

# Updating spatialLIBD

From SingleCellExperiment to  
VisiumExperiment classes

**spatialLIBD version 1.1.7**

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@PardoBree



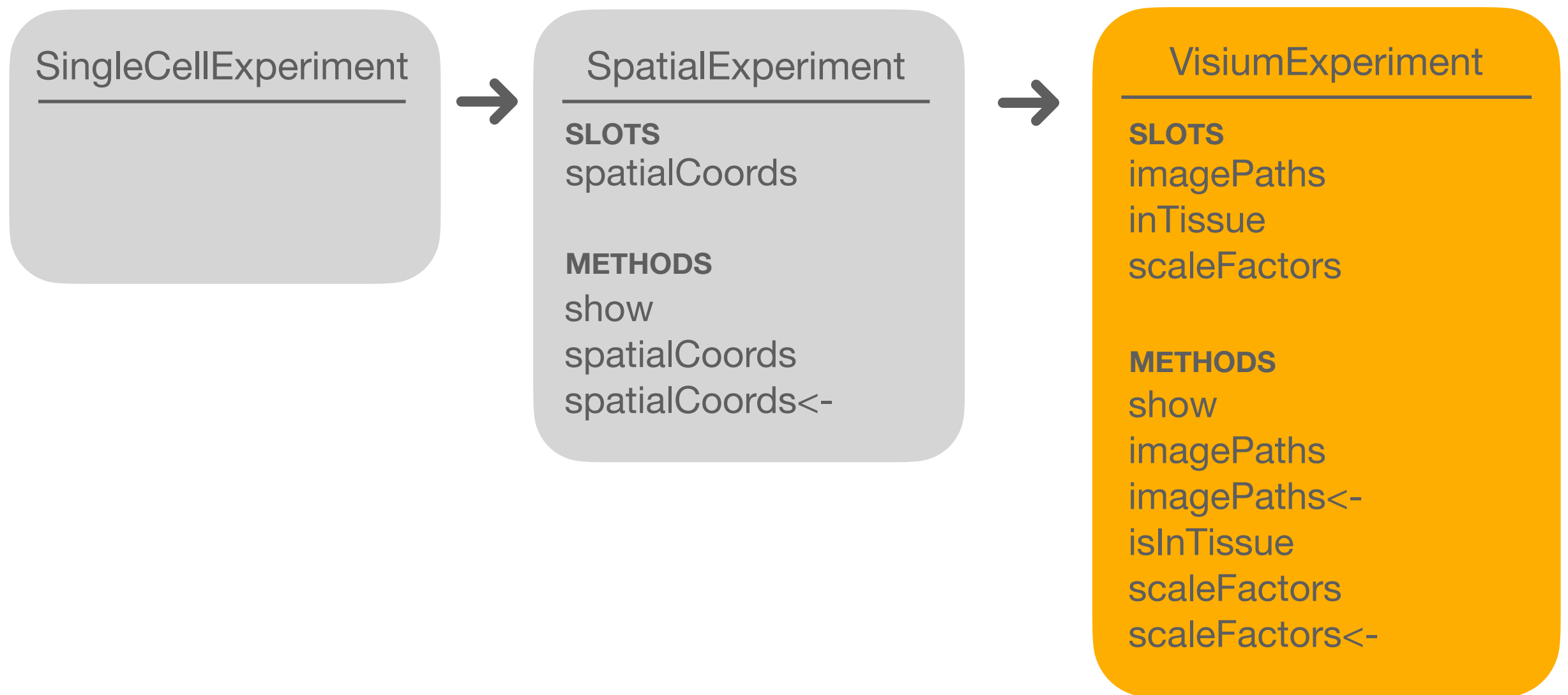
bpardo99



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# VisiumExperiment class contains new attributes and methods



# Before starting

Install spatialLIBD

```
if (!requireNamespace("BiocManager", quietly = TRUE)) {  
  install.packages("BiocManager")  
}  
  
BiocManager::install("spatialLIBD")
```

Load packages

```
library("spatialLIBD")
```

# Downloading DLPFC data contained in a VisiumExperiment object

- Retrieving data with `fetch_data()`

```
## Connect to ExperimentHub
ehub <- ExperimentHub::ExperimentHub()
## Download ve object
ve <- fetch_data(type = "ve", eh = ehub)
```

# Downloading DLPFC data contained in a VisiumExperiment object

- `sce_to_ve()` takes data from `sce` and rearranges it to the structure of `VisiumExperiment` class

```
#Download data in a SingleCellExperiment object  
if (!exists("sce")) sce <- fetch_data("sce")  
#Subset data  
sce_sub <- sce[, sce$sample_name == "151673"]  
#Make the SingleCellExperiment object a VisiumExperiment one  
ve_sub <- sce_to_ve(sce_sub)
```

