Package 'synapsis'

July 21, 2025

Type Package

Title An R package to automate the analysis of double-strand break repair during meiosis

Version 1.15.0

Description Synapsis is a Bioconductor software package for automated (unbiased and reproducible) analysis of meiotic immunofluorescence datasets. The primary functions of the software can i) identify cells in meiotic prophase that are labelled by a synaptonemal complex axis or central element protein, ii) isolate individual synaptonemal complexes and measure their physical length, iii) quantify foci and co-localise them with synaptonemal complexes, iv) measure interference between synaptonemal complex-associated foci. The software has applications that extend to multiple species and to the analysis of other proteins that label meiotic prophase chromosomes. The software converts meiotic immunofluorescence images into R data frames that are compatible with machine learning methods. Given a set of microscopy images of meiotic spread slides, synapsis crops images around individual single cells, counts colocalising foci on strands on a per cell basis, and measures the distance between foci on any given strand.

biocViews Software, SingleCell

Depends R (>= 4.1)

Imports EBImage, stats, utils, graphics

License MIT + file LICENSE

Encoding UTF-8

RoxygenNote 7.1.1

VignetteBuilder knitr

Suggests knitr, rmarkdown, testthat (>= 3.0.0), ggplot2, tidyverse, BiocStyle

Config/testthat/edition 3

git_url https://git.bioconductor.org/packages/synapsis

git_branch devel

git_last_commit 6ff9c64

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-07-20

Author Lucy McNeill [aut, cre, cph] (ORCID:
<https://orcid.org/0000-0003-1752-4882>),
Wayne Crismani [rev, ctb] (ORCID:
<https://orcid.org/0000-0003-0143-8293>)

Maintainer Lucy McNeill <luc.mcneill@gmail.com>

Contents

`annotate_foci_counting` *annotate_foci_counting*

Description

Contains all plotting routines for count foci annotation

Usage

```
annotate_foci_counting(
  img_file,
  cell_count,
  img_orig,
  img_orig_foci,
  artificial_amp_factor,
  strands,
  coincident_foci,
  foci_label,
  alone_foci,
  percent_px,
  foci_per_cell
)
```

Arguments

img_file	cell's file name
cell_count	unique cell counter
img_orig	original strand crop
img_orig_foci	cropped foci channel
artificial_amp_factor	amplification factor
strands	black white mask of strand channel
coincident_foci	mask of overlap between strand and foci channel
foci_label	black and white mask of foci channel
alone_foci	estimated number of foci that are NOT on a strand.
percent_px	percentage of foci mask that coincides with strand channel small number indicates potentially problematic image.
foci_per_cell	number of foci counted per cell

Value

displays key steps from raw image to coincident foci count

---

annotate_foci_counting_adjusted *annotate_foci_counting_adjusted*

Description

Contains all plotting routines for count foci annotation

Usage

```
annotate_foci_counting_adjusted(
  img_file,
  cell_count,
  img_orig,
  img_orig_foci,
  artificial_amp_factor,
  strands,
  coincident_foci,
  foci_label,
  alone_foci,
  percent_px,
  foci_per_cell
)
```

Arguments

`img_file`	cell's file name
`cell_count`	unique cell counter
`img_orig`	original strand crop
`img_orig_foci`	cropped foci channel
`artificial_amp_factor`	amplification factor
`strands`	black white mask of strand channel
`coincident_foci`	mask of overlap between strand and foci channel
`foci_label`	black and white mask of foci channel
`alone_foci`	estimated number of foci that are NOT on a strand.
`percent_px`	percentage of foci mask that coincides with strand channel small number indicates potentially problematic image.
`foci_per_cell`	number of foci counted per cell

Value

displays key steps from raw image to coincident foci count

`append_data_frame` *append_data_frame*

Description

applies new row to data frame

Usage

```
append_data_frame(
  WT_str,
  KO_str,
  WT_out,
  KO_out,
  img_file,
  foci_areas,
  df_cells,
  cell_count,
  stage,
  foci_per_cell,
  image_mat,
  percent_px,
  alone_foci,
  discrepant_category,
  C1
)
```

