Package: CytoPipelineGUI (via r-universe)

November 25, 2026

Title GUI's for visualization of flow cytometry data analysis pipelines

Version 1.12.0

Description This package is the companion of the `CytoPipeline` package. It provides GUI's (shiny apps) for the visualization of flow cytometry data analysis pipelines that are run with `CytoPipeline`. Two shiny applications are provided, i.e. an interactive flow frame assessment and comparison tool and an interactive scale transformations visualization and adjustment tool.

License GPL-3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

BugReports https://github.com/UCLouvain-CBIO/CytoPipelineGUI/issues

URL https://uclouvain-cbio.github.io/CytoPipelineGUI

biocViews FlowCytometry, Preprocessing, QualityControl, WorkflowStep, ImmunoOncology, Software, Visualization, GUI, ShinyApps

Collate plots.R shiny-functions.R shiny-scaleTransform-module.R shiny.R CytoPipelineGUI-package.R

Depends R (>= 4.4), CytoPipeline (>= 1.9.3)

Imports shiny, plotly, ggplot2, flowCore

Suggests testthat (>= 3.0.0), vdiffr, diffviewer, knitr, rmarkdown, BiocStyle, patchwork

VignetteBuilder knitr

Config/testthat/edition 3

Config/pak/sysreqs cmake make libicu-dev libpng-dev libuv1-dev libxml2-dev libssl-dev perl zlib1g-dev

Repository Bioconductor 3.24

Date/Publication 2026-11-23 22:51:10 UTC

RemoteUrl https://github.com/bioc/CytoPipelineGUI

RemoteRef RELEASE_3_24

RemoteSha a09f7ec359ebb45bc86dff09c49fc3d1049bd451

Contents

CytoPipelineCheckApp 2
plotDiffFlowFrame 3
plotScaleTransformedChannel 6
plotSelectedFlowFrame 9
plotSelectedWorkflow 11
ScaleTransformApp 13

Index **15**

`CytoPipelineCheckApp` *interactive visualization of flow cytometry data analysis pipeline objects stored in cache*

Description

interactive visualization of flow cytometry data analysis pipeline objects stored in cache

Usage

```
CytoPipelineCheckApp(dir = ".", debug = FALSE)
```

Arguments

`dir`	the root directory into which the engine will look for existing CytoPipeline experiments
`debug`	if TRUE, will output messages on the console tracking the shiny events, for debugging purposes

Value

no return value

Examples

```
# run CytoPipeline object first

outputDir <- base::tempdir()


rawDataDir <-
    system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
```

```
sampleFiles <-
    file.path(
        rawDataDir,
        list.files(
            rawDataDir,
            pattern = "Donor"))
jsonDir <- system.file("extdata", package = "CytoPipeline")
jsonPath <- file.path(jsonDir, "pipelineParams.json")

pipL2 <- CytoPipeline(
    jsonPath,
    experimentName = experimentName,
    sampleFiles = sampleFiles)

suppressWarnings(execute(
    pipL2,
    rmCache = TRUE,
    path = outputDir))

# run shiny app

if (interactive())
    CytoPipelineCheckApp(dir = outputDir)
```

`plotDiffFlowFrame` *Plot the difference plot between two flow frames from a CytoPipeline run*

Description

Based on an experiment name, this function will gather the required flowFrames from the CytoPipeline disk cache and display a difference plot using the user chosen 1D or 2D view.

Usage

```
plotDiffFlowFrame(
  experimentNameFrom,
  experimentNameTo,
  whichQueueFrom,
  whichQueueTo,
  sampleFileFrom,
  sampleFileTo,
  path,
  flowFrameNameFrom,
  flowFrameNameTo,
  xChannelLabelFrom,
  xChannelLabelTo,
  yChannelLabelFrom,
```

```
  yChannelLabelTo,
  interactive = FALSE,
  useAllCells,
  nDisplayCells,
  useFixedLinearRange,
  linearRange,
  transfoListName = " "
)
```