# Downloading DLPFC data contained in a VisiumExperiment object

- ve object structure

ve

```
## class: VisiumExperiment
## dim: 33538 47681
## metadata(0):
## assays(2): counts logcounts
## rownames(33538): ENSG00000243485 ENSG00000237613 ... ENSG00000277475
##      ENSG00000268674
## rowData names(9): source type ... gene_search is_top_hvg
## colnames(47681): AAACAACGAATAGTTC-1 AAACAAGTATCTCCCA-1 ...
##      TTGTTTCCATACAACACT-1 TTGTTTGTGTAAATTC-1
## colData names(66): Cluster height ... pseudobulk_UMAP_spatial
##      markers_UMAP_spatial
## reducedDimNames(6): PCA TSNE_perplexity50 ... TSNE_perplexity80
##      UMAP_neighbors15
## altExpNames(0):
## spatialCoordinates(7): Cell_ID sample_name ... pxl_row_in_fullres
##      pxl_col_in_fullres
## inTissue(1): 47681
## imagePaths(12):
##      /Users/brendapardo/Library/Caches/BiocFileCache/6e17e40d5ec_151507
##      _tissue_lowres_image.png
##      /Users/brendapardo/Library/Caches/BiocFileCache/6e134363fac_151508
##      _tissue_lowres_image.png
##      ...
##      /Users/brendapardo/Library/Caches/BiocFileCache/6e17b9ee30f_151675
##      _tissue_lowres_image.png
##      /Users/brendapardo/Library/Caches/BiocFileCache/6e17c4d2d30_151676
##      _tissue_lowres_image.png
```

# Storing and retrieving scale factors from a VisiumExperiment object

- scaleFactors contains
  - a list with the required four scale factors names.
  - a fifth list element with the full list of scale factors for all our samples.

```
#Get scale factors  
scaleFactors(ve)
```

```
## $spot_diameter_fullres  
## [1] 96.37511  
##  
## $tissue_hires_scalef  
## [1] 0.150015  
##  
## $fiducial_diameter_fullres  
## [1] 144.5627  
##  
## $tissue_lowres_scalef  
## [1] 0.0450045  
##  
## $all_images  
## $all_images$`151507`  
## $all_images$`151507`$spot_diameter_fullres  
## [1] 96.37511  
##  
## $all_images$`151507`$tissue_hires_scalef  
## [1] 0.150015  
##  
## $all_images$`151507`$fiducial_diameter_fullres  
## [1] 144.5627  
##  
## $all_images$`151507`$tissue_lowres_scalef  
## [1] 0.0450045  
##
```

# Storing and retrieving scale factors from a VisiumExperiment object

- `update_scaleFactors()` generates a VisiumExperiment object with updated scale factors for a given input sample ID

```
## Check the default scale factors  
scaleFactors(ve)[1:4]
```

```
## $spot_diameter_fullres  
## [1] 96.37511  
##  
## $tissue_hires_scalef  
## [1] 0.150015  
##  
## $fiducial_diameter_fullres  
## [1] 144.5627  
##  
## $tissue_lowres_scalef  
## [1] 0.0450045
```



# Storing and retrieving scale factors from a VisiumExperiment object

- `update_scaleFactors()` generates a VisiumExperiment object with updated scale factors for a given input sample ID

```
## Replace them for those for the second image and check them  
ve <- update_scaleFactors(ve, "151508")  
scaleFactors(ve)[1:4]
```

```
## $spot_diameter_fullres  
## [1] 96.36957  
##  
## $tissue_hires_scalef  
## [1] 0.150015  
##  
## $fiducial_diameter_fullres  
## [1] 144.5543  
##  
## $tissue_lowres_scalef  
## [1] 0.0450045
```

# Visualizing the histology image from a VisiumExperiment object

- Tissue images are downloaded at the moment ve is created in sce\_to\_ve
  - Paths in imagePaths have to be local

```
imagePaths(ve)[1:2]
```