Arguments

WT_str	string in filename corresponding to wildtype genotype. Defaults to ++.
KO_str	string in filename corresponding to knockout genotype. Defaults to –.
WT_out	string in output csv in genotype column, for knockout. Defaults to +/+.
KO_out	string in output csv in genotype column, for knockout. Defaults to -/-.
img_file	cell's file name
foci_areas	pixel area of each foci
df_cells	current data frame
cell_count	unique cell counter
stage	meiosis stage of interest. Currently count_foci determines this with thresholding/ object properties in the synaptonemal complex channel by previosly calling the get_pachytene function. Note that if using this option, the count_foci function requires that the input directory contains a folder called "pachytene" with the crops in it.
foci_per_cell	foci count for cell
image_mat	matrix with all pixel values above zero
percent_px	percentage of foci mask that coincides with strand channel small number indicates potentially problematic image.
alone_foci	estimated number of foci that are NOT on a strand.
discrepant_category	estimated number of foci that are NOT on a strand.
C1	criteria

Value

data frame with new row

---

auto_crop_fast *auto_crop_fast*

Description

crop an image around each viable cell candidate.

Usage

```
auto_crop_fast(
  img_path,
  max_cell_area = 20000,
  min_cell_area = 7000,
  mean_pix = 0.08,
  annotation = "off",
  blob_factor = 15,
  bg_blob_factor = 10,
  offset = 0.2,
  final_blob_amp = 10,
```

```
  test_amount = 0,
  brush_size_blob = 51,
  sigma_blob = 15,
  channel3_string = "DAPI",
  channel2_string = "SYCP3",
  channel1_string = "MLH3",
  file_ext = "jpeg",
  third_channel = "off",
  cell_aspect_ratio = 2,
  strand_amp = 2,
  path_out = img_path,
  resize_l = 720,
  crowded_cells = "FALSE",
  watershed_radius = 50,
  watershed_tol = 0.2,
  cropping_factor = 1.3
)
```

Arguments

`img_path`	path containing image data to analyse
`max_cell_area`	Maximum pixel area of a cell candidate
`min_cell_area`	Minimum pixel area of a cell candidate
`mean_pix`	Mean pixel intensity of cell crop (in SYCP3 channel) for normalisation
`annotation`	Choice to output pipeline choices (recommended to knit)
`blob_factor`	Contrast factor to multiply original image by before smoothing/smudging
`bg_blob_factor`	Contrast factor to multiply original image by to take background. Used prior to thresholding.
`offset`	Pixel value offset from bg_blob_factor. Used in thresholding to make blob mask.
`final_blob_amp`	Contrast factor to multiply smoothed/smudged image. Used in thresholding to make blob mask.
`test_amount`	Optional number of first N images you want to run function on. For troubleshooting/testing/variable calibration purposes.
`brush_size_blob`	Brush size for smudging the synaptonemal complex channel to make blobs
`sigma_blob`	Sigma in Gaussian brush for smudging the synaptonemal complex channel to make blobs
`channel3_string`	Optional. String appended to the files showing the channel illuminating cell structures. Defaults to DAPI, if third channel == "on".
`channel2_string`	String appended to the files showing the channel illuminating synaptonemal complexes. Defaults to SYCP3
`channel1_string`	String appended to the files showing the channel illuminating foci. Defaults to MLH3
`file_ext`	file extension of your images e.g. tif jpeg or png.
`third_channel`	Optional, defaults to "off". Set to "on" if you would also like crops of the third channel.

`cell_aspect_ratio`
: Maximum aspect ratio of blob to be defined as a cell

`strand_amp`
: multiplication of strand channel for get_blobs function.

`path_out`
: user specified output path. Defaults to img_path

`resize_l`
: length for resized image

`crowded_cells`
: TRUE or FALSE, defaults to FALSE. Set to TRUE if you have many cells in a frame that almost touch

`watershed_radius`
: Radius (ext variable) in watershed method used in strand channel. Defaults to 1 (small)

`watershed_tol`
: Intensity tolerance for watershed method. Defaults to 0.05.

