Package 'furrowSeg'

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Type Package

Title Furrow Segmentation

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Depends R (>= 3.3), EBImage

Suggests BiocStyle, ggplot2, knitr

VignetteBuilder knitr

Imports abind, dplyr, locfit, tiff

Description Image feature data and analysis codes for the Guglielmi, Barry et al. paper describing the application of an optogenetics tools to disrupt Drosophila embryo furrowing.

biocViews ExperimentData, Drosophila_melanogaster_Data, Tissue, ReproducibleResearch

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NeedsCompilation no

R topics documented:

constructBox *Construct Box*

Description

Calculates dimensions of box for at a given DV position. Ensures that box does not exceed dimensions of image.

Usage

```
constructBox(dvPos, Lx=100, Ly=50, w=512, mid=NA)
```

Arguments

dvPos	Pixel location along DV of box center.
Lx	Half of box width in pixels.
Ly	Half of box height in pixels.
w	Image width in pixels.
mid	Location of midpoint along AP in pixels. If not specified defaults to half of the image width.

Value

A vector with locations of box corners. Nonclemature is 'xleft', 'ybottom', 'xright' and 'ytop'.

Author(s)

Joseph Barry, 2014

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="furrowSeg")
```

exampleFurrowMovie *Example Furrow Movie*

Description

An example movie on which furrowSeg segmention can be performed.

Usage

```
exampleFurrowMovie
```

Value

A 4D array.

Examples

```
data(exampleFurrowMovie, package="furrowSeg")
dim(exampleFurrowMovie)
```

`identifyFurrowPosition` *Identify Furrow Position*

Description

Identifies furrowing line by identifying DV position of minimum area.

Usage

```
identifyFurrowPosition(x, nbinsExclude=3, h=100, plot=FALSE, myCex=1.4, w=512,
    px=0.293)
```

Arguments

`x`	Feature table.
`nbinsExclude`	Number of pixel columns to exclude at the DV edges of the image.
`h`	Smoothing bandwidth, passed to locfit.
`plot`	Logical specifying whether or not to plot data and fit.
`myCex`	Size of axis labels.
`w`	Width of image in number of pixels.
`px`	Pixel dimensions in microns (assumed isotropic).

Value

The pixel index along DV indicating the furrowing position.

Author(s)

Joseph Barry, 2014

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="furrowSeg")
```

`identifyTimeMinArea` *Identify Time Point of Tissue Invagination*

Description

Identifies time point where the cell areas attain a minimum.

Usage

```
identifyTimeMinArea(x, h=2, px=0.293, plot=FALSE, myCex=1.4)
```

Arguments

x	Feature table.
h	Smoothing bandwidth, passed to locfit.
px	Pixel dimensions in microns (assumed isotropic).
plot	Logical specifying whether or not to plot data and fit.
myCex	Size of axis labels.

Value

Returns the time at which the tissue invaginates ('tstar') and the index of the corresponding time point ('tindex').

Author(s)

Joseph Barry, 2014

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="furrowSeg")
```

---

isOdd *isOdd*

Description

Checks if a number is odd or adds one to make it odd. Useful for constructing filters.

Usage

```
isOdd(x)
makeOdd(x)
```

Arguments

x	An integer.

Value

A logical indicating if number is odd or an odd integer.

Author(s)

Joseph Barry, 2014

Examples

```
isOdd(seq(1:10))
```

isolateBoxCells *Isolate Box Cells*

Description

Subsets feature table to include only cells whose center are in the interior of the specified box dimensions.

Usage

```
isolateBoxCells(x, box)
```

Arguments

x	Feature table containing centroid positions as 'x.0.m.cx' and 'x.0.m.cy'.
box	Coordinates of box corners, specified as 'xleft', 'ybottom', 'xright' and 'ytop'.

Value

A subsetted 'x' containing box cells.

Author(s)

Joseph Barry, 2014

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="furrowSeg")
```

opto *Cell Feature Data*

Description

Table containing all cell feature data for optogenetically perturbed samples and controls. Contains the following columns:

`sample` Unique sample identifier referring to the .rda object from which the image analysis was loaded.

`t` Integer index of time point.

`z` Integer index of z-stack.

`x.0.m.cx` x position (along anterior-posterior axis) of cell center in number of pixel lengths.

`x.0.m.cy` y position (along dorsal-ventral axis) of cell center in number of pixel lengths.

