Package: spaSim (via r-universe)

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Title Spatial point data simulator for tissue images

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Description A suite of functions for simulating spatial patterns of cells in tissue images. Output images are multitype point data in SingleCellExperiment format. Each point represents a cell, with its 2D locations and cell type. Potential cell patterns include background cells, tumour/immune cell clusters, immune rings, and blood/lymphatic vessels.

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bg1 *Background cells (4915 cells in a 2000*2000 window)*

Description

A data frame containing 4915 background cells on 2000 by 2000 size window

Usage

```
bg1
```

Format

A data frame with 4915 rows (cells) and 3 columns:

Cell.X.Position X coordinate

Cell.Y.Position Y coordinate

Cell.Type cell type

format_spe *format_spe*

Description

Format a data frame object into a SpatialExperiment class object where the count assay is empty.

Usage

```
format_spe(df)
```

Arguments

df	A data frame where each row contains information about a cell. The columns of the data frame will become the colData of the SpatialExperiment object.

Value

An SPE object

multiple_background_images *Simulate multiple background images (mixed cell types)*

Description

Generate a set of background images with different proportions of mixed cell types all at once. The default values for the arguments give an example of multiple image simulation which enable an automatic multiple image simulation without the specification of any argument.

Usage

```
multiple_background_images(
  bg_sample = bg1,
  idents = c("Tumour", "Immune", "Others"),
  props = list(rep(0.1, 9), seq(0, 0.4, 0.05), seq(0.9, 0.5, -0.05)),
  plot_image = TRUE,
  plot_colours = NULL
)
```

Arguments

bg_sample	A data frame or SpatialExperiment class object with locations of points representing background cells. Further cell types will be simulated based on this background sample. The data.frame or the spatialCoords() of the SPE object should have colnames including "Cell.X.Positions" and "Cell.Y.Positions". By default use the internal bg1 background image.
idents	String Vector. Names of the cell types to generate.
props	List. Each element is a vector of proportions of the corresponding cell type. The length of the vector is how many images to generate. All vectors should be of the same length, also equal to the number of images.
plot_image	Boolean. Whether plot the simulated images or not. Default is TRUE.
plot_colours	String Vector. If plot_image is TRUE, this param is the corresponding colours for the idents arg. Default is NULL, the predefined colour vector would be used for plotting.

Value

A list of SPE objects

See Also

multiple_images_with_clusters for simulating multiple images with clusters, and multiple_images_with_immune_rin for simulating multiple images with immune rings.

Other simulate multiple images functions: multiple_images_with_clusters(), multiple_images_with_immune_rings(

Examples

```
idents <- c("Tumour","Immune","Others")
prop1 <- rep(0.1,9)
prop2 <- seq(0, 0.4, 0.05)
prop3 <- seq(0.9,0.5,-0.05)
set.seed(610)
bg_image_list <- multiple_background_images(bg_sample = bg1,
idents = idents, props = list(prop1, prop2, prop3), plot_image = FALSE)
```

---

multiple_images_with_clusters

Simulate multiple images with clusters

Description

Generate a set of images with different cluster properties. Trying out the default parameters is recommended for understanding this function. The default values for the arguments give an example of multiple image simulation which enable an automatic multiple image simulation without the specification of any argument.

Usage

```
multiple_images_with_clusters(
  bg_sample = bg1,
  cluster_shape = 2,
  prop_infiltration = 0.1,
  cluster_size = seq(200, 1000, 100),
  cluster_loc_x = 0,
  cluster_loc_y = 0,
  plot_image = TRUE,
  plot_categories = NULL,
  plot_colours = NULL
)
```