`cropping_factor`
: size of cropping window square, as factor of characteristic blob radius. Defaults to 1. May need to increase if using watershed.

Details

This function takes all images in a directory, and crops around individual cells according to the antibody that stains synaptonemal complexes e.g. SYCP3. First, it increases the brightness and smudges the image with a Gaussian brush, and creates a mask using thresholding (get_blobs). Then it deletes cell candidates in the mask deemed too large, too small, or too long (keep_cells). Using the computeFeatures functions from EBImage to locate centre and radius, the cropping area is determined and the original image cropped. These images are saved in either a user specified directory, or a crops folder at the location of the image files.

Value

cropped synaptonemal complex and foci channels around single cells, regardless of stage

Author(s)

Lucy McNeill

Examples

```
demo_path = paste0(system.file("extdata",package = "synapsis"))
auto_crop_fast(demo_path, annotation = "on", max_cell_area = 30000,
min_cell_area = 7000, file_ext = "tif",crowded_cells = TRUE)
```

`count_foci` *count_foci*

Description

Calculates coincident foci in synaptonemal complex and foci channel, per cell

Usage

```
count_foci(
  img_path,
  stage = "none",
  offset_px = 0.2,
  offset_factor = 2,
  brush_size = 3,
  brush_sigma = 3,
  foci_norm = 0.01,
  annotation = "off",
  channel2_string = "SYCP3",
  channel1_string = "MLH3",
  file_ext = "jpeg",
  KO_str = "--",
  WT_str = "++",
  KO_out = "-/-",
  WT_out = "+/+",
  watershed_stop = "off",
  watershed_radius = 1,
  watershed_tol = 0.05,
  crowded_foci = TRUE,
  artificial_amp_factor = 1,
  strand_amp = 2,
  min_foci = -1,
  disc_size = 51,
  modify_problematic = "off",
  disc_size_foci = 5,
  C1 = 0.02,
  C2 = 0.46,
  C_weigh_foci_number = TRUE
)
```

Arguments

img_path	path containing crops to analyse
stage	meiosis stage of interest. Currently count_foci determines this with thresholding/ object properties in the synaptonemal complex channel by previosly calling the get_pachytene function. Note that if using this option, the count_foci function requires that the input directory contains a folder called "pachytene" with the crops in it.
offset_px	Pixel value offset used in thresholding of synaptonemal complex channel
offset_factor	Pixel value offset used in thresholding of foci channel
brush_size	size of brush to smooth the foci channel. Should be small to avoid erasing foci.
brush_sigma	sigma for Gaussian smooth of foci channel. Should be small to avoid erasing foci.
foci_norm	Mean intensity to normalise all foci channels to.
annotation	Choice to output pipeline choices (recommended to knit)
channel2_string	String appended to the files showing the channel illuminating synaptonemal complexes. Defaults to SYCP3

`channel1_string`
: String appended to the files showing the channel illuminating foci. Defaults to MLH3

`file_ext`
: file extension of your images e.g. tiff jpeg or png.

`KO_str`
: string in filename corresponding to knockout genotype. Defaults to –.

`WT_str`
: string in filename corresponding to wildtype genotype. Defaults to ++.

`KO_out`
: string in output csv in genotype column, for knockout. Defaults to -/-.

`WT_out`
: string in output csv in genotype column, for knockout. Defaults to +/+.

`watershed_stop`
: Stop default watershed method with "on"

`watershed_radius`
: Radius (ext variable) in watershed method used in foci channel. Defaults to 1 (small)

`watershed_tol`
: Intensity tolerance for watershed method. Defaults to 0.05.

`crowded_foci`
: TRUE or FALSE, defaults to FALSE. Set to TRUE if you have foci > 100 or so.

`artificial_amp_factor`
: Amplification of foci channel, for annotation only.

