Package 'MerfishData'

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Title Collection of public MERFISH datasets

Version 1.16.0

Description MerfishData is an ExperimentHub package that serves publicly available datasets obtained with Multiplexed Error-Robust Fluorescence in situ Hybridization (MERFISH). MERFISH is a massively multiplexed single-molecule imaging technology capable of simultaneously measuring the copy number and spatial distribution of hundreds to tens of thousands of RNA species in individual cells. The scope of the package is to provide MERFISH data for benchmarking and analysis.

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VignetteBuilder knitr

LazyData false

URL https://github.com/ccb-hms/MerfishData

BugReports https://github.com/ccb-hms/MerfishData/issues

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Contents

MerfishData-package 2
addHolesToPolygons 3
MouseColonIbdCadinu2024 3
MouseHypothalamusMoffitt2018 4
MouseIleumPetukhov2021 5
plotRasterImage 7
plotTabset 7
plotXY 8

Index **10**

`MerfishData-package` *Collection of public MERFISH datasets*

Description

MerfishData is an ExperimentHub package that serves publicly available datasets obtained with Multiplexed Error-Robust Fluorescence in situ Hybridization (MERFISH). MERFISH is a massively multiplexed single-molecule imaging technology capable of simultaneously measuring the copy number and spatial distribution of hundreds to tens of thousands of RNA species in individual cells. The scope of the package is to provide MERFISH data for benchmarking and analysis.

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See Also

Useful links:

- https://github.com/ccb-hms/MerfishData
- Report bugs at https://github.com/ccb-hms/MerfishData/issues

addHolesToPolygons *Add holes to polygons*

Description

Add holes to a `data.frame` of cell polygon coordinates

Usage

```
addHolesToPolygons(poly)
```

Arguments

`poly`	A `data.frame` storing cell polygon coordinates. Expected columns include • `"cell"` storing the cell ID, • `"x"` storing x-coordinates of the polygon corners, • `"y"` storing the y-coordinates of the polygon corners.

Value

A `data.frame`

Examples

```
x <- c(2053, 2053, 2053, 2056, 2059, 2059)
y <- c(51, 54, 57, 57, 57, 54)
poly <- data.frame(cell = 1, x = x, y = y)
poly <- addHolesToPolygons(poly)
```

MouseColonIbdCadinu2024 *MERFISH mouse colon IBD dataset from Cadinu et al., 2024*

Description

Obtain the MERFISH mouse colon IBD dataset from Cadinu et al., 2024

Usage

```
MouseColonIbdCadinu2024()
```

Details

Gut inflammation involves contributions from immune and non-immune cells, whose interactions are shaped by the spatial organization of the healthy gut and its remodeling during inflammation. The crosstalk between fibroblasts and immune cells is an important axis in this process, but our understanding has been challenged by incomplete cell-type definition and biogeography.

To address this challenge, Cadinu et al., 2024 used multiplexed error-robust fluorescence in situ hybridization (MERFISH) to profile the expression of 943 genes in 1.35 million cells imaged across the onset and recovery from a mouse colitis model. They identified diverse cell populations, charted their spatial organization, and revealed their polarization or recruitment in inflammation.

The barcoding scheme contained 990 possible barcodes; 943 of them were used to code the RNAs of the genes assayed via combinatorial smFISH across different stages of colitis in a mouse model; 47 of these barcodes were left unassigned ("blank"), providing a direct measure of the false-positive rate in MERFISH. Measurements for these 47 blank barcodes is stored in an `altExp` named `"blank"`.

The dataset includes cell type labels with three levels of granularity. Data were collected at multiple time points: prior to the onset of colitis (`sample_type="Healthy"`) and at intervals of 3 days, 9 days, and 21 days post-onset.

Value

An object of class `SpatialExperiment`.

Source

https://doi.org/10.5061/dryad.rjdfn2zh3

References

Cadinu et al. (2024) Charting the cellular biogeography in colitis reveals fibroblast trajectories and coordinated spatial remodeling. Cell, 187(8).