Arguments

`experimentNameFrom`	the experiment name (representing a pipeline run) from which to extract the flow frame ('from' situation)
`experimentNameTo`	the experiment name (representing a pipeline run) from which to extract the flow frame ('to' situation)
`whichQueueFrom`	"pre-processing" or "scale transform" ('from' situation)
`whichQueueTo`	"pre-processing" or "scale transform" ('to' situation)
`sampleFileFrom`	in case 'whichQueueFrom' is set to 'pre-processing, which sample file to look at for the 'from' situation. This can be a number or a character. • if whichQueueFrom == "scale transform", the sampleFileFrom is ignored • if NULL and whihQueueFrom == "pre-processing", the sampleFileFrom is defaulted to the first one belonging to the experiment
`sampleFileTo`	same as sampleFileFrom, but for the 'to' situation
`path`	the root path to look for the CytoPipeline experiment cache
`flowFrameNameFrom`	for the 'from' situation, the name of the object to fetch (as referenced in the pipeline workflow)
`flowFrameNameTo`	for the 'to' situation, the name of the object to fetch (as referenced in the pipeline workflow)
`xChannelLabelFrom`	the label of the channel to be displayed on the x axis: the conventional syntax is : `channelName` + " - " + `channelMarker`
`xChannelLabelTo`	should be equal to xChannelLabelFrom (otherwise no plot is returned but NULL)
`yChannelLabelFrom`	the label of the channel to be displayed on the y axis: the conventional syntax is : `channelName` + " - " + `channelMarker`
`yChannelLabelTo`	should be equal to yChannelLabelFrom (otherwise no plot is returned but NULL)
`interactive`	if TRUE, uses ggplot_shiny
`useAllCells`	if TRUE, no subsampling will be done
`nDisplayCells`	if useAllCells == FALSE, the number of subsampled cells

useFixedLinearRange
: if TRUE, all channels using a linear scale will use a fixed range set by linearRange

linearRange
: set for all channels using a linear scale, if useFixedLinearRange == TRUE

transfoListName
: if not set to " ", the transformation list (as an object name ending with "_obj", as referenced in the pipeline workflow) to be used for for display.

Value

a ggplot (or plotly if interactive = TRUE) object

Examples

```
# run CytoPipeline object first

outputDir <- base::tempdir()


rawDataDir <-
    system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <-
    file.path(
        rawDataDir,
        list.files(rawDataDir, pattern = "Donor"))
jsonDir <- system.file("extdata", package = "CytoPipeline")
jsonPath <- file.path(jsonDir, "pipelineParams.json")

pipL2 <- CytoPipeline(
    jsonPath,
    experimentName = experimentName,
    sampleFiles = sampleFiles)

suppressWarnings(execute(
    pipL2,
    rmCache = TRUE,
    path = outputDir))


plotDiffFlowFrame(
    experimentNameFrom = experimentName,
    whichQueueFrom = "pre-processing",
    sampleFileFrom = 1,
    flowFrameNameFrom = "remove_doublets_obj",
    xChannelLabelFrom = "FSC-A : NA",
    yChannelLabelFrom = "SSC-A : NA",
    path = outputDir,
    experimentNameTo = experimentName,
    whichQueueTo = "pre-processing",
    sampleFileTo = 1,
    flowFrameNameTo = "remove_debris_obj",
```

```
    xChannelLabelTo = "FSC-A : NA",
    yChannelLabelTo = "SSC-A : NA",
    useAllCells = TRUE,
    nDisplayCells = 0,
    useFixedLinearRange = TRUE,
    linearRange = c(-100, 262144))

plotDiffFlowFrame(
    experimentNameFrom = experimentName,
    whichQueueFrom = "pre-processing",
    sampleFileFrom = 1,
    flowFrameNameFrom = "remove_doublets_obj",
    xChannelLabelFrom = "FSC-A : NA",
    yChannelLabelFrom = "SSC-A : NA",
    path = outputDir,
    experimentNameTo = experimentName,
    whichQueueTo = "pre-processing",
    sampleFileTo = 1,
    flowFrameNameTo = "remove_debris_obj",
    xChannelLabelTo = "FSC-A : NA",
    yChannelLabelTo = "SSC-A : NA",
    useAllCells = FALSE,
    nDisplayCells = 100,
    useFixedLinearRange = FALSE,
    linearRange = NULL)

plotDiffFlowFrame(
    experimentNameFrom = experimentName,
    whichQueueFrom = "pre-processing",
    sampleFileFrom = 1,
    flowFrameNameFrom = "remove_debris_obj",
    xChannelLabelFrom = "FSC-A : NA",
    yChannelLabelFrom = "Comp-525/50Violet-A : L/D Aqua - Viability",
    path = outputDir,
    experimentNameTo = experimentName,
    whichQueueTo = "pre-processing",
    sampleFileTo = 1,
    flowFrameNameTo = "remove_dead_cells_obj",
    xChannelLabelTo = "FSC-A : NA",
    yChannelLabelTo = "Comp-525/50Violet-A : L/D Aqua - Viability",
    useAllCells = TRUE,
    nDisplayCells = 0,
    useFixedLinearRange = FALSE,
    linearRange = NULL,
    transfoListName = "scale_transform_estimate_obj")
```

---

plotScaleTransformedChannel

Plot a flow frame in 1D with explicit user given scale transform

---

Description

This function plots a 1D view, i.e. the marginal distribution for one specified channel, of the given flow frame, using the specific user-provided scale transformation parameters.