`strand_amp`
: multiplication of strand channel to make masks

`min_foci`
: minimum pixel area for a foci. Depends on your dpi etc. Defaults to 4

`disc_size`
: size of disc for local background calculation in synaptonemal complex channel

`modify_problematic`
: option for synapsis to try and "save" images which have likely been counted incorrectly due to a number of reasons. Default settings are optimized for mouse pachytene. Defaults to "off"

`disc_size_foci`
: size of disc for local background calculation in foci channel

`C1`
: Default crispness criteria = sd(foci_area)/(mean(foci_area)+1)

`C2`
: Alternative crisp criteria.

`C_weigh_foci_number`
: choose crispness criteria- defaults to TRUE to use C1 (weighing with number). Otherwise set to FALSE to use C2

Details

In this function, masks for the synaptonemal complex (SC) and foci channel are created from the saved crops of single/individual cells. These masks are computed using (optional) input parameters related to meiosis stage/ how well spread chromosomes are (for the former) and related to smoothing, thresholding and how "crowded" foci are for the latter. Finally, these two masks are multiplied, and the number of objects found with EBImage's computeFeatures are the colocalizing foci.

The file, cell number, foci count etc. are output as a data frame.

Value

data frame with foci count per cell

Author(s)

Lucy McNeill

Examples

```
demo_path = paste0(system.file("extdata",package = "synapsis"))
foci_counts <- count_foci(demo_path,offset_factor = 3, brush_size = 3,
brush_sigma = 3, annotation = "on",stage = "pachytene")
```

---

crop_single_object_fast *crop_single_object_fast*

Description

Creates mask for every individual cell candidate in mask

Usage

```
crop_single_object_fast(
  retained,
  OOI_final,
  counter_final,
  img_orig,
  img_orig_foci,
  img_orig_DAPI = "blank",
  file_sc,
  file_foci,
  file_DAPI = "blank",
  cell_count,
  mean_pix,
  annotation,
  file_base,
  img_path,
  r_max,
  cx,
  cy,
  channel3_string,
  channel2_string,
  channel1_string,
  file_ext,
  third_channel,
  path_out,
  img_orig_highres,
  resize_l,
  crowded_cells,
  cropping_factor
)
```

Arguments

retained	Mask of cell candidates which meet size criteria. After smoothing/smudging and thresholding.
OOI_final	Objects of interest count. Total number of cell candidates in retained.

counter_final	Counter for single cell we are focussing on. Remove all other cells where counter_single not equal to counter_final.
img_orig	description
img_orig_foci	description
img_orig_DAPI	description
file_sc	filename of synaptonemal complex channel image
file_foci	filename of foci channel image
file_DAPI	filename of DAPI channel image
cell_count	counter for successful crops around cells
mean_pix	Mean pixel intensity of cell crop (in SYCP3 channel) for normalisation
annotation	Choice to output pipeline choices (recommended to knit)
file_base	filename base common to all three channels i.e. without -MLH3.jpeg etc.
img_path	path containing image data to analyse
r_max	maximum radius of blob for cropping
cx	centre of blob x
cy	centre of blob y
channel3_string	Optional. String appended to the files showing the channel illuminating cell structures. Defaults to DAPI, if third channel == "on".
channel2_string	String appended to the files showing the channel illuminating synaptonemal complexes. Defaults to SYCP3
channel1_string	String appended to the files showing the channel illuminating foci. Defaults to MLH3
file_ext	file extension of your images e.g. tif jpeg or png.
third_channel	Optional, defaults to "off". Set to "on" if you would also like crops of the third channel.
path_out	user specified output path. Defaults to img_path
img_orig_highres	the original strand image with original resolution
resize_l	length of square to resize original image to.
crowded_cells	TRUE or FALSE, defaults to FALSE. Set to TRUE if you have many cells in a frame that almost touch
cropping_factor	size of cropping window square, as factor of characteristic blob radius. Defaults to 1. May need to increase if using watershed.

