

# Package ‘tpSVG’

July 4, 2025

**Title** Thin plate models to detect spatially variable genes

**Version** 1.5.0

**Description** The goal of ‘tpSVG’ is to detect and visualize spatial variation in the gene expression for spatially resolved transcriptomics data analysis. Specifically, ‘tpSVG’ introduces a family of count-based models, with generalizable parametric assumptions such as Poisson distribution or negative binomial distribution. In addition, comparing to currently available count-based model for spatially resolved data analysis, the ‘tpSVG’ models improves computational time, and hence greatly improves the applicability of count-based models in SRT data analysis.

**License** MIT + file LICENSE

**URL** <https://github.com/boyigu01/tpSVG>

**BugReports** <https://github.com/boyigu01/tpSVG/issues>

**biocViews** Spatial, Transcriptomics, GeneExpression, Software,  
StatisticalMethod, DimensionReduction, Regression,  
Preprocessing

**Encoding** UTF-8

**Depends** mgcv, R (>= 4.4)

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Imports** stats, BiocParallel, MatrixGenerics, methods,  
SingleCellExperiment, SummarizedExperiment, SpatialExperiment

**Suggests** BiocStyle, knitr, nnSVG, rmarkdown, scan, scuttle,  
STexampleData, escheR, ggpubr, colorspace, BumpyMatrix,  
sessioninfo, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Config/testthat/edition** 3

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

**git\_branch** devel

**git\_last\_commit** 98f4d48

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-07-03

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## Contents

tpSVG . . . . .	2
<b>Index</b>	<b>5</b>

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tpSVG	<i>Thin Plate Spline Model to Detect Spatially Variable Genes</i>
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## Description

Thin Plate Spline Model to Detect Spatially Variable Genes

## Usage

```
tpSVG(
  input,
  spatial_coords = NULL,
  X = NULL,
  family = poisson(),
  offset = log(input$sizeFactor),
  weights = NULL,
  assay_name = "counts",
  n_threads = 1,
  BPPARAM = NULL,
  verbose = FALSE,
  ...
)
```

## Arguments

<b>input</b>	SpatialExperiment or numeric matrix: Input data, which can either be a SpatialExperiment object or a numeric matrix of values. If it is a SpatialExperiment object, it is assumed to have an assay slot containing either logcounts (e.g. from the scran package) or deviance residuals (e.g. from the scry package), and a spatialCoords slot containing spatial coordinates of the measurements. If it is a numeric matrix, the values are assumed to already be normalized and transformed (e.g. logcounts), formatted as rows = genes and columns = spots, and a separate numeric matrix of spatial coordinates must also be provided with the spatial_coords argument.
<b>spatial_coords</b>	numeric matrix: Matrix containing columns of spatial coordinates, formatted as rows = spots. This must be provided if input is provided as a numeric matrix of values, and is ignored if input is provided as a SpatialExperiment object. Default = NULL.

<code>X</code>	numeric matrix: Optional design matrix containing columns of covariates per spatial location, e.g. known spatial domains. Number of rows must match the number of spatial locations. Default = NULL, which fits an intercept-only model.
<code>family</code>	a description of the error distribution and link function to be used in the model. Currently support two distributions <code>poisson</code> and <code>gaussian</code>
<code>offset</code>	This can be used to account for technician variation when <code>family = poisson</code> model is used to model raw counts. <code>offset</code> should take in the log-transformed scale factor, e.g. <code>offset = log(spe\$sizeFactor)</code> , library size, or other normalization factor.
<code>weights</code>	Reserved for future development, e.g. correcting mean-var relationship for Gaussian models. Please use with caution.
<code>assay_name</code>	character: If input is provided as a <code>SpatialExperiment</code> object, this argument selects the name of the assay slot in the input object containing the pre-processed gene expression values. For example, <code>logcounts</code> for log-transformed normalized counts from the <code>scran</code> package, or <code>binomial_deviance_residuals</code> for deviance residuals from the <code>scry</code> package. Default = "logcounts", or ignored if input is provided as a numeric matrix of values.
<code>n_threads</code>	integer: Number of threads for parallelization. Default = 1. We recommend setting this equal to the number of cores available (if working on a laptop or desktop) or around 10 or more (if working on a compute cluster).
<code>BPPARAM</code>	<code>BiocParallelParam</code> : Optional additional argument for parallelization. This argument is provided for advanced users of <code>BiocParallel</code> for further flexibility for parallelization on some operating systems. If provided, this should be an instance of <code>BiocParallelParam</code> . For most users, the recommended option is to use the <code>n_threads</code> argument instead. Default = NULL, in which case <code>n_threads</code> will be used instead.
<code>verbose</code>	logical: Whether to display verbose output for model fitting and parameter estimation from BRISC. Default = FALSE.
<code>...</code>	Reserved for future arguments.

## Value

If the input was provided as a `SpatialExperiment` object, the output values are returned as additional columns in the `rowData` slot of the input object. If the input was provided as a numeric matrix of values, the output is returned as a numeric matrix. The output values include p-values without any adjustment and statistics reporting reporting the thinplate spline model. The `test_stat` entry of the returned object is the test statistic for the corresponding model, that is F statistics for the gaussian model and the Chi-squared statistics for generalized models.

## Examples

```
library(SpatialExperiment)
library(STexampleData)
library(scran)
library(nnSVG)

# load example dataset from STexampleData package
spe <- Visium_humanDLPFC()

# preprocessing steps
```

```
# keep only spots over tissue
spe <- spe[, colData(spe)$in_tissue == 1]

# skip spot-level quality control, since this has been performed previously
# on this dataset
# Add library size
spe <- addPerCellQCMetrics(spe)

# filter low-expressed and mitochondrial genes
spe <- filter_genes(spe)

# calculate logcounts (log-transformed normalized counts) using scran package
# using library size factors
spe <- computeLibraryFactors(spe)
spe <- logNormCounts(spe)

# select small number of genes for faster runtime in this example
set.seed(123)
ix <- sample(seq_len(nrow(spe)), 4)
spe <- spe[ix, ]

# run tpSVG
set.seed(123)

# Gaussian Model
spe_gaus <- tpSVG(
  spe,
  family = gaussian(),
  assay_name = "logcounts"
)

# Poisson Model
spe_poisson <- tpSVG(
  spe,
  family = poisson,
  assay_name = "counts",
  offset = log(spe$sizeFactor) # Natural log library size
)
```

# Index

tpSVG, [2](#)