

# Package: CytoPipelineGUI (via r-universe)

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

**Version** 1.11.1

**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

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**URL** <https://uclouvain-cbio.github.io/CytoPipelineGUI>

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**Contents**

|                                       |           |
|---------------------------------------|-----------|
| CytoPipelineCheckApp . . . . .        | 2         |
| plotDiffFlowFrame . . . . .           | 3         |
| plotScaleTransformedChannel . . . . . | 6         |
| plotSelectedFlowFrame . . . . .       | 9         |
| plotSelectedWorkflow . . . . .        | 11        |
| ScaleTransformApp . . . . .           | 13        |
| <b>Index</b>                          | <b>15</b> |

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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)

```

---

|                   |                                                                                 |
|-------------------|---------------------------------------------------------------------------------|
| 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 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 (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**

|                             |                                                                                                                                                                                                                                                                          |
|-----------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <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>t</code>              | the max scale parameter of the logicle transformation.                                                                                                                                                                                                                   |
| <code>m</code>              | the number of positive decades of the logicle transformation.                                                                                                                                                                                                            |
| <code>w</code>              | the width parameter of the logicle transformation.                                                                                                                                                                                                                       |
| <code>a</code>              | 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. <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 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,
xChannellLabel = "FSC-A : NA",
yChannellLabel = "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,
  xChannellLabel = "FSC-A : NA",
  yChannellLabel = "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**

|                             |                                                                                                                                                                                                                                                                                                                                                                                                                                        |
|-----------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>experimentName</code> | the experiment name (representing a pipeline run) from which to extract the workflow                                                                                                                                                                                                                                                                                                                                                   |
| <code>whichQueue</code>     | "pre-processing" or "scale transform"                                                                                                                                                                                                                                                                                                                                                                                                  |
| <code>sampleFile</code>     | 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 <code>whichQueue == "scale transform"</code>, the <code>sampleFile</code> is ignored</li> <li>• if <code>NULL</code> and <code>whichQueue == "pre-processing"</code>, the <code>sampleFile</code> is defaulted to the first one belonging to the experiment</li> </ul> |
| <code>path</code>           | 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)
```

# Index

CytoPipelineCheckApp, [2](#)

plotDiffFlowFrame, [3](#)

plotScaleTransformedChannel, [6](#)

plotSelectedFlowFrame, [9](#)

plotSelectedWorkflow, [11](#)

ScaleTransformApp, [13](#)