

Package ‘cytoviewer’

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Version 1.5.0

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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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 <code>CytoImageList</code> object containing single or multi-channel <code>Image</code> objects.
mask	(optional) a <code>CytoImageList</code> containing single-channel <code>Image</code> objects.
object	(optional) a <code>SingleCellExperiment</code> or <code>SpatialExperiment</code> object.
cell_id	character specifying the <code>colData(object)</code> entry, in which the integer cell IDs are stored. These IDs should match the integer pixel values in the segmentation mask object (<code>mask</code>).
img_id	character specifying the <code>colData(object)</code> and <code>mcols(mask)</code> and/or <code>mcols(image)</code> 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

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

# 3. Use cytoviewer with images and masks
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  
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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