

# Package ‘CytoPipelineGUI’

April 23, 2025

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

**Version** 1.6.0

**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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**Author** Philippe Hauchamps [aut, cre] (ORCID: [<https://orcid.org/0000-0003-2865-1852>](https://orcid.org/0000-0003-2865-1852)),  
Laurent Gatto [aut] (ORCID: [<https://orcid.org/0000-0002-1520-2268>](https://orcid.org/0000-0002-1520-2268)),  
Dan Lin [ctb]

**Maintainer** Philippe Hauchamps <philippe.hauchamps@uclouvain.be>

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

---

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 CytoProcessing-Steps 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()`

**Author(s)**

**Maintainer:** Philippe Hauchamps <philippe.hauchamps@uclouvain.be> ([ORCID](#))

Authors:

- Laurent Gatto <laurent.gatto@uclouvain.be> ([ORCID](#))

Other contributors:

- Dan Lin <dan.8.lin@gsk.com> [contributor]

**See Also**

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

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|                   |                                                                                 |
|-------------------|---------------------------------------------------------------------------------|
| plotDiffFlowFrame | <i>Plot the difference plot between two flow frames from a CytoPipeline run</i> |
|-------------------|---------------------------------------------------------------------------------|

---

**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. <ul style="list-style-type: none"> <li>• if whichQueueFrom == "scale transform", the sampleFileFrom is ignored</li> <li>• if NULL and whichQueueFrom == "pre-processing", the sampleFileFrom is defaulted to the first one belonging to the experiment</li> </ul> |
| 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

|                             |                                                                                                                                                                                                                                                                          |
|-----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>ff</code>             | the flowFrame to be plotted                                                                                                                                                                                                                                              |
| <code>channel</code>        | 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).                                                                                                                                |
| <code>applyTransform</code> | 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. |
| <code>transfoType</code>    | the transformation type, currently only linear and logicle(bi-exponential) are supported.                                                                                                                                                                                |
| <code>linA</code>           | the intercept parameter of the linear transformation.                                                                                                                                                                                                                    |
| <code>linB</code>           | the slope parameter of the linear transformation.                                                                                                                                                                                                                        |
| <code>negDecades</code>     | the number of additional decades on the negative side for the logicle transformation.                                                                                                                                                                                    |
| <code>width</code>          | the width parameter of the logicle transformation.                                                                                                                                                                                                                       |
| <code>posDecades</code>     | 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
)

```

**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. <ul style="list-style-type: none"> <li>• if whichQueue == "scale transform", the sampleFile is ignored</li> <li>• if NULL and whichQueue == "pre-processing", the sampleFile is defaulted to the first one belonging to the experiment</li> </ul> |
| 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 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,
  xChannellLabel = "Comp-670/30Violet-A : BV785 - CD3",
  yChannellLabel = "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. <ul style="list-style-type: none"> <li>if whichQueue == "scale transform", the sampleFile is ignored</li> <li>if NULL and whichQueue == "pre-processing", the sampleFile is defaulted to the first one belonging to the experiment</li> </ul> |
| 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 transformation list and flow frame for visualization needs to be read from a CytoPipeline experiments stored in cache.

**Usage**

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

**Arguments**

|                  |                                                                                          |
|------------------|------------------------------------------------------------------------------------------|
| <code>dir</code> | 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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