Value

Crops around all candidates in both channels

get_blobs *get_blobs*

Description

Makes mask of all objects bright enough to be classified as a cell cadidate

Usage

```
get_blobs(
  img_orig,
  blob_factor,
  bg_blob_factor,
  offset,
  final_blob_amp,
  brush_size_blob,
  sigma_blob,
  watershed_tol,
  watershed_radius,
  crowded_cells,
  annotation
)
```

Arguments

img_orig	Original image
blob_factor	Contrast factor to multiply original image by before smoothing/smudging
bg_blob_factor	Contrast factor to multiply original image by to take background. Used prior to thresholding.
offset	Pixel value offset from bg_blob_factor. Used in thresholding to make blob mask.
final_blob_amp	Contrast factor to multiply smoothed/smudged image. Used in thresholding to make blob mask.
brush_size_blob	Brush size for smudging the synaptonemal complex channel to make blobs
sigma_blob	Sigma in Gaussian brush for smudging the synaptonemal complex channel to make blobs
watershed_tol	Intensity tolerance for watershed method. Defaults to 0.05.
watershed_radius	Radius (ext variable) in watershed method used in strand channel. Defaults to 1 (small)
crowded_cells	TRUE or FALSE, defaults to FALSE. Set to TRUE if you have many cells in a frame that almost touch
annotation	Choice to output pipeline choices (recommended to knit) have many cells in a frame that almost touch

Value

Mask with cell candidates

get_C1 *get_C1*

Description

calculates the statistic to compare to crisp_criteria, which determines whether the foci count will be reliable

Usage

```
get_C1(foci_areas, foci_per_cell, C_weigh_foci_number)
```

Arguments

foci_areas	pixel area of each foci
foci_per_cell	foci count for cell
C_weigh_foci_number	choose crispness criteria- defaults to TRUE to use C1 (weighing with number). Otherwise set to FALSE to use C2

Value

statistic to comapre to crisp_criteria

get_coincident_foci *get_coincident_foci*

Description

calculates the statistic to compare to crisp_criteria, which determines whether the foci count will be reliable

Usage

```
get_coincident_foci(
  offset_px,
  offset_factor,
  brush_size,
  brush_sigma,
  annotation,
  watershed_stop,
  watershed_radius,
  watershed_tol,
  crowded_foci,
  artificial_amp_factor,
  strand_amp,
  disc_size,
  disc_size_foci,
  img_file,
```

```
  cell_count,
  img_orig,
  img_orig_foci,
  stage,
  WT_str,
  KO_str,
  WT_out,
  KO_out,
  C1_search,
  discrepant_category,
  C1,
  C2,
  df_cells,
  C_weigh_foci_number
)
```

Arguments

offset_px	Pixel value offset used in thresholding of synaptonemal complex channel
offset_factor	Pixel value offset used in thresholding of foci channel
brush_size	size of brush to smooth the foci channel. Should be small to avoid erasing foci.
brush_sigma	sigma for Gaussian smooth of foci channel. Should be small to avoid erasing foci.
annotation	Choice to output pipeline choices (recommended to knit)
watershed_stop	Stop default watershed method with "on"
watershed_radius	Radius (ext variable) in watershed method used in foci channel. Defaults to 1 (small)
watershed_tol	Intensity tolerance for watershed method. Defaults to 0.05.
crowded_foci	TRUE or FALSE, defaults to FALSE. Set to TRUE if you have foci > 100 or so.
artificial_amp_factor	Amplification of foci channel, for annotation only.
strand_amp	multiplication of strand channel to make masks
disc_size	size of disc for local background calculation in synaptonemal complex channel
disc_size_foci	size of disc for local background calculation in foci channel
img_file	cell's file name
cell_count	unique cell counter
img_orig	original strand crop
img_orig_foci	cropped foci channel
stage	meiosis stage of interest. Currently count_foci determines this with thresholding/ object properties in the synaptonemal complex channel by previosly calling the get_pachytene function. Note that if using this option, the count_foci function requires that the input directory contains a folder called "pachytene" with the crops in it.
WT_str	string in filename corresponding to wildtype genotype. Defaults to ++.
KO_str	string in filename corresponding to knockout genotype. Defaults to –.
WT_out	string in output csv in genotype column, for knockout. Defaults to +/+.