`x.0.m.majoraxis` Length of major axis of the cell.

`x.0.m.theta` Angle between the major axis of the cell and the anterior-posterior axis of the embryo.

`x.0.s.area` Area of the cell in number of pixels.

`x.0.s.perimeter` Perimeter length of cell in number of pixel lengths.

`x.0.s.radius.mean` Mean radius of cell in number of pixel lengths.

`x.0.s.radius.max` Maximum radius of cell in number of pixel lengths.

`e.x` First component of anisotropy vector. Referred to as AP anisotropy in the paper.

`e.y` Second component of anisotropy vector. Referred to as DV anisotropy in the paper.

`dt` Time between frames in seconds

`px` Side length of a (square) pixel in microns. Note that the z-stack spacing is longer.

`condition` Factor identifying which experimental condition cell is associated with.

Usage

```
opto
```

Value

A data table.

Examples

```
data(opto, package="furrowSeg")
head(opto)
```

---

plotFeatureEvolution *Plot Feature Evolution*

Description

Plots mean and standard deviation of area and elongation features over time.

Usage

```
plotFeatureEvolution(x, dt=32.6/60, tMax, myTitle="", cex=1.4, cex.axis=1,
    px=0.293, mar=c(5.1, 5.1, 4.1, 4.1), legend=TRUE, line=2.5)
```

Arguments

`x`	A feature table, as supplied by `constructFeatureTable`.
`dt`	Timestep in minutes (numeric).
`tMax`	Latest time point to plot in minutes (numeric).
`myTitle`	Plot title (string).
`cex`	Label size.
`cex.axis`	See help for `par`.
`px`	Pixel width in microns.
`mar`	See help for `par`.
`legend`	A logical. Should figure legend be displayed or not?
`line`	Determines placement of right-hand axis label. See help for `mtext`.

Value

Nothing is returned from this function.

Author(s)

Joseph Barry, 2014

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="furrowSeg")
```

`px2area` *px2area*

Description

Converts area in pixels to microns squared and vice versa.

Usage

```
px2area(x, px)
area2px(x, px)
```

Arguments

`x`	A vector of numbers.
`px`	Side-length of a pixel in microns.

Value

A vector of areas in new units.

Author(s)

Joseph Barry, 2014

Examples

```
# pixels side-length half a micron, square of 10x10 pixels
px2area(x=10*10, px=0.5)
```

px2microns *px2microns*

Description

Converts length in pixels to microns and vice versa.

Usage

```
px2microns(x, px)
microns2px(x, px)
```

Arguments

x	A vector of numbers.
px	Side-length of a pixel in microns.

Value

A vector of lengths in new units.

Author(s)

Joseph Barry, 2014

Examples

```
# map a contiguous block of 8 pixels to position in microns (here pixel side-length is half a micron)
px2microns(x=seq(1:8), px=0.5)
```

sampeTable *Table of image names with metadata*

Description

Contains names of the images used in study, and assigns them to their respective experimental groupings. The time interval between frames is listed in seconds and the (isotropic) pixel dimensions in microns.

Usage

```
sampleTable
```

Value

A data table.

Examples

```
data(sampleTable, package="furrowSeg")
head(sampleTable)
```

segmentFurrowAllStacks

Cell segmentation of furrow images.

Description

Performs segmentation on furrow images using smoothing, adaptive thresholding and watershed algorithms.

Usage

```
segmentFurrowAllStacks(x, L=17, filterSize=3, threshOffset=0.001, closingSize=3,
    minObjectSize=2^5, maxObjectSize=2^10)
```

Arguments

x	A 4-dimensional image with dimensions x, y, z, t
L	The characterisitc diameter of a cell in pixels.
filterSize	The size of the filter for gaussian smoothing.
threshOffset	The offset value for the adaptive thresholding algorithm that is used to segment cytoplasmic fluorescence signal.
closingSize	The size of the brush that is used to perform a closing operation that smooths the cytoplasmic mask after the adaptive thresholding.
minObjectSize	Determines the threshold below which objects in the cytoplasmic mask are removed.
maxObjectSize	Determines the threshold above which objects in the cytoplasmic mask are removed.

Value

A list with items.

x	A smoothed version of the original image array
mask	Cell masks
hs	An image showing highlighted segmentation of the cell masks

Author(s)

Joseph Barry, 2014

Examples

```
if (interactive()) vignette(topic="exampleFurrowSegmentation", package="furrowSeg")
```

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