Package: SpaGER (via r-universe)

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Type Package

Title Spatial Gene Expression Prediction using scRNA-seq

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Description Integrates spatial transcriptomics data with single-cell RNA sequencing (scRNA-seq) data to predict expression of unmeasured genes in spatial data. Uses Principal Vectors (PVs) for domain adaptation followed by k-nearest neighbor weighted imputation. This R implementation provides identical results to the original Python SpaGE package with efficient C++ acceleration.

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URL `https://github.com/Zaoqu-Liu/SpaGER`

BugReports `https://github.com/Zaoqu-Liu/SpaGER/issues`

Encoding UTF-8

RoxygenNote 7.3.2

Roxygen list(markdown = TRUE)

Depends R (>= 4.0.0)

Imports stats, Matrix, methods, Rcpp (>= 1.0.0), irlba, FNN, parallel, future, future.apply, MASS

Suggests Seurat (>= 4.0.0), SeuratObject, fastICA, NMF, pls, psych, testthat (>= 3.0.0), knitr, rmarkdown, ggplot2

LinkingTo Rcpp, RcppArmadillo

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation yes

SystemRequirements C++

Repository https://zaoqu-liu.r-universe.dev

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RemoteUrl https://github.com/Zaoqu-Liu/SpaGER

RemoteRef main

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