KO_out	string in output csv in genotype column, for knockout. Defaults to -/-.
C1_search	TRUE or FALSE whether the image is still being modified until it meets the crispness criteria
discrepant_category	estimated number of foci that are NOT on a strand.
C1	Default crispness criteria = sd(foci_area)/(mean(foci_area)+1)
C2	Alternative crisp criteria.
df_cells	current data frame
C_weigh_foci_number	choose crispness criteria- defaults to TRUE to use C1 (weighing with number). Otherwise set to FALSE to use C2

Value

data frame with new row with most recent foci per cell appended

---

`get_foci_per_cell` *get_foci_per_cell*

Description

creates mask for coincident foci

Usage

```
get_foci_per_cell(
  img_file,
  offset_px,
  stage,
  strands,
  watershed_stop,
  foci_label,
  annotation,
  cell_count,
  img_orig,
  img_orig_foci,
  artificial_amp_factor,
  coincident_foci
)
```

Arguments

img_file	cell's file name
offset_px	Pixel value offset used in thresholding of synaptonemal complex channel
stage	meiosis stage of interest. Currently count_foci determines this with thresholding/ object properties in the synaptonemal complex channel by previosly calling the get_pachytene function. Note that if using this option, the count_foci function requires that the input directory contains a folder called "pachytene" with the crops in it.

strands	black white mask of strand channel
watershed_stop	Stop default watershed method with "on"
foci_label	black and white mask of foci channel
annotation	Choice to output pipeline choices (recommended to knit)
cell_count	unique cell counter
img_orig	original strand crop
img_orig_foci	cropped foci channel
artificial_amp_factor	amplification factor
coincident_foci	mask of coincident foci

Value

number of foci per cell

`get_overlap_mask` *get_overlap_mask*

Description

creates mask for coincident foci

Usage

```
get_overlap_mask(
  strands,
  foci_label,
  watershed_stop,
  img_orig_foci,
  watershed_radius,
  watershed_tol
)
```

Arguments

strands	black white mask of strand channel
foci_label	black and white mask of foci channel
watershed_stop	Stop default watershed method with "on"
img_orig_foci	cropped foci channel
watershed_radius	Radius (ext variable) in watershed method used in foci channel. Defaults to 1 (small)
watershed_tol	Intensity tolerance for watershed method. Defaults to 0.05.

Value

mask with coincident foci on strands

get_pachytene *get_pachytene*

Description

Identifies crops in pachytene

Usage

```
get_pachytene(
  img_path,
  species_num = 20,
  offset = 0.2,
  ecc_thresh = 0.85,
  area_thresh = 0.06,
  annotation = "off",
  channel2_string = "SYCP3",
  channel1_string = "MLH3",
  file_ext = "jpeg",
  KO_str = "--",
  WT_str = "++",
  KO_out = "-/-",
  WT_out = "+/+",
  path_out = img_path,
  artificial_amp_factor = 3,
  strand_amp = 2,
  resize_l = 120
)
```

Arguments

img_path	path containing crops analyse
species_num	number of chromosomes in the species
offset	Pixel value offset used in therholding for the synaptonemal complex (SYCP3) channel
ecc_thresh	The minimum average eccentricity of all objects in mask determined by computefeatures, for a cell to be pachytene.
area_thresh	The minimum ratio of pixels included in mask to total, for a cell to be classified as pachytene.
annotation	Choice to output pipeline choices (recommended to knit)
channel2_string	String appended to the files showing the channel illuminating synaptonemal complexes. Defaults to SYCP3
channel1_string	String appended to the files showing the channel illuminating foci. Defaults to MLH3
file_ext	file extension of your images e.g. tiff jpeg or png.
KO_str	string in filename corresponding to knockout genotype. Defaults to –.

