

Package ‘CytoPipelineGUI’

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

Version 1.7.0

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.

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CytoPipelineCheckApp	<i>interactive visualization of flow cytometry data analysis pipeline objects stored in cache</i>
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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)

```

CytoPipelineGUI

CytoPipelineGUI package

Description

CytoPipelineGUI is the companion package of CytoPipeline, and is used for interactive visualization. It implements two shiny applications :

- a shiny app for interactive comparison of flow frames that are the results of CytoProcessingSteps of the same or different CytoPipeline experiments. It is launched using the following statement: `CytoPipelineCheckApp()`
- a shiny app for interactive visualization and manual adjustments of scale transformation objects. It is launched using the following statement: `ScaleTransformApp()`

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See Also

[CytoPipeline](#), [CytoPipelineCheckApp](#), [ScaleTransformApp](#)

plotDiffFlowFrame	<i>Plot the difference plot between two flow frames from a CytoPipeline run</i>
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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 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,
  negDecades,
  width,
  posDecades
)

```

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 scale 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.
negDecades	the number of additional decades on the negative side for the logicle transformation.
width	the width parameter of the logicle transformation.
posDecades	the number of positive decades of 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",
  negDecades = 1,
  width = 0.5,
  posDecades = 4
)

plotScaleTransformedChannel(
  ff,
  channel = "CD3",
```

```

    applyTransform = "data",
    transfoType = "logicle",
    negDecades = 1,
    width = 0.5,
    posDecades = 4
)

```

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 linear-
 Range
 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	<i>interactive display and modification of scale transform list</i>
-------------------	---

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 transformation 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)
```

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