Examples

```
spe <- MouseColonIbdCadinu2024()
```

MouseHypothalamusMoffitt2018

MERFISH mouse hypothalamus dataset from Moffitt et al., 2018

Description

Obtain the MERFISH mouse hypothalamic preoptic region dataset from Moffitt et al., 2018

Usage

```
MouseHypothalamusMoffitt2018(center.coords = TRUE)
```

Arguments

`center.coords`	logical. Should spatial x- and y-coordinates be centered for each z-layer (bregma slice)? This is useful for making coordinates comparable between bregma slices for visualization and analysis. Defaults to `TRUE`. Use `FALSE` to obtain the coordinates as provided in the data release.

Details

The hypothalamus controls essential social behaviors and homeostatic functions. However, the cellular architecture of hypothalamic nuclei, including the molecular identity, spatial organization, and function of distinct cell types, is not well understood.

Moffitt et al., 2018, developed an imaging-based cell type identification and mapping method and combined it with single-cell RNA-sequencing to create a molecularly annotated and spatially resolved cell atlas of the mouse hypothalamic preoptic region.

The MERFISH measurements were obtained via combinatorial smFISH imaging for 135 genes (main experiment named `"smFISH"`), followed by sequential rounds of non-combinatorial seqFISH for 20 additional genes (stored as an `altExp` named `"seqFISH"`). These genes were considered neuronal markers and important for discriminating neuronal cell populations. For behavioral measurements, cFos was added to the set of genes measured with sequential rounds of FISH.

The barcoding scheme contained 140 possible barcodes; 135 of them were used to code the RNAs of the genes assayed via combinatorial smFISH; 5 of these barcodes were left unassigned ("blank"), providing a direct measure of the false-positive rate in MERFISH. Measurements for these 5 blank barcodes is stored in an `altExp` named `"blank"`.

Value

An object of class `SpatialExperiment`.

Source

https://doi.org/10.5061/dryad.8t8s248

References

Moffitt et al. (2018) Molecular, spatial, and functional single-cell profiling of the hypothalamic preoptic region. Science, 362(6416), eaau5324.

Examples

```
spe <- MouseHypothalamusMoffitt2018()
```

`MouseIleumPetukhov2021` *MERFISH mouse ileum dataset from Petukhov et al., 2021*

Description

Obtain the MERFISH mouse ileum dataset from Petukhov et al., 2021

Usage

```
MouseIleumPetukhov2021(
  segmentation = c("baysor", "cellpose"),
  use.images = TRUE,
  use.polygons = TRUE
)
```

Arguments

segmentation	character. Should be either "baysor" or "cellpose". Defaults to "baysor". See details.
use.images	logical. Should DAPI and Membrane Na+/K+ - ATPase images be loaded into memory and annotated to the imgData slot of the returned SpatialExperiment? Defaults to TRUE. See details.
use.polygons	logical. Should polygon cell boundaries be annotated to the metadata of the returned SpatialExperiment? Defaults to TRUE. Only available for Baysor segmentation.

Details

Spatial transcriptomics protocols based on in situ sequencing or multiplexed RNA fluorescent hybridization can reveal detailed tissue organization. Distinguishing the boundaries of individual cells in such data is challenging. Current segmentation methods typically approximate cells positions using nuclei stains.

Petukhov et al., 2021, describe Baysor, a segmentation method, which optimizes 2D or 3D cell boundaries considering joint likelihood of transcriptional composition and cell morphology. Baysor can also perform segmentation based on the detected transcripts alone.

Petukhov et al., 2021, compare the results of Baysor segmentation (mRNA-only) to the results of a deep learning-based segmentation method called Cellpose from Stringer et al., 2021. Cellpose applies a machine learning framework for the segmentation of cell bodies, membranes and nuclei from microscopy images.

The function allows to obtain segmented MERFISH mouse ileum data for both segmentation methods.

A note on storing images within a SpatialExperiment: The default use.images = TRUE reduces the 9-frame z-stack images for DAPI stain and Membrane Na+/K+ - ATPase fluorecense to single-frame images (taking the first frame). For working with the 9-frame z-stack images it is recommended to load the images individually from ExperimentHub.