WT_str	string in filename corresponding to wildtype genotype. Defaults to ++.
KO_out	string in output csv in genotype column, for knockout. Defaults to -/-.
WT_out	string in output csv in genotype column, for knockout. Defaults to +/+.
path_out	user specified output path. Defaults to img_path
artificial_amp_factor	Amplification of foci channel, for RGB output files. Deaults to 3.
strand_amp	multiplication of strand channel.
resize_l	length of resized square cell image.

Details

This function takes the crops make by auto_crop fast, and determines the number of synaptonemal complex candidates by considering the local background and using EBImage functions. In general, very bright objects which contrast highly with the background will be classified as the same object. Dim objects will likely be classified as many different objects. If the number of objects is too high compared to the species number (species_num) then the cell is determined to not be in pachytene. Note that this function has been optimized for mouse cells which can be very well spread / separated.

Value

Pairs of foci and synaptonemal channel crops for pachytene

Author(s)

Lucy McNeill

Examples

```
demo_path = paste0(system.file("extdata",package = "synapsis"))
SYCP3_stats <- get_pachytene(demo_path,ecc_thresh = 0.8, area_thresh = 0.04, annotation = "on")
```

---

keep_cells *keep_cells*

Description

Deletes objects in mask which are too small, large, oblong i.e. unlikely to be a cell

Usage

```
keep_cells(
  candidate,
  max_cell_area,
  min_cell_area,
  cell_aspect_ratio,
  crowded_cells,
  annotation
)
```

Arguments

candidate	Mask of individual cell candidates
max_cell_area	Maximum pixel area of a cell candidate
min_cell_area	Minimum pixel area of a cell candidate
cell_aspect_ratio	Maximum aspect ratio of blob to be defined as a cell
crowded_cells	TRUE or FALSE, defaults to FALSE. Set to TRUE if you
annotation	Choice to output pipeline choices (recommended to knit) have many cells in a frame that almost touch

Value

Mask of cell candidates which meet size criteria

---

make_foci_mask *make_foci_mask*

Description

creates foci mask for foci channel crop

Usage

```
make_foci_mask(
  offset_factor,
  bg,
  crowded_foci,
  img_orig_foci,
  brush_size,
  brush_sigma,
  disc_size_foci
)
```

Arguments

offset_factor	Pixel value offset used in thresholding of foci channel
bg	background value- currently just mean pixel value of whole image
crowded_foci	TRUE or FALSE, defaults to FALSE. Set to TRUE if you have foci > 100 or so.
img_orig_foci	cropped foci channel
brush_size	size of brush to smooth the foci channel. Should be small to avoid erasing foci.
brush_sigma	sigma for Gaussian smooth of foci channel. Should be small to avoid erasing foci.
disc_size_foci	size of disc for local background calculation in foci channel

Value

foci mask

make_strand_mask *make_strand_mask*

Description

creates strand mask for strand channel crop

Usage

```
make_strand_mask(
  offset_px,
  stage,
  img_orig,
  disc_size,
  brush_size,
  brush_sigma
)
```

Arguments

offset_px	Pixel value offset used in thresholding of synaptonemal complex channel
stage	meiosis stage of interest. Currently count_foci determines this with thresholding/ object properties in the synaptonemal complex channel by previosly calling the get_pachytene function. Note that if using this option, the count_foci function requires that the input directory contains a folder called "pachytene" with the crops in it.
img_orig	original strand crop
disc_size	size of disc for local background calculation in synaptonemal complex channel
brush_size	size of brush to smooth the foci channel. Should be small to avoid erasing foci.
brush_sigma	sigma for Gaussian smooth of foci channel. Should be small to avoid erasing foci.

Value

strand mask

remove_XY *remove_XY*

Description

applies new row to data frame

Usage

```
remove_XY(foci_label, foci_candidates, foci_areas)
```

Arguments

`foci_label`	black and white mask of foci channel
`foci_candidates`	computeFeatures data frame of foci channel
`foci_areas`	the areas of the foci objects

Value

mask with XY blob removed

Index