
    than raw space? Default is the value of transform. Only relevant when transform
    = TRUE.
max_search_depth
    Integer. Maximum directory depth when searching for FCS files. Default 5.
stop_on_multiple
    Logical. Stop if multiple FCS files match a sample? When TRUE, stops on both
    missing files and multiple matches. When FALSE, only stops on missing files
    and continues with multiple matches. Default TRUE.
mc.cores
    Integer. Number of cores for parallel processing. Default 1.
strip_comp_prefix
    Logical. Strip "Comp-" prefix from gate parameter names when adding popula-
    tions? Default TRUE. Set to FALSE if compensation has already been applied
    and gate names should match the compensated parameter names.
sanitize_slashes
    Logical. Replace "/" with "_" in parameter names? Default TRUE (matches
    flowCore behavior). Set to FALSE if you want to preserve "/" in marker names
    (e.g., "CD3/CD4" stays as-is).
...
    Additional arguments passed to FCS parser.

```

Details

The subset argument can be:

Numeric vector: Sample indices to import

Character vector: FCS filenames to import

Expression: Logical expression to filter pData (requires keywords argument)

FlowJo v11 stores data differently than v10:

populationDefinitions: Master gate definitions

desyncTable: Per-sample gate variations (tailored gates)

groups: Sample groupings

dataSources: FCS file references

Value

A named list of GatingSet objects, one per sample. Each element contains the full gating hierarchy, gates, compensation, and transformations for that sample. To obtain a single merged GatingSet for downstream analysis, call `flowWorkspace::merge_list_to_gs(gsList)` on the returned list.

Examples

```

ws_path <- system.file("extdata", "min_test.flowjo", package = "CyFj11")
fcs_path <- system.file("extdata", package = "CyFj11")
ws      <- read_flowjo11_workspace(ws_path)
gsList  <- fj11_to_gatingset(ws, group_name = 1, path = fcs_path)
length(gsList) # Number of GatingSets created

```

get_sanitize_slashes	<i>Get slash sanitization mode</i>
----------------------	------------------------------------

Description

Check whether "/" characters in parameter names are being replaced with "_".

Usage

```
get_sanitize_slashes()
```

Value

Logical. TRUE if "/" is replaced with "_", FALSE if preserved

Examples

```
# Check current setting
is_sanitize_slashes <- get_sanitize_slashes()
```

get_verbose	<i>Get verbose mode</i>
-------------	-------------------------

Description

Check whether verbose output is currently enabled.

Usage

```
get_verbose()
```

Value

Logical. TRUE if verbose output is enabled, FALSE otherwise

Examples

```
# Check current verbose setting
is_verbose <- get_verbose()
is_verbose # Should be FALSE by default
```

`load_example_workspace`*Load Example FlowJo v11 Workspace*

Description

Loads the example FlowJo v11 workspace from `inst/extdata/min_test.flowjo` for use in tests and examples. This workspace contains a simple gating hierarchy (Ungated -> Lymphocytes -> CD8, CD3 subset) and references `sample04.fcs`.

Usage

```
load_example_workspace()
```

Value

A `flowjo11_workspace` object

Examples

```
ws <- load_example_workspace()
length(ws$samples) # Number of samples
```

`pretty_print_flowjo` *Pretty Print FlowJo Workspace*

Description

This function takes a FlowJo v11 workspace file (`.flowjo`) and extracts the JSON content, then pretty prints it to a text file with `"_pretty.json"` suffix.

Usage

```
pretty_print_flowjo(flowjo_file)
```

Arguments

`flowjo_file` Path to the FlowJo workspace file (`.flowjo`)

Value

Path to the created pretty printed JSON file

Examples

```
# Pretty print a FlowJo workspace to readable JSON
ws_path <- system.file("extdata", "min_test.flowjo", package = "CyFj11")
out_file <- pretty_print_flowjo(ws_path)
file.exists(out_file) # Verify output was created
# Clean up
unlink(out_file)
```

```
read_flowjo11_workspace
```

Read FlowJo v11 Workspace

Description

Main wrapper function to read and parse FlowJo v11 workspace files.

Usage

```
read_flowjo11_workspace(workspace_path)
```

Arguments

`workspace_path` Path to the FlowJo workspace file (.flowjo)

Value

Parsed workspace object containing manifest and JSON data

Examples

```
ws_path <- system.file("extdata", "min_test.flowjo", package = "CyFj11")
ws <- read_flowjo11_workspace(ws_path)
length(ws$samples) # Number of samples in workspace
names(ws$groups)   # Group names
```

```
set_sanitize_slashes Set parameter name slash sanitization behavior
```

Description

Control whether "/" characters in parameter/marker names are automatically replaced with ". This is important because flowCore sanitizes parameter names by replacing "/" with "." when reading FCS files.

Usage

```
set_sanitize_slashes(v)
```

Arguments

`v` Logical. TRUE to replace "/" with "_" (default), FALSE to preserve "/"

Details

By default, this is TRUE to match flowCore's behavior, ensuring that gate parameter names match the flowFrame column names. Set to FALSE if you want to preserve "/" in marker names (e.g., "CD3/CD4" stays as-is).

Value

Invisible NULL. Called for side effects.

Examples

```
# Preserve "/" in marker names
set_sanitise_slashes(FALSE)
# Use default behavior (replace "/" with "_")
set_sanitise_slashes(TRUE)
```

`set_verbose`*Set verbose mode*

Description

Enable or disable verbose output for debugging and monitoring package operations. When enabled, the package will print detailed information about its operations, including file processing, gate conversion, and data extraction steps.

Usage

```
set_verbose(v)
```

Arguments

`v` Logical. TRUE to enable verbose output, FALSE to disable it

Value

Invisible NULL. Called for side effects.

Examples

```
set_verbose(TRUE)
set_verbose(FALSE)
```

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