Arguments

`bg_sample`	A data frame or `SpatialExperiment` class object with locations of points representing background cells. Further cell types will be simulated based on this background sample. The data.frame or the `spatialCoords()` of the SPE object should have colnames including "Cell.X.Positions" and "Cell.Y.Positions". By default use the internal bg1 background image.
`cluster_shape`	Number. Choose from one of the following pre-designed shapes (1 or 2 for tumour cluster or 3 for immune cluster). The pre-designed shape contains information of the cell names of the cluster, the infiltration cell types, the proportions of infiltration, the cluster size, and the cluster centre locations. In order to simulate a set of images, use the arguments below to specify the ranges of the properties. The predefined cell types can not be changed, while users can change them manually after the simulation.
`prop_infiltration`	Numeric Vector. The degree of infiltration. If numeric, all simulated images have the same infiltration degree. If vector, images with a range of different infiltration proportions will be simulated.
`cluster_size`	Numeric Vector. The size of the cluster. If numeric, all simulated images have the same cluster size. If vector, images with a range of different cluster sizes will be simulated. The size should not exceed the limit of the image sides.
`cluster_loc_x`	Numeric or Vector. The X location of the cluster center offset. If numeric, all simulated images have the same center X location. If vector, images with a range of different center locations will be simulated.
`cluster_loc_y`	Numeric or Vector of the same length of `cluster_loc_x`. The Y location of the cluster center offset.
`plot_image`	Boolean Whether plot the simulated images or not.Default is TRUE.
`plot_categories`	String Vector specifying the order of the cell categories to be plotted. Default is NULL - the cell categories under the "Cell.Type" column would be used for plotting.
`plot_colours`	String Vector specifying the order of the colours that correspond to the `plot_categories` arg. Default is NULL - the predefined colour vector would be used for plotting.

Value

A list of SPE objects

See Also

multiple_background_images for simulating multiple mixed background images, and multiple_images_with_immune_r for simulating multiple images with immune rings.

Other simulate multiple images functions: multiple_background_images(), multiple_images_with_immune_rings()

Examples

```
set.seed(610)
cluster_image_list <- multiple_images_with_clusters(bg_sample=bg1,
cluster_shape=2, prop_infiltration=0.1, cluster_size = seq(200,1000,100),
cluster_loc_x = 0, cluster_loc_y = 0, plot_image = TRUE)
```

---

multiple_images_with_immune_rings

Simulate multiple images with immune rings

Description

Generate a set of images with different immune ring properties. The default values for the arguments give an example of multiple image simulation which enable an automatic multiple image simulation without the specification of any argument.

Usage

```
multiple_images_with_immune_rings(
  bg_sample = bg1,
  cluster_size = 200,
  ring_shape = 1,
  prop_infiltration = 0,
  ring_width = seq(50, 100, 10),
  cluster_loc_x = 0,
  cluster_loc_y = 0,
  prop_ring_infiltration = seq(0, 0.2, 0.05),
  plot_image = TRUE,
  plot_categories = NULL,
  plot_colours = NULL
)
```

Arguments

bg_sample	A data frame or SpatialExperiment class object with locations of points representing background cells. Further cell types will be simulated based on this background sample. The data.frame or the spatialCoords() of the SPE object should have colnames including "Cell.X.Positions" and "Cell.Y.Positions". By default use the internal bg1 background image.
cluster_size	Numeric Vector. The size of the cluster. If numeric, all simulated images have the same cluster size. If vector, images with a range of different cluster sizes will be simulated. The size should not exceed the limit of the image sides.
ring_shape	Number. Choose from one of the following pre-designed shapes (1,2 or 3). The pre-designed shape contains information of the cell names of the cluster, the infiltration cell types, the proportions of infiltration, the cluster size, the ring width, the proportions of infiltrated cells into immune rings and the cluster centre locations. In order to simulate a set of images, use the arguments below to specify the ranges of the properties. The predefined cell types can not be changed, while users can change them manually after the simulation.
prop_infiltration	Numeric Vector. The degree of infiltration. If numeric, all simulated images have the same infiltration degree. If vector, images with a range of different infiltration proportions will be simulated.
ring_width	Numeric Vector. The width of the immune ring. If numeric, all simulated images have the same ring width. If vector, images with a range of different ring widths will be simulated.
cluster_loc_x	Numeric or Vector. The X location of the cluster center offset. If numeric, all simulated images have the same center X location. If vector, images with a range of different center locations will be simulated.
cluster_loc_y	Numeric or Vector of the same length of cluster_loc_x. The Y location of the cluster center offset.
prop_ring_infiltration	Numeric or Vector. The degree of tumour infiltration in the region of immune rings.
plot_image	Boolean Whether plot the simulated images or not.Default is TRUE.
plot_categories	String Vector specifying the order of the cell cateories to be plotted. Default is NULL - the cell categories under the "Cell.Type" column would be used for plotting.
plot_colours	String Vector specifying the order of the colours that correspond to the plot_categories arg. Default is NULL - the predefined colour vector would be used for plotting.

