Package ‘furrowSeg’

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Type Package
Title Furrow Segmentation
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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
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R topics documented:

constructBox ................................................................. 2
exampleFurrowMovie ...................................................... 3
identifyFurrowPosition .................................................. 3
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 segmentation 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).
identifyTimeMinArea

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

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

**Usage**

```r
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**

```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**

```r
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

```r
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**

```r
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**

**Description**

Converts area in pixels to microns squared and vice versa.

**Usage**

```r
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**

```r
# 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**

```r
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)

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 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

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

* datasets
  exampleFurrowMovie, 3
  opto, 6
  sampeTable, 9

* furrow
  constructBox, 2
  identifyFurrowPosition, 3
  identifyTimeMinArea, 4
  isOdd, 5
  isolateBoxCells, 5
  plotFeatureEvolution, 7
  px2area, 8
  px2microns, 8
  segmentFurrowAllStacks, 9

area2px (px2area), 8

constructBox, 2

eampleFurrowMovie, 3

identifyFurrowPosition, 3
identifyTimeMinArea, 4
isOdd, 5
isolateBoxCells, 5

makeOdd (isOdd), 5
microns2px (px2microns), 8
mtext, 7

opto, 6

par, 7
plotFeatureEvolution, 7
px2area, 8
px2microns, 8

sampeTable, 9
sampeTable (sampeTable), 9
segmentFurrowAllStacks, 9