

Package ‘cytoviewer’

May 14, 2024

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

Suggests BiocStyle, knitr, rmarkdown, markdown, testthat

biocViews ImmunoOncology, Software, SingleCell, OneChannel, TwoChannel, MultiChannel, Spatial, DataImport

VignetteBuilder knitr

URL <https://github.com/BodenmillerGroup/cytoviewer>

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

RoxygenNote 7.2.3

Encoding UTF-8

git_url <https://git.bioconductor.org/packages/cytoviewer>

git_branch RELEASE_3_19

git_last_commit 8756af3

git_last_commit_date 2024-04-30

Repository Bioconductor 3.19

Date/Publication 2024-05-14

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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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