Value

A list of spe objects

See Also

multiple_background_images for simulating multiple mixed background images, and multiple_images_with_clusters for simulating multiple images with clusters.

Other simulate multiple images functions: multiple_background_images(), multiple_images_with_clusters()

Examples

```
set.seed(610)
ring_image_list <- multiple_images_with_immune_rings(bg_sample = bg1,
ring_shape = 1, prop_infiltration = 0, ring_width = seq(50,100,10),
cluster_size = 200, cluster_loc_x = 0, cluster_loc_y = 0,
prop_ring_infiltration = seq(0, 0.2,0.05), plot_image = TRUE)
```

---

plot_cells *plot_cells*

Description

Produces a scatter plot of the cells in the tissue. Cells are coloured categorically by Cell.Type column. Cell categories not specified will be coloured "lightgrey" and labled "Unspecified".

Usage

```
plot_cells(
  spe_object,
  categories_of_interest = NULL,
  colour_vector = NULL,
  feature_colname = "Cell.Type"
)
```

Arguments

spe_object	SpatialExperiment object or a data.frame that has cell locations and cell type info.
categories_of_interest	String Vector of cell categories to be coloured.
colour_vector	String Vector specifying the colours of each cell type.
feature_colname	String specifying the column the cell categories belong to.

Value

A plot is returned

simulate_background_cells *Simulate background cells*

Description

Simulate cell locations. The 2D locations of the cells are simulated and plotted in a rectangular window. Users can specify the window size, cell number and the minimum distance between two cells. All cells have the same cell type, specified by the "Cell.Type" param.

Usage

```
simulate_background_cells(
  n_cells,
  width,
  height,
  method = "Hardcore",
  min_d,
  oversampling_rate = 1.2,
  jitter = 0.3,
  Cell.Type = "Others",
  plot_image = TRUE
)
```

Arguments

n_cells	Numeric. Number of cells to simulate in the background.
width, height	Numeric. The width and height of the image.
method	String. The distribution model for the background cells. Options are "Hardcore" for tumour tissues and "Even" for normal tissues. Default is "Hardcore".
min_d	(OPTIONAL) Numeric. Use when method is "Hardcore". The minimum distance between two cells.
oversampling_rate	(OPTIONAL) Numeric. Use when method is "Hardcore". The multiplier for oversampling. Without oversampling, the simulation deletes cells that are within min_d from each other, resulting in a less total number of cells than n_cells. Default is 1.2 (this should be set based on n_cells and min_d; should always be larger than 1).
jitter	(OPTIONAL) Numeric. Use when method is "Even". The uniform distribution parameter to generate the jitter distance for each cell from the vertices of the hexagon.
Cell.Type	(OPTIONAL) String. The name of the background cell type. Default is "Others" since there shouldn't be any identity of the background cells.
plot_image	(OPTIONAL) Boolean. Default is TRUE.

Details

There are two options for the background cell distribution model. 1) Hardcore model for tumour tissues. This model uses `rHardcore` spatstat.random. Since `rHardcore` deletes cells that are within the distance of `min_d` to another cell, resulting in fewer cell specified by users, we here introduce parameter `oversampling_rate` to generate more cells than specified. 2) Normal tissues use an evenly-spaced model where the cells are distributed approximately according to the vertices of a hexagon. The function accomplishes this by generating cells on a hexagonal grid and individually applying a bounded uniform random jitter. In our algorithm, `jitter` is the parameter to define the uniform distribution of the jitter of the cells from the hexagon vertices. If there is a reference image, `jitter` can be estimated by comparing the average minimum distance between cells of the simulated image and the reference image. If without a reference image, We suggest 0.3 as the default value of `jitter` as this gives a sensible outcome.

Value

A data.frame of the simulated background image

See Also

`simulate_mixing` for mixed background simulation, `simulate_clusters` for cluster simulation, `simulate_immune_rings`/`simulate_double_rings` for immune ring simulation, and `simulate_stripes` for vessel simulation.