Value

An object of class SpatialExperiment.

Source

https://doi.org/10.5061/dryad.jm63xsjb2

References

Petukhov et al. (2021) Cell segmentation in imaging-based spatial transcriptomics. Nat Biotechnol, 40(3), 345-54.

Stringer et al. (2021) Cellpose: a generalist algorithm for cellular segmentation. Nat Methods, 18(1), 100-6.

Examples

```
spe <- MouseIleumPetukhov2021()
```

plotRasterImage *Plot raster image*

Description

Small helper function to plot a raster image.

Usage

```
plotRasterImage(img)
```

Arguments

img	a raster object representing a bitmap image.

Value

A ggplot object.

Examples

```
hgrid <- hcl(0, 80, seq(50, 80, 10))
img <- as.raster(matrix(hgrid, nrow = 4, ncol = 5))
plotRasterImage(img)
```

plotTabset *Plot a tabset*

Description

Plot a tabset of colData annotations of one or more SpatialExperiment objects over an image.

Usage

```
plotTabset(spe.list, img)
```

Arguments

spe.list	A named list of SpatialExperiment objects.
img	a raster object representing a bitmap image.

Value

None. Produces a tabset for rendering with rmarkdown.

Examples

```
# create simulated data as described in the SpatialExperiment man page
n <- 1000; ng <- 50; nc <- 20
x <- runif(n)
y <- runif(n)

# assign each molecule to some gene-cell pair
gs <- paste0("gene", seq(ng))
cs <- paste0("cell", seq(nc))
gene <- sample(gs, n, TRUE)
cell <- sample(cs, n, TRUE)

# generate molecule coordinates
df <- data.frame(gene, cell, x, y)
df$gene <- factor(df$gene, gs)
df$cell <- factor(df$cell, cs)

mol <- BumpyMatrix::splitAsBumpyMatrix(
        df[, c("x", "y")],
        row = df$gene, column = df$cell)

# generate gene x cell molecule count matrix
y <- with(df, table(gene, cell))
y <- as.matrix(unclass(y))

# construct SpatialExperiment
spe <- SpatialExperiment(assays = list(counts = y, molecules = mol))

# add simulated cell centroids
s <- cbind(x = runif(20), y = runif(20))
spatialCoords(spe) <- s

# add simulated cell type and cell cycle annotation
ct <- c("ct1", "ct2", "ct3")
cc <- c("G1", "G2", "S", "M")
spe$type <- sample(ct, ncol(spe), replace = TRUE)
spe$cycle <- sample(cc, ncol(spe), replace = TRUE)

# create an example image
hgrid <- hcl(0, 80, seq(50, 80, 10))
img <- as.raster(matrix(hgrid, nrow = 4, ncol = 5))

# plotTabset
spe.list <- list(myseg = spe)
plotTabset(spe.list, img)
```

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plotXY *Plot spatial image with data overlay*

Description

A helper function to overlay data onto a spatial image.

Usage

```
plotXY(df, col, img = NULL)
```

Arguments

df	A data.frame storing the data to plot.
col	character. A column of df to use for overlay onto the image.
img	a raster object representing a bitmap image.

Value

A ggplot.

Examples

```
gene <- rep(c("Cd44", "Cd8b1", "Cd79b"), each = 2)
x <- c(1693, 1701, 1820, 3188, 1631, 1881)
y <- c(1831, 1666, 1855, 6612, 1533, 942)
df <- data.frame(gene = gene, x = x, y = y)
plotXY(df, "gene")
```

Index

addHolesToPolygons, 3

imgData, *6*

MerfishData *(*MerfishData-package*)*, 2
MerfishData-package, 2
metadata, *6*
MouseColonIbdCadinu2024, 3
MouseHypothalamusMoffitt2018, 4
MouseIleumPetukhov2021, 5

plotRasterImage, 7
plotTabset, 7
plotXY, 8

SpatialExperiment, *4–7*