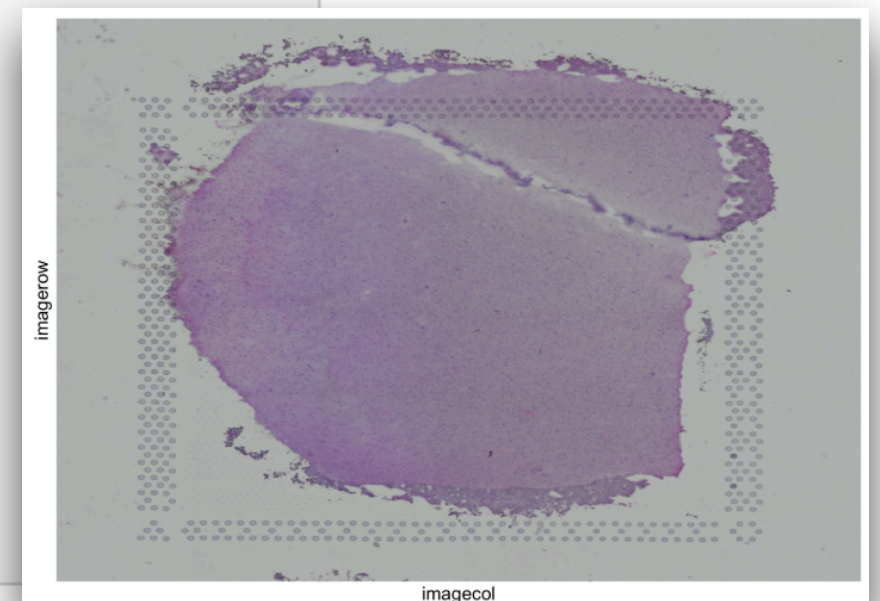
```
##  
                151507  
## "/Users/brendapardo/Library/Caches/BiocFileCache/6e17e40d5ec_15150  
7_tissue_lowres_image.png"  
##  
                151508  
## "/Users/brendapardo/Library/Caches/BiocFileCache/6e134363fac_15150  
8_tissue_lowres_image.png"
```

# Visualizing the histology image from a VisiumExperiment object

- `read_image()` makes possible to give `geom_spatial()` a VisiumExperiment object
  - It takes the image path of the desired samples, creates the grobs and puts them on a tibble

```
## Extract data from a sample (with ID 151507)
sample_id <- "151507"
ve_sub <- ve[, SpatialExperiment::spatialCoords(ve)$sample_name == sample_id]
sample_df <- as.data.frame(SpatialExperiment::spatialCoords(ve_sub))

## Plot with geom_spatial
ggplot2::ggplot(
  sample_df,
  ggplot2::aes(
    x = imagecol,
    y = imagerow,
  )
) +
geom_spatial(
  data = read_image(ve_sub, sample_id),
  ggplot2::aes(grob = grob),
  x = 0.5,
  y = 0.5
)
```



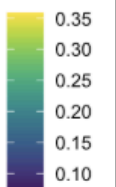
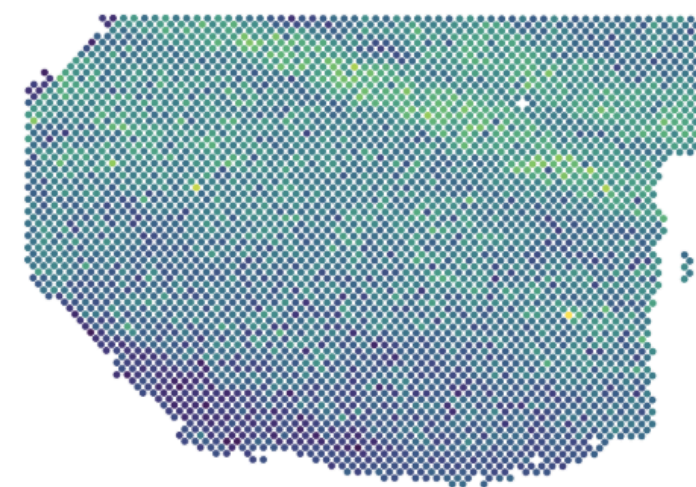
# Making other functions compatible with VisiumExperiment class

- `ve_image_colData()` generates an input data frame for `sce_image_clus_p()` and `sce_image_gene_p()`.

```
## Use the data previously extracted for a sample
## Prepare the data for the plotting function
df <- colData(ve_sub)
df$COUNT <- df$expr_chrM_ratio

sce_image_gene_p(
  sce = ve_sub,
  d = df,
  sampleid = sample_id,
  title = "151507 chrM expr ratio",
  spatial = FALSE
)
```

