

# Package ‘spatialSimGP’

December 19, 2024

**Title** Simulate Spatial Transcriptomics Data with the Mean-variance Relationship

**Version** 1.1.0

**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

**License** MIT + file LICENSE

**Encoding** UTF-8

**Suggests** testthat (>= 3.0.0), STestexampleData, ggplot2, knitr

**biocViews** Spatial, Transcriptomics, GeneExpression

**Depends** R (>= 4.4)

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/spatialSimGP>

**git\_branch** devel

**git\_last\_commit** ea76aca

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-12-18

**Author** Kinnary Shah [aut, cre] (ORCID:

<<https://orcid.org/0000-0001-7098-2116>>),

Boyi Guo [aut] (ORCID: <<https://orcid.org/0000-0003-2950-2349>>),

Stephanie C. Hicks [aut] (ORCID:

<<https://orcid.org/0000-0002-7858-0231>>)

**Maintainer** Kinnary Shah <kinnaryshahh@gmail.com>

## Contents

spatial\_simulate . . . . . 2

**Index** . . . . . 4

---

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")
```

# Index

`spatial_simulate`, [2](#)