Usage

```
plotScaleTransformedChannel(
  ff,
  channel,
  applyTransform = c("axis scale only", "data"),
  transfoType = c("linear", "logicle"),
  linA,
  linB,
  t,
  m,
  w,
  a
)
```

Arguments

ff	the flowFrame to be plotted
channel	the name of the channel of which to display the marginal distribution (i.e. the channel name used as column in the ff expression matrix).
applyTransform	if "data", data are explicitly transformed using the user provided sclae transformation parameters, before display if "axis scale only" (default), the data are not transformed, i.e. only the x axis scale is defined according to the scale transformation parameters.
transfoType	the transformation type, currently only linear and logicle(bi-exponential) are supported.
linA	the intercept parameter of the linear transformation.
linB	the slope parameter of the linear transformation.
t	the max scale parameter of the logicle tranformation.
m	the number of positive decades of the logicle tranformation.
w	the width parameter of the logicle transformation.
a	the number of additional decades on the negative side for the logicle transformation.

Value

a ggplot object

Examples

```
# run CytoPipeline object first

outputDir <- base::tempdir()


rawDataDir <-
    system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <-
    file.path(
        rawDataDir,
        list.files(rawDataDir, pattern = "Donor"))
jsonDir <- system.file("extdata", package = "CytoPipeline")
jsonPath <- file.path(jsonDir, "pipelineParams.json")

pipL2 <- CytoPipeline(
    jsonPath,
    experimentName = experimentName,
    sampleFiles = sampleFiles)

suppressWarnings(execute(
    pipL2,
    rmCache = TRUE,
    path = outputDir))

ff <- CytoPipeline::getCytoPipelineFlowFrame(
pipL2,
path = outputDir,
whichQueue = "scale transform",
objectName = "flowframe_aggregate_obj"
)

plotScaleTransformedChannel(
    ff,
    channel = "FSC-A",
    transfoType = "linear",
    linA = 0.0002,
    linB = -0.5)

plotScaleTransformedChannel(
    ff,
    channel = "Comp-670/30Violet-A",
    transfoType = "logicle",
    t = 262144,
    m = 4.5,
    w = 0.5,
    a = 1.0
)

plotScaleTransformedChannel(
    ff,
```

```
    channel = "CD3",
    applyTransform = "data",
    transfoType = "logicle",
    t = 262144,
    m = 4.5,
    w = 0.5,
    a = 1.0
)
```

`plotSelectedFlowFrame` *Plot a flow frame from a CytoPipeline run*

Description

Based on an experiment name, this function will gather the required flowFrame from the CytoPipeline disk cache and display it using the user chosen 1D or 2D view.

Usage

```
plotSelectedFlowFrame(
  experimentName,
  whichQueue,
  sampleFile,
  flowFrameName,
  path,
  xChannelLabel,
  yChannelLabel,
  useAllCells,
  nDisplayCells,
  useFixedLinearRange,
  linearRange,
  transfoListName = " "
)
```

Arguments

`experimentName`	the experiment name (representing a pipeline run) from which to extract the flow frame
`whichQueue`	"pre-processing" or "scale transform"
`sampleFile`	in case 'whichQueue' is set to 'pre-processing, which sample file to look at. This can be a number or a character. • if whichQueue == "scale transform", the sampleFile is ignored • if NULL and whichQueue == "pre-processing", the sampleFile is defaulted to the first one belonging to the experiment
`flowFrameName`	the name of the object to fetch (as referenced in the pipeline workflow)

path	the root path to look for the CytoPipeline experiment cache
xChannelLabel	the label of the channel to be displayed on the x axis: the conventional syntax is : channelName + " - " + channelMarker
yChannelLabel	the label of the channel to be displayed on the y axis: the conventional syntax is : channelName + " - " + channelMarker
useAllCells	if TRUE, no subsampling will be done
nDisplayCells	if useAllCells == FALSE, the number of subsampled cells
useFixedLinearRange	if TRUE, all channels using a linear scale will use a fixed range set by linearRange
linearRange	set for all channels using a linear scale, if useFixedLinearRange == TRUE
transfoListName	if not set to " ", the transformation list (as an object name ending with "_obj", as referenced in the pipeline workflow) to be used for for display.