Other simulate pattern functions: `simulate_clusters()`, `simulate_double_rings()`, `simulate_immune_rings()`, `simulate_mixing()`, `simulate_stripes()`

Examples

```
set.seed(610) # set seed for this background image simulation for reproducibility
background_image <- simulate_background_cells(n_cells = 5000, width = 2000,
                                              height = 2000, method = "Hardcore",
                                              min_d = 10,
                                              oversampling_rate = 1.5,
                                              Cell.Type = "Others",
                                              plot_image = TRUE)
```

---

simulate_clusters *Simulate clusters*

Description

Based on an existing background image, simulate clusters of cells where the same type of cells aggregate. The default values for the arguments give an example of cluster simulation which enable an automatic simulation of clusters without the specification of any argument.

Usage

```
simulate_clusters(
  bg_sample = bg1,
  n_clusters = 2,
  bg_type = "Others",
 cluster_properties = list(C1 = list(name_of_cluster_cell = "Tumour", size = 300, shape
    = "Oval", centre_loc = data.frame(x = 500, y = 500), infiltration_types =
    c("Immune1", "Others"), infiltration_proportions = c(0.1, 0.05)), C2 =
   list(name_of_cluster_cell = "Immune1", size = 500, shape = "Irregular", centre_loc =
    data.frame(x = 1500, y = 500), infiltration_types = c("Immune2", "Others"),
    infiltration_proportions = c(0.1, 0.05))),
  plot_image = TRUE,
  plot_categories = NULL,
  plot_colours = NULL
)
```

Arguments

bg_sample	(OPTIONAL) A data frame or SpatialExperiment class object with locations of points representing background cells. Further cell types will be simulated based on this background sample. The data.frame or the spatialCoords() of the SPE object should have colnames including "Cell.X.Positions" and "Cell.Y.Positions". By default use the internal bg1 background image.
n_clusters	Numeric. Number of clusters. This must match the length(cluster_properties).
bg_type	(OPTIONAL) String. The name of the background cell type if the background sample does not have a "Cell.Type" column. By default is "Others".
cluster_properties	List of properties of the clusters. See examples for the format of this arg.
plot_image	Boolean. Whether the simulated image is plotted.
plot_categories	String Vector specifying the order of the cell categories to be plotted. Default is NULL - the cell categories under the "Cell.Type" column would be used for plotting.
plot_colours	String Vector specifying the order of the colours that correspond to the plot_categories arg. Default is NULL - the predefined colour vector would be used for plotting.

Value

A data.frame of the simulated image

See Also

simulate_background_cells for all cell simulation, simulate_mixing for mixed background simulation, simulate_immune_rings/simulate_double_rings for immune ring simulation, and simulate_stripes for vessel simulation.

Other simulate pattern functions: simulate_background_cells(), simulate_double_rings(), simulate_immune_rings(), simulate_mixing(), simulate_stripes()

Examples

```
set.seed(610)
cluster_image <- simulate_clusters(bg_sample = bg1,
n_clusters=2, cluster_properties=list(C1=list(name_of_cluster_cell="Tumour",
size=300, shape="Oval", centre_loc=data.frame("x"=500, "y"=500),
infiltration_types=c("Immune1", "Others"), infiltration_proportions=c(0.1, 0.05)),
C2=list(name_of_cluster_cell="Immune1", size=500, shape="Irregular",
centre_loc=data.frame("x"=1500,"y"=500), infiltration_types=c("Immune2", "Others"),
infiltration_proportions=c(0.1, 0.05))))
```

---

simulate_double_rings *Simulate double immune rings*

Description

Based on an existing background image, simulate double rings of immune cells that surround tumour clusters. The inner ring is the internal margin of a tumour cluster. The outer ring is the external tumour margin. The tumour clusters and the double immune rings are simulated at the same time. The default values for the arguments give an example of double ring simulation which enable an automatic simulation of double rings without the specification of any argument.

