Package ‘cytoviewer’

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Version 1.4.0

Title An interactive multi-channel image viewer for R

Description This R package supports interactive visualization of multi-channel images and segmentation masks generated by imaging mass cytometry and other highly multiplexed imaging techniques using shiny. The cytoviewer interface is divided into image-level (Composite and Channels) and cell-level visualization (Masks). It allows users to overlay individual images with segmentation masks, integrates well with SingleCellExperiment and SpatialExperiment objects for metadata visualization and supports image downloads.

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Imports shiny, shinydashboard, utils, colourpicker, shinycssloaders, svgPanZoom, viridis, archive, grDevices, RColorBrewer, svglite, EBImage, methods, cytomapper, SingleCellExperiment, S4Vectors, SummarizedExperiment

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VignetteBuilder knitr

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BugReports https://github.com/BodenmillerGroup/cytoviewer/issues

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Description

This shiny R application allows users to interactively visualize multi-channel images and segmentation masks generated by imaging mass cytometry and other highly multiplexed imaging techniques. The cytoviewer interface is divided into image-level (Composite and Channels) and cell-level visualization (Masks). It allows users to overlay individual images with segmentation masks, integrates well with SingleCellExperiment and SpatialExperiment objects for metadata visualization and supports image downloads.

Usage

cytoviewer(
    image = NULL,
    mask = NULL,
    object = NULL,
    cell_id = NULL,
    img_id = NULL
)

Arguments

image  (optional) a CytoImageList object containing single or multi-channel Image objects.

mask  (optional) a CytoImageList containing single-channel Image objects.

object  (optional) a SingleCellExperiment or SpatialExperiment object.

cell_id  character specifying the colData(object) entry, in which the integer cell IDs are stored. These IDs should match the integer pixel values in the segmentation mask object (mask).

img_id  character specifying the colData(object) and mcols(mask) and/or mcols(image) entry, in which the image IDs are stored.
**Value**

A Shiny app object for interactive multi-channel image visualization and exploration

**The input objects**

The functionality of cytoviewer depends on which input objects are user-provided. Below we describe the four use cases in respect to input objects and functionality.

1. **Usage of cytoviewer with images, masks and object**

   The full functionality of cytoviewer can be leveraged when image, mask and object are provided. This allows image-level visualization (Composite and Channels), cell-level visualization, overlaying images with segmentation masks as well as metadata visualization.

2. **Usage of cytoviewer with images only**

   If only image is specified, image-level visualization (Composite and Channels) is possible.

3. **Usage of cytoviewer with images and masks**

   Image-level visualization (Composite and Channels), overlaying of images with masks and cell-level visualization is feasible when image and mask are provided.

4. **Usage of cytoviewer with masks and object**

   If mask and object are specified, cell-level visualization as well as metadata visualization is possible.

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**See Also**

plotPixels for the function underlying image-level visualization

plotCells for the function underlying cell-level visualization

cytomapperShiny for a shiny application that visualizes gated cells on images

**Examples**

```r
# Load example datasets from cytomapper
library(cytomapper, quietly = TRUE)
data("pancreasImages")
data("pancreasMasks")
data("pancreasSCE")

# 1. Use cytoviewer with images, masks and object
app <- cytoviewer(image = pancreasImages,
                   mask = pancreasMasks,
                   object = pancreasSCE,
                   img_id = "ImageNb",
                   cell_id = "CellNb")
if (interactive()) {
  shiny::runApp(app, launch.browser = TRUE)
}
```
## Other input variations (see "The input objects" section):

### 2. Use cytoviewer with images
```r
app_1 <- cytoviewer(image = pancreasImages)
if (interactive()) {
  shiny::runApp(app_1, launch.browser = TRUE)
}
```

### 3. Use cytoviewer with images and masks
```r
app_2 <- cytoviewer(image = pancreasImages,
                    mask = pancreasMasks,
                    img_id = "ImageNb")
if (interactive()) {
  shiny::runApp(app_2, launch.browser = TRUE)
}
```

### 4. Use cytoviewer with masks and object
```r
app_3 <- cytoviewer(mask = pancreasMasks,
                      object = pancreasSCE,
                      img_id = "ImageNb",
                      cell_id = "CellNb")
if (interactive()) {
  shiny::runApp(app_3, launch.browser = TRUE)
}
```
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