Value

a ggplot object

Examples

```
# run CytoPipeline object first

outputDir <- base::tempdir()


rawDataDir <-
    system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <-
    file.path(
        rawDataDir,
        list.files(rawDataDir, pattern = "Donor"))
jsonDir <- system.file("extdata", package = "CytoPipeline")
jsonPath <- file.path(jsonDir, "pipelineParams.json")

pipL2 <- CytoPipeline(
    jsonPath,
    experimentName = experimentName,
    sampleFiles = sampleFiles)

suppressWarnings(execute(
    pipL2,
    rmCache = TRUE,
    path = outputDir))

plotSelectedFlowFrame(
    experimentName = experimentName,
    whichQueue = "pre-processing",
```

```
    sampleFile = 1,
    flowFrameName = "remove_debris_obj",
    path = outputDir,
    xChannelLabel = "FSC-A : NA",
    yChannelLabel = "SSC-A : NA",
    useAllCells = TRUE,
    nDisplayCells = 0,
    useFixedLinearRange = TRUE,
    linearRange = c(-100, 262144))

plotSelectedFlowFrame(
    experimentName = experimentName,
    whichQueue = "pre-processing",
    sampleFile = 1,
    flowFrameName = "remove_debris_obj",
    path = outputDir,
    xChannelLabel = "FSC-A : NA",
    yChannelLabel = "SSC-A : NA",
    useAllCells = FALSE,
    nDisplayCells = 100,
    useFixedLinearRange = FALSE,
    linearRange = NULL)

plotSelectedFlowFrame(
    experimentName = experimentName,
    whichQueue = "pre-processing",
    sampleFile = 1,
    flowFrameName = "remove_debris_obj",
    path = outputDir,
    xChannelLabel = "Comp-670/30Violet-A : BV785 - CD3",
    yChannelLabel = "Comp-780/60Red-A : APCCy7 - CD4",
    useAllCells = TRUE,
    nDisplayCells = 0,
    useFixedLinearRange = FALSE,
    linearRange = NULL,
    transfoListName = "scale_transform_estimate_obj")
```

`plotSelectedWorkflow` *Plot a pipeline workflow from a CytoPipeline run*

Description

Plot a pipeline workflow from a CytoPipeline run

Usage

```
plotSelectedWorkflow(experimentName, whichQueue, sampleFile, path = path)
```

Arguments

experimentName	the experiment name (representing a pipeline run) from which to extract the workflow
whichQueue	"pre-processing" or "scale transform"
sampleFile	in case 'whichQueue' is set to 'pre-processing, which sample file to look at. This can be a number or a character. • if whichQueue == "scale transform", the sampleFile is ignored • if NULL and whichQueue == "pre-processing", the sampleFile is defaulted to the first one belonging to the experiment
path	the root path to look for the CytoPipeline experiment cache

Value

nothing, but displays the plot as a side effect

Examples

```
# run CytoPipeline object first

outputDir <- base::tempdir()


rawDataDir <-
    system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <-
    file.path(
        rawDataDir,
        list.files(rawDataDir, pattern = "Donor"))
jsonDir <- system.file("extdata", package = "CytoPipeline")
jsonPath <- file.path(jsonDir, "pipelineParams.json")

pipL2 <- CytoPipeline(
    jsonPath,
    experimentName = experimentName,
    sampleFiles = sampleFiles)

suppressWarnings(execute(
    pipL2,
    rmCache = TRUE,
    path = outputDir))

plotSelectedWorkflow(
    experimentName = experimentName,
    whichQueue = "pre-processing",
    sampleFile = sampleFiles[1],
    path = outputDir)

plotSelectedWorkflow(
    experimentName = experimentName,
```

```
    whichQueue = "scale transform",
    sampleFile = NULL,
    path = outputDir)
```

ScaleTransformApp *interactive display and modification of scale transform list*

Description

this application allows the user to visualize a scale transformation list, possibly amending it channel after channel, and save the results on disk. The needed input tranformation list and flow frame for visualization needs to be read from a CytoPipeline experiments stored in cache.

Usage

```
ScaleTransformApp(dir = ".")
```

Arguments

dir	the root directory into which the engine will look for existing CytoPipeline experiments

Value

no return value

Examples

```
# run CytoPipeline object first

outputDir <- base::tempdir()


rawDataDir <-
    system.file("extdata", package = "CytoPipeline")
experimentName <- "OMIP021_PeacoQC"
sampleFiles <-
    file.path(rawDataDir, list.files(rawDataDir, pattern = "Donor"))
jsonDir <- system.file("extdata", package = "CytoPipeline")
jsonPath <- file.path(jsonDir, "pipelineParams.json")

pipL2 <-
    CytoPipeline(
        jsonPath,
        experimentName = experimentName,
        sampleFiles = sampleFiles)

suppressWarnings(execute(
```

```
    pipL2,
    rmCache = TRUE,
    path = outputDir))

# run shiny app

if (interactive())
    ScaleTransformApp(dir = outputDir)
```

Index

CytoPipelineCheckApp, 2

plotDiffFlowFrame, 3
plotScaleTransformedChannel, 6
plotSelectedFlowFrame, 9
plotSelectedWorkflow, 11

ScaleTransformApp, 13