Usage

```
simulate_double_rings(
  bg_sample = bg1,
  bg_type = "Others",
  n_dr = 2,
 dr_properties = list(D1 = list(name_of_cluster_cell = "Tumour", size = 300, shape =
    "Circle", centre_loc = data.frame(x = 1000, y = 1000), infiltration_types =
   c("Immune1", "Immune2", "Others"), infiltration_proportions = c(0.15, 0.05, 0.05),
    name_of_ring_cell = "Immune1", immune_ring_width = 150,
   immune_ring_infiltration_types = c("Others"), immune_ring_infiltration_proportions =
    c(0.15), name_of_double_ring_cell = "Immune2", double_ring_width = 100,
   double_ring_infiltration_types = c("Others"), double_ring_infiltration_proportions =
    c(0.15)),
     D2 = list(name_of_cluster_cell = "Tumour", size = 300, shape =
    "Oval", centre_loc = data.frame(x = 1200, y = 1200), infiltration_types =
   c("Immune1", "Immune2", "Others"), infiltration_proportions = c(0.15, 0.05, 0.05),
    name_of_ring_cell = "Immune1", immune_ring_width = 150,
   immune_ring_infiltration_types = c("Others"), immune_ring_infiltration_proportions =
    c(0.15), name_of_double_ring_cell = "Immune2", double_ring_width = 100,
   double_ring_infiltration_types = c("Others"), double_ring_infiltration_proportions =
    c(0.15))),
  plot_image = TRUE,
  plot_categories = NULL,
  plot_colours = NULL
)
```

Arguments

bg_sample	(OPTIONAL) A data frame or SpatialExperiment class object with locations of points representing background cells. Further cell types will be simulated based on this background sample. The data.frame or the spatialCoords() of the SPE object should have colnames including "Cell.X.Positions" and "Cell.Y.Positions". By default use the internal bg1 background image.
bg_type	(OPTIONAL) String The name of the background cell type. By default is "Others".
n_dr	Number of double immune rings. This must match the length(dr_properties).
dr_properties	List of properties of the double immune rings. Please refer to the examples for the structure of dr_properties.
plot_image	Boolean. Whether the simulated image is plotted.
plot_categories	String Vector specifying the order of the cell categories to be plotted. Default is NULL - the cell categories under the "Cell.Type" column would be used for plotting.
plot_colours	String Vector specifying the order of the colours that correspond to the plot_categories arg. Default is NULL - the predefined colour vector would be used for plotting.

Value

A data.frame of the simulated image

See Also

simulate_background_cells for all cell simulation, simulate_mixing for mixed background simulation, simulate_clusters for cluster simulation, simulate_immune_rings for single immune ring simulation, and simulate_stripes for vessel simulation.

Other simulate pattern functions: simulate_background_cells(), simulate_clusters(), simulate_immune_rings(), simulate_mixing(), simulate_stripes()

Examples

```
set.seed(610)
# manually define the properties of the immune ring
dr_properties <- list(D1 = list(name_of_cluster_cell = "Tumour",size = 300,
shape = "Circle",centre_loc = data.frame("x" = 1000, "y" = 1000),infiltration_types
= c("Immune1", "Immune2", "Others"),infiltration_proportions = c(0.15, 0.05, 0.05),
name_of_ring_cell = "Immune1",immune_ring_width = 150,immune_ring_infiltration_types
= c("Others"),immune_ring_infiltration_proportions = c(0.15),name_of_double_ring_cell
= "Immune2",double_ring_width = 100,double_ring_infiltration_types = c("Others"),
double_ring_infiltration_proportions = c(0.15)),
D2 = list(name_of_cluster_cell = "Tumour",size = 300,shape = "Oval",centre_loc
= data.frame("x" = 1200, "y" = 1200),infiltration_types = c("Immune1", "Immune2", "Others"),
infiltration_proportions = c(0.15, 0.05, 0.05),name_of_ring_cell = "Immune1",
immune_ring_width = 150,immune_ring_infiltration_types = c("Others"),
immune_ring_infiltration_proportions = c(0.15),name_of_double_ring_cell = "Immune2",
double_ring_width = 100,double_ring_infiltration_types = c("Others"),
```

```
double_ring_infiltration_proportions = c(0.15)))

double_ring_image <- simulate_double_rings(bg_sample = bg1,
n_dr = 2, dr_properties = dr_properties)
```

`simulate_immune_rings` *simulate_immune_rings*

Description

Based on an existing background image, simulate rings of immune cells that surround tumour clusters. The tumour clusters and immune rings are simulated at the same time. The default values for the arguments give an example of immune ring simulation which enable an automatic simulation of immune rings without the specification of any argument.