151507 chrM expr ratio

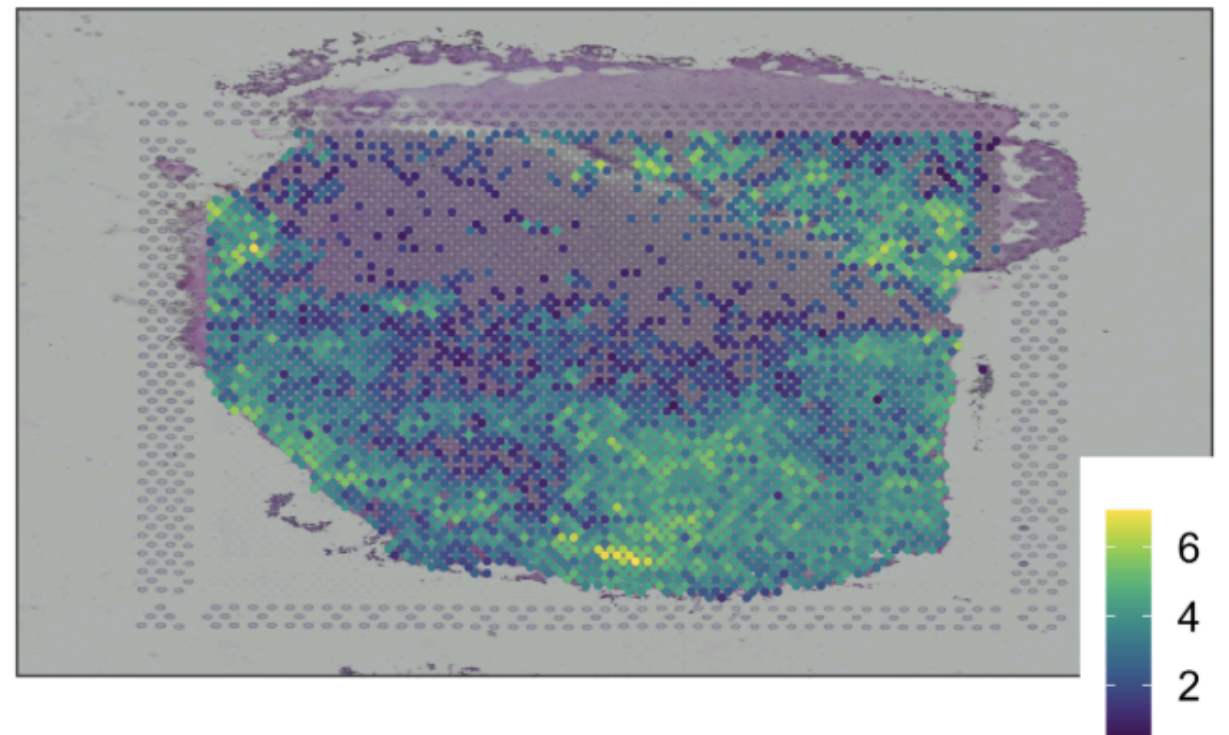


# Making other functions compatible with VisiumExperiment class

- `sce_image_gene()`, `sce_image_clus()`, `sce_image_grid()` and `sce_image_grid_gene()` access sample IDs from the slot `spatialCoords`.

```
sce_image_gene(  
  sce = ve_sub,  
  sampleid = sample_id,  
  spatial = TRUE  
)
```

