

Package: shinyDSP (via r-universe)

October 12, 2026

Title A Shiny App For Visualizing Nanostring GeoMx DSP Data

Version 1.5.0

Description This package is a Shiny app for interactively analyzing and visualizing Nanostring GeoMX Whole Transcriptome Atlas data. Users have the option of exploring a sample data to explore this app's functionality. Regions of interest (ROIs) can be filtered based on any user-provided metadata. Upon taking two or more groups of interest, all pairwise and ANOVA-like testing are automatically performed. Available outputs include PCA, Volcano plots, tables and heatmaps. Aesthetics of each output are highly customizable.

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Imports AnnotationHub, BiocGenerics, bsicons, bslib, circlize, ComplexHeatmap, cowplot, dplyr, DT, edgeR, ExperimentHub, ggplot2, ggpubr, ggrepel, grDevices, grid, htmltools, limma, magrittr, pals, readr, S4Vectors, scales, scater, shiny, shinycssloaders, shinyjs, shinyvalidate, shinyWidgets, SingleCellExperiment, standR, stats, stringr, SummarizedExperiment, tibble, tidyr, utils, withr

biocViews DifferentialExpression, GeneExpression, ShinyApps, Spatial, Transcriptomics

URL <https://github.com/kimsjune/shinyDSP>, <http://joonkim.ca/shinyDSP/>

BugReports <https://github.com/kimsjune/shinyDSP/issues>

Suggests BiocStyle, knitr, rmarkdown, shinytest2, spelling, svglite, testthat (>= 3.0.0)

Language en-US

Depends R (>= 4.5)

Config/testthat/edition 3

VignetteBuilder knitr

Config/pak/sysreqs cmake make libmagick++-dev gsfonts libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev perl libx11-dev xz-utils zlib1g-dev

Repository <https://bioc.r-universe.dev>

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Description

Creates the shiny app, ready to be loaded

Usage

```
shinyDSP()
```

Value

A `shiny::shinyApp()` object

Author(s)

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Examples

```
library(shinyDSP)
app <- shinyDSP()
if (interactive()) {
  shiny::runApp(app)
}
```

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