Usage

```
simulate_immune_rings(
  bg_sample = bg1,
  bg_type = "Others",
  n_ir = 2,
 ir_properties = list(I1 = list(name_of_cluster_cell = "Tumour", size = 600, shape =
    "Circle", centre_loc = data.frame(x = 930, y = 1000), infiltration_types =
   c("Immune1", "Immune2", "Others"), infiltration_proportions = c(0.15, 0.05, 0.05),
    name_of_ring_cell = "Immune1", immune_ring_width = 150,
   immune_ring_infiltration_types = c("Others"), immune_ring_infiltration_proportions =
   c(0.15)), I2 = list(name_of_cluster_cell = "Tumour", size = 500, shape = "Oval",
    centre_loc = data.frame(x = 1330, y = 1100), infiltration_types = c("Immune1",

    "Immune2", "Others"), infiltration_proportions = c(0.15, 0.05, 0.05),
    name_of_ring_cell = "Immune1", immune_ring_width = 150,
   immune_ring_infiltration_types = c("Others"), immune_ring_infiltration_proportions =
    c(0.15))),
  plot_image = TRUE,
  plot_categories = NULL,
  plot_colours = NULL
)
```

Arguments

bg_sample	(OPTIONAL) A data frame or SpatialExperiment class object with locations of points representing background cells. Further cell types will be simulated based on this background sample. The data.frame or the spatialCoords() of the SPE object should have colnames including "Cell.X.Positions" and "Cell.Y.Positions". By default use the internal bg1 background image.
bg_type	(OPTIONAL) String The name of the background cell type. By default is "Others".

n_ir	Number of immune rings. This must match the arg length(ir_properties).
ir_properties	List of properties of the immune rings. Please refer to the examples for the structure of ir_properties.
plot_image	Boolean. Whether the simulated image is plotted.
plot_categories	String Vector specifying the order of the cell categories to be plotted. Default is NULL - the cell categories under the "Cell.Type" column would be used for plotting.
plot_colours	String Vector specifying the order of the colours that correspond to the plot_categories arg. Default is NULL - the predefined colour vector would be used for plotting.

Value

A data.frame of the simulated image

See Also

simulate_background_cells for all cell simulation, simulate_mixing for mixed background simulation, simulate_clusters for cluster simulation, simulate_double_rings for double immune ring simulation, and simulate_stripes for vessel simulation.

Other simulate pattern functions: simulate_background_cells(), simulate_clusters(), simulate_double_rings(), simulate_mixing(), simulate_stripes()

Examples

```
set.seed(610)
# manually define the properties of the immune ring
ir_properties <- list(I1=list(name_of_cluster_cell="Tumour", size=600,
shape="Circle",centre_loc=data.frame("x"=930, "y"=1000),
infiltration_types=c("Immune1", "Immune2", "Others"), infiltration_proportions
=c(0.15, 0.05, 0.05), name_of_ring_cell="Immune1", immune_ring_width=150,
immune_ring_infiltration_types=c("Others"), immune_ring_infiltration_proportions=c(0.15)),
I2=list(name_of_cluster_cell="Tumour", size=500, shape="Oval",
centre_loc=data.frame("x"=1330, "y"=1100), infiltration_types=c("Immune1", "Immune2", "Others"),
infiltration_proportions=c(0.15, 0.05, 0.05), name_of_ring_cell="Immune1",
immune_ring_width=150, immune_ring_infiltration_types=c("Others"),
immune_ring_infiltration_proportions=c(0.15)))
# simulate immune rings (`n_ir` should match the length of `ir_properties`)
immune_ring_image <- simulate_immune_rings(bg_sample=bg1,
n_ir=2, ir_properties=ir_properties)
```

simulate_mixing *Simulate mixed background image*

Description

Based on an existing background image, simulate mixed cell types with specified cell types and proportions. The default values for the arguments give an example of mixed cell type simulation which enable an automatic simulation of mixed cell types without the specification of any argument.

