Package ‘spatialSimGP’

December 31, 2024

Title Simulate Spatial Transcriptomics Data with the Mean-variance Relationship

Version 1.0.0

Description This packages simulates spatial transcriptomics data with the mean-variance relationship using a Gaussian Process model per gene.

URL `https://github.com/kinnaryshah/spatialSimGP`

BugReports `https://github.com/kinnaryshah/spatialSimGP/issues`

Imports SpatialExperiment, MASS, SummarizedExperiment

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Encoding UTF-8

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Contents

`spatial_simulate` *Simulate SpatialExperiment object*

Description

Simulate a SpatialExperiment object with spatially varying genes

Usage

```
spatial_simulate(
  n_genes,
  proportion,
  coords,
  range_sigma.sq,
  range_beta,
  length_scale,
  length_scale_option = "fixed"
)
```

Arguments

`n_genes`	an integer specifying the number of genes to simulate.
`proportion`	a numeric value specifying the proportion of genes that will have no spatially varying patterns.
`coords`	a matrix of coordinates.
`range_sigma.sq`	a numeric vector of length 2 specifying the range of the spatial variance parameter.
`range_beta`	a numeric vector of length 2 specifying the range of the mean expression value.
`length_scale`	if length_scale_option is "fixed", a numeric value specifying the length scale parameter. If length_scale_option is "unique", a numeric vector of length n_genes specifying the length scale parameter for each gene.
`length_scale_option`	a character string specifying the length scale option. Options are "fixed" for a single length scale for all genes or "unique" for a unique length scale for each gene.

Details

This function simulates a SpatialExperiment object with spatially varying genes. The function takes in the number of genes to simulate, the proportion of genes that will have no spatially varying patterns, a matrix of coordinates, the range of the spatial variance parameter, the range of the mean expression value, the length scale parameter, and the length scale option.

Value

A SpatialExperiment object with the simulated data.

Examples

```
library(STexampleData)

set.seed(1)
n_genes <- 1
proportion <- 0.5
range_sigma.sq <- c(0.2, 3)
range_beta <- c(0.5, 9)
length_scale <- 60

spe_demo <- Visium_mouseCoronal()
colData(spe_demo)$subset <- ifelse(
  colData(spe_demo)$array_row > 20 &
  colData(spe_demo)$array_row < 65 &
  colData(spe_demo)$array_col > 30 &
  colData(spe_demo)$array_col < 65,
  TRUE, FALSE
)
spe_demo <- spe_demo[, colData(spe_demo)$subset]
coords <- spatialCoords(spe_demo)

spe <- spatial_simulate(n_genes, proportion, coords, range_sigma.sq, range_beta,
   length_scale, length_scale_option = "fixed")
```

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