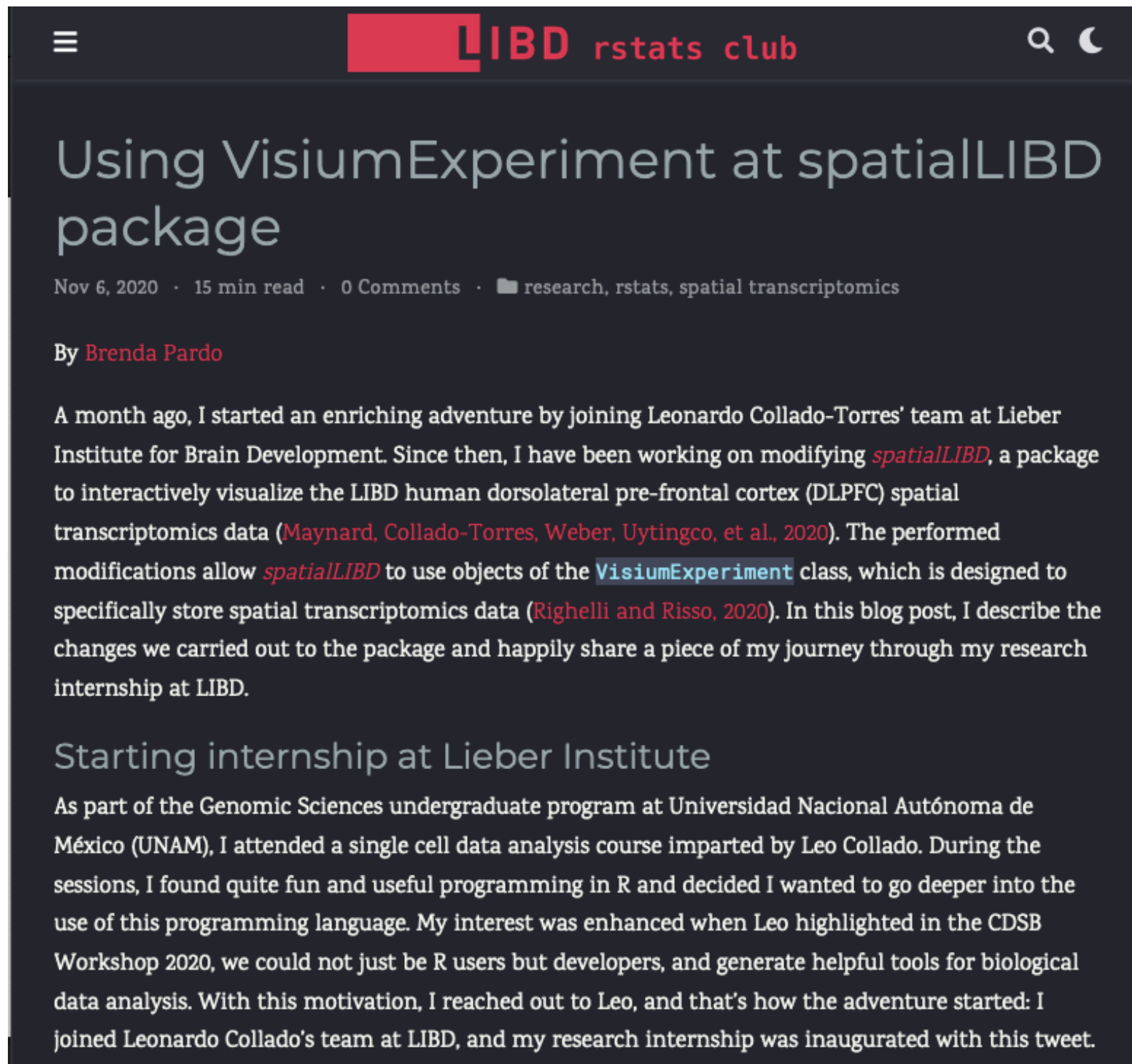
151507 SCGB2A2; ENSG000000110484



logcounts min > 0



# Blog post at LIBD rstats club



The screenshot shows a web browser displaying a blog post on the LIBD rstats club website. The header features a hamburger menu icon, the site name 'LIBD rstats club' in red, and search and moon icons. The main title of the post is 'Using VisiumExperiment at spatialLIBD package'. Below the title, it shows the date 'Nov 6, 2020', a reading time of '15 min read', '0 Comments', and tags 'research, rstats, spatial transcriptomics'. The author is 'Brenda Pardo'. The first paragraph describes the author's experience joining the Lieber Institute for Brain Development and working on the *spatialLIBD* package. The second paragraph is titled 'Starting internship at Lieber Institute' and describes the author's background and how they joined the team.

LIBD rstats club

## Using VisiumExperiment at spatialLIBD package

Nov 6, 2020 · 15 min read · 0 Comments · research, rstats, spatial transcriptomics

By Brenda Pardo

A month ago, I started an enriching adventure by joining Leonardo Collado-Torres' team at Lieber Institute for Brain Development. Since then, I have been working on modifying *spatialLIBD*, a package to interactively visualize the LIBD human dorsolateral pre-frontal cortex (DLPFC) spatial transcriptomics data (Maynard, Collado-Torres, Weber, Uytingco, et al., 2020). The performed modifications allow *spatialLIBD* to use objects of the *VisiumExperiment* class, which is designed to specifically store spatial transcriptomics data (Righelli and Risso, 2020). In this blog post, I describe the changes we carried out to the package and happily share a piece of my journey through my research internship at LIBD.

### Starting internship at Lieber Institute

As part of the Genomic Sciences undergraduate program at Universidad Nacional Autónoma de México (UNAM), I attended a single cell data analysis course imparted by Leo Collado. During the sessions, I found quite fun and useful programming in R and decided I wanted to go deeper into the use of this programming language. My interest was enhanced when Leo highlighted in the CDSB Workshop 2020, we could not just be R users but developers, and generate helpful tools for biological data analysis. With this motivation, I reached out to Leo, and that's how the adventure started: I joined Leonardo Collado's team at LIBD, and my research internship was inaugurated with this tweet.

Check it out here!



<http://research.libd.org/rstatsclub/2020/11/06/using-visiumexperiment-at-spatiallibd-package/#starting-internship-at-lieber-institute>