Usage

```
simulate_mixing(
  bg_sample = bg1,
  idents = c("Tumour", "Immune", "Others"),
  props = c(0.2, 0.4, 0.4),
  plot_image = TRUE,
  plot_colours = NULL
)
```

Arguments

bg_sample	(OPTIONAL) A data frame or SpatialExperiment class object with locations of points representing background cells. Further cell types will be simulated based on this background sample. The data.frame or the spatialCoords() of the SPE object should have colnames including "Cell.X.Positions" and "Cell.Y.Positions". By default use the internal bg1 background image.
idents	String Vector of the mixed cell types.
props	Numeric Vector of the proportions of the mixed cell types.
plot_image	Boolean. Whether the simulated image is plotted.
plot_colours	String Vector specifying the order of the colours that correspond to the idents arg. Default is NULL - the predefined colour vector would be used for plotting..

Value

A data.frame of the simulated image

See Also

simulate_background_cells for all cell simulation, simulate_clusters for cluster simulation, simulate_immune_rings/simulate_double_rings for immune ring simulation, and simulate_stripes for vessel simulation.

Other simulate pattern functions: simulate_background_cells(), simulate_clusters(), simulate_double_rings(), simulate_immune_rings(), simulate_stripes()

Examples

```
set.seed(610)
mix_background <- simulate_mixing(bg_sample=bg1,
idents=c("Tumour","Immune", "Others"), props=c(0.2, 0.4,  0.4),
plot_image=TRUE)
```

---

simulate_stripes *simulate_stripes*

Description

Based on an existing background image, simulate stripes of cells representing vessels. The cell types and widths of the stripes can be specified. The locations of the stripes are randomly simulated. Please refer to the examples to check what properties of the stripes can be specified. The default values for the arguments give an example of vessel simulation which enable an automatic simulation of vessels without the specification of any argument.

Usage

```
simulate_stripes(
  bg_sample = bg1,
  n_stripe_type = 2,
  stripe_properties = list(S1 = list(number_of_stripes = 1, name_of_stripe_cell =
    "Others", width_of_stripe = 80, infiltration_types = c("Immune"),
    infiltration_proportions = c(0.08)), S2 = list(number_of_stripes = 1,
    name_of_stripe_cell = "Others", width_of_stripe = 80, infiltration_types =
    c("Immune"), infiltration_proportions = c(0.08))),
  plot_image = TRUE,
  plot_categories = NULL,
  plot_colours = NULL
)
```

Arguments

bg_sample	(OPTIONAL) A data frame or SpatialExperiment class object with locations of points representing background cells. Further cell types will be simulated based on this background sample. The data.frame or the spatialCoords() of the SPE object should have colnames including "Cell.X.Positions" and "Cell.Y.Positions". By default use the internal bg1 background image.
n_stripe_type	Number of stripe types. Should be the same as length(stripe_properties.
stripe_properties	List of the properties of the stripes. See examples for the format of the properties. Please refer to the examples for the structure of stripe_properties.
plot_image	Boolean. Whether the simulated image is plotted. Default is TRUE.

plot_categories
: String Vector specifying the order of the cell categories to be plotted. Default is NULL - the cell categories under the "Cell.Type" column would be used for plotting.

plot_colours
: String Vector specifying the order of the colours that correspond to the plot_categories arg. Default is NULL - the predefined colour vector would be used for plotting.

Value

A data.frame of the simulated image

See Also

simulate_background_cells for all cell simulation, simulate_mixing for mixed background simulation, simulate_clusters for cluster simulation, and simulate_immune_rings/simulate_double_rings for immune ring simulation

Other simulate pattern functions: simulate_background_cells(), simulate_clusters(), simulate_double_rings(), simulate_immune_rings(), simulate_mixing()

Examples

```
stripe_properties <- list(
S1 = list(
  number_of_stripes = 1,
  name_of_stripe_cell = "Others",
  width_of_stripe = 80,
  infiltration_types = c("Immune"),
  infiltration_proportions = c(0.08)
), S2 = list(
  number_of_stripes = 1,
  name_of_stripe_cell = "Others",
  width_of_stripe = 80,
  infiltration_types = c("Immune"),
  infiltration_proportions = c(0.08)))
set.seed(610)
stripe_image <- simulate_stripes(bg_sample = bg1, n_stripe_type=2,
stripe_properties = stripe_properties, plot_image = TRUE)
```

TIS *Tissue Image Simulator (TIS)*

Description

Tissue Image Simulator (TIS) integrates the basic simulation functions in spaSim, including simulating (mixed) background image, clusters, immune rings, double immune rings and stripes. The patterns are simulated on separate layers sequentially (e.g. immune rings are simulated after/on top of background cells). And each layer is also plot sequentially.

