Package ‘furrowSeg’
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Type Package
Title Furrow Segmentation
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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
License Artistic-2.0
NeedsCompilation no

R topics documented:

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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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>dvPos</td>
<td>Pixel location along DV of box center.</td>
</tr>
<tr>
<td>Lx</td>
<td>Half of box width in pixels.</td>
</tr>
<tr>
<td>Ly</td>
<td>Half of box height in pixels.</td>
</tr>
<tr>
<td>w</td>
<td>Image width in pixels.</td>
</tr>
<tr>
<td>mid</td>
<td>Location of midpoint along AP in pixels. If not specified defaults to half of the image width.</td>
</tr>
</tbody>
</table>

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")

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

exampleFurrowMovie   

Example Furrow Movie

Description
An example movie on which furrowSeg segmentation can be performed.

Usage
data(exampleFurrowMovie, package="furrowSeg")
identifyFurrowPosition

**Identify Furrow Position**

**Description**

Identifies furrowing line by identifying DV position of minimum area.

**Usage**

```r
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**

```r
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**

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

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

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

isOdd

Description

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

Usage

```r
isOdd(x)
makеOdd(x)
```

Arguments

- **x**: An integer.

Value

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

Author(s)

Joseph Barry, 2014

Examples

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

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.
plotFeatureEvolution

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")

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

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)

sampleTable

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)
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 characteristic 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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