

# Package ‘HistoImagePlot’

April 20, 2026

**Title** Plotting functionality for Histopathology pipeline datasets

**Version** 0.99.10

**Description** Create side-by-side visualizations of tissue thumbnail image and HoverNet cell segmentation with colored cell type labels. Functionality automatically retrieves the thumbnail image associated with a HoverNet JSON file and overlays the segmentation data. This package is intended for researchers working with histopathological images, facilitating exploratory analysis, and integrates with the imageFeatureTCGA Bioconductor package.

**biocViews** Software, Visualization, Spatial

**Depends** R (>= 4.5.0)

**Imports** BiocBaseUtils, cowplot, ggplot2, grDevices, imageFeatureTCGA, methods, RColorBrewer, S4Vectors, SpatialExperiment, SummarizedExperiment

**Suggests** anndataR, BiocStyle, dplyr, knitr, magick, rmarkdown, tinytest

**License** Artistic-2.0

**Encoding** UTF-8

**VignetteBuilder** knitr

**BugReports** <https://github.com/waldronlab/HistoImagePlot/issues>

**URL** <https://github.com/waldronlab/HistoImagePlot>

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plotHoverNetH5ADOverlay

*Plot HoverNet H5AD Segmentation Overlay with Thumbnail*

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## Description

Creates a side-by-side visualization of the original tissue thumbnail image and the HoverNet cell segmentation with colored cell type labels. This function works with HoverNet data stored in h5ad format and imported as a SpatialExperiment object.

## Usage

```
plotHoverNetH5ADOverlay(
  hovernet,
  thumbnail_path,
  title = NULL,
  point_size = 0.01,
  legend_point_size = 2,
  color_palette = NULL,
  ncol = 2,
  rel_widths = c(1, 1.08),
  title_size = 25,
  flip_image = TRUE
)
```

## Arguments

|                |  |
|----------------|--|
| hovernet       | A SpatialExperiment or SpatialFeatureExperiment object containing HoverNet segmentation data from h5ad format. |
| thumbnail_path | Path or URL to the thumbnail PNG image file.   |
| title          | Optional. Title for the combined plot. If NULL, uses "HoverNet Segmentation". Default is NULL.                 |
| point_size     | Numeric value for the size of points in the segmentation plot. Default is 0.01.                                |

|                   |   |
|-------------------|---|
| legend_point_size | Numeric value for the size of points in the legend. Default is 2.                                       |
| color_palette     | Optional. A named vector of colors for cell types. If NULL, uses RColorBrewer palette. Default is NULL. |
| ncol              | Number of columns for the side-by-side plots. Default is 2.   |
| rel_widths        | Relative widths of the image and segmentation plots. Default is c(1, 1.08).                             |
| title_size        | Font size for the main title. Default is 25.  |
| flip_image        | Logical. Whether to flip the image vertically to match coordinate system. Default is TRUE.              |

### Details

The function performs the following steps:

1. Loads the thumbnail PNG image (from local path or URL with caching)
2. Creates a segmentation plot colored by cell type using the type column from colData
3. Combines the thumbnail and segmentation side-by-side
4. Adds an optional title

The function expects the SpatialExperiment to have:

- spatialCoords with columns x\_centroid and y\_centroid
- colData with a type column for cell type classification

Remote PNG files are automatically cached using BiocFileCache for efficient handling without manual downloads.

### Value

A ggplot object combining the thumbnail image and segmentation overlay with an optional title.

### Examples

```
# Load h5ad HoverNet data
h5ad_url <- paste0(
  "https://store.cancerdatasci.org/hovernet/h5ad/",
  "TCGA-VG-A8L0-01A-01-DX1.B39A4D64-82A1-4A04-8AB6-918F3058B83B.h5ad"
)
hn_spe <- HoverNet(h5ad_url, outClass = "SpatialExperiment") |> import()

thumb_url <- paste0(
  "https://store.cancerdatasci.org/hovernet/thumb/",
  "TCGA-VG-A8L0-01A-01-DX1.B39A4D64-82A1-4A04-8AB6-918F3058B83B.png"
)
plotHoverNetH5ADOverlay(hn_spe, thumbnail_path = thumb_url)
```

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plotHoverNetOverlay *Plot HoverNet Segmentation Overlay with Thumbnail*

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### Description

Creates a side-by-side visualization of the original tissue thumbnail image and the HoverNet cell segmentation with colored cell type labels. The function automatically retrieves the thumbnail image associated with a HoverNet JSON file and overlays the segmentation data.

### Usage

```
plotHoverNetOverlay(
  hovernet,
  json_path = NULL,
  title = NULL,
  point_size = 0.01,
  legend_point_size = 2,
  color_palette = NULL,
  ncol = 2,
  rel_widths = c(1, 1.08),
  title_size = 25,
  flip_image = TRUE
)
```

### Arguments

|                   |   |
|-------------------|---|
| hovernet          | A <code>SpatialExperiment</code> or <code>SpatialFeatureExperiment</code> object created by importing a HoverNet JSON file, or a path/URL to a HoverNet JSON file.  |
| json_path         | Optional. Path or URL to the HoverNet JSON file. Only required if <code>hovernet</code> is a <code>SpatialExperiment</code> object and the original JSON path is not stored in metadata. Default is <code>NULL</code> . |
| title             | Optional. Title for the combined plot. If <code>NULL</code> , uses the basename of the JSON file. Default is <code>NULL</code> .  |
| point_size        | Numeric value for the size of points in the segmentation plot. Default is <code>0.01</code> .   |
| legend_point_size | Numeric value for the size of points in the legend. Default is <code>2</code> .   |
| color_palette     | Optional. A named vector of colors for cell types. If <code>NULL</code> , uses the colors from the HoverNet type map or <code>RColorBrewer</code> . Default is <code>NULL</code> .                                      |
| ncol              | Number of columns for the side-by-side plots. Default is <code>2</code> .   |
| rel_widths        | Relative widths of the image and segmentation plots. Default is <code>c(1, 1.08)</code> .   |
| title_size        | Font size for the main title. Default is <code>25</code> .  |
| flip_image        | Logical. Whether to flip the image vertically to match coordinate system. Default is <code>TRUE</code> .  |

**Details**

The function performs the following steps:

1. If `hovernet` is a file path, imports it using `HoverNet()` and `import()`
2. Retrieves the associated thumbnail PNG
3. Creates a segmentation plot colored by cell type
4. Combines the thumbnail and segmentation side-by-side
5. Adds an optional title

The thumbnail is automatically downloaded and cached if a URL is provided. The segmentation uses the `type` column from the `colData` and colors are taken from the `type_map` metadata if available.

**Value**

A `ggplot` object combining the thumbnail image and segmentation overlay with an optional title.

**Examples**

```
json_url <- paste0(
  "https://store.cancerdatasci.org/hovernnet/json/",
  "TCGA-VG-A8LO-01A-01-DX1.B39A4D64-82A1-4A04-8AB6-918F3058B83B.json.gz"
)
plotHoverNetOverlay(json_url, title = "TCGA-VG-A8LO Sample")
```

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