Pattern properties (e.g. `properties_of_clusters`) contain the properties of a pattern in the format of list where each element is one pattern. These properties need to be manually defined. Details about the format of the properties see the examples in simulate_clusters simulate_immune_rings simulate_double_rings simulate_stripes

Usage

```
TIS(
  bg_sample = NULL,
  n_cells = NULL,
  width = NULL,
  height = NULL,
  bg_method = NULL,
  min_d = NULL,
  oversampling_rate = 1.2,
  jitter = 0.3,
  names_of_bg_cells = NULL,
  proportions_of_bg_cells = NULL,
  n_clusters = NULL,
  properties_of_clusters = NULL,
  n_immune_rings = NULL,
  properties_of_immune_rings = NULL,
  n_double_rings = NULL,
  properties_of_double_rings = NULL,
  n_stripe_type = NULL,
  properties_of_stripes = NULL,
  image_name = NULL,
  plot_image = FALSE,
  plot_categories = NULL,
  plot_colours = NULL
)
```

Arguments

`bg_sample`	(OPTIONAL) A data frame or `SpatialExperiment` class object with locations of points representing background cells. Further cell types will be simulated based on this background sample. The data.frame or the `spatialCoords` of the SPE object should have colnames including "Cell.X.Positions" and "Cell.Y.Positions". By default use the internal bg1 background image.
`n_cells`	(OPTIONAL) Number of background cells to simulate. Only when `bg_sample` is NULL.
`width`	(OPTIONAL) Number The width of the image.
`height`	(OPTIONAL) Number The height of the image.
`bg_method`	(OPTIONAL) String specifying the distribution of the background cells. Choose from "Hardcore" and "Even".
`min_d`	(OPTIONAL) Number The minimum distance between two cells.

`oversampling_rate`
: (OPTIONAL) Numeric. The multiplier for oversampling. Without oversampling, the simulation deletes cells that are within `min_d` from each other, resulting in a less total number of cells than `n_cells`. Default is 1.2 (this should be set based on `n_cells` and `min_d`; should always be larger than 1).

`jitter`
: (OPTIONAL) Numeric. Use when `method` is "Even". The uniform distribution parameter to generate the jitter distance for each cell from the vertices of the hexagon.

`names_of_bg_cells`
: (OPTIONAL) Vector The cell types of the background cells. If NULL, the background cells are of one type.

`proportions_of_bg_cells`
: (OPTIONAL) Vector The corresponding proportion of each cell type in the background cells.

`n_clusters`
: (OPTIONAL) Number of cell clusters. If NULL, no clusters to simulate.

`properties_of_clusters`
: (OPTIONAL) List of parameters to define the clusters.

`n_immune_rings`
: (OPTIONAL) Number of immune rings. If NULL, no immune rings to simulate.

`properties_of_immune_rings`
: (OPTIONAL) List of parameters to define the immune rings.

`n_double_rings`
: (OPTIONAL) Number of double immune rings. If NULL, no double rings to simulate.

`properties_of_double_rings`
: (OPTIONAL) List of parameters to define the double immune rings.

`n_stripe_type`
: (OPTIONAL) Number of stripe (vessel) types. If NULL, no stripes to simulate.

`properties_of_stripes`
: (OPTIONAL) List of parameters to define the stripes.

`image_name`
: (OPTIONAL) String to name the output tissue image.

`plot_image`
: Boolean. Whether the simulated image is plotted.

`plot_categories`
: String Vector specifying the order of the cell categories to be plotted. Default is NULL - the cell categories under the "Cell.Type" column would be used for plotting.

`plot_colours`
: String Vector specifying the order of the colours that correspond to the `plot_categories` arg. Default is NULL - the predefined colour vector would be used for plotting.

Value

An spe object of the simulated image

Examples

```
set.seed(610)
double_ring_image <- TIS(bg_sample=bg1, n_clusters=1,
properties_of_clusters=list(C1=list( name_of_cluster_cell="Tumour",
size=300, shape="Oval", centre_loc=data.frame("x"=500, "y"=500),
```

```
infiltration_types=c("Immune1", "Others"), infiltration_proportions=c(0.1, 0.05))),
plot_image=TRUE)
```

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