Package ‘furrowSeg’

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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:

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constructBox

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

Usage

calculateBox(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**  
```r
exampleFurrowMovie
```

**Value**  
A 4D array.

**Examples**  
```r
data(exampleFurrowMovie, package="furrowSeg")
dim(exampleFurrowMovie)
```

---

**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).
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")
Description

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

Usage

isOdd(x)
makesOdd(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))

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

---

**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

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

---

**plotFeatureEvolution**  
**Plot Feature Evolution**

**Description**

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

**Usage**

```r
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**

```r
if (interactive()) vignette(topic="genPaperFigures", package="furrowSeg")
```
px2area

Description
Converting 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
Converting 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.
sampeTable

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

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