Package 'shinyDSP'

November 12, 2026

Title A Shiny App For Visualizing Nanostring GeoMx DSP Data

Version 1.4.0

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 ouputs 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

git_url https://git.bioconductor.org/packages/shinyDSP

git_branch RELEASE_3_23

git_last_commit 959b62d

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-11

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`shinyDSP-package` *shinyDSP: A Shiny App For Visualizing Nanostring GeoMx DSP Data*

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 ouputs include PCA, Volcano plots, tables and heatmaps. Aesthetics of each output are highly customizable.

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See Also

Useful links:

- https://kimsjune.github.com/shinyDSP
- http://joonkim.ca/shinyDSP/
- Report bugs at https://kimsjune.github.com/ShinyDSP/issues

`.interfaceHeatmapNavPanel` *Create the "Heatmap" nav panel*

Description

Create the "Heatmap" nav panel

Usage

```
.interfaceHeatmapNavPanel()
```

Value

`bslib::nav_panel()`

Author(s)

Seung J. Kim

`.interfacePcaNavPanel` *Create the "PCA" nav panel*

Description

Create the "PCA" nav panel

Usage

```
.interfacePcaNavPanel()
```

Value

`bslib::nav_panel()`

Author(s)

Seung J. Kim

.interfaceQcNavPanel *Create the "QC" nav panel*

Description

Create the "QC" nav panel

Usage

```
.interfaceQcNavPanel()
```

Value

`bslib::nav_panel()`

Author(s)

Seung J. Kim

.interfaceSetupNavPanel *Create the "setup" nav panel*

Description

Create the "setup" nav panel

Usage

```
.interfaceSetupNavPanel()
```

Value

`bslib::nav_panel()`

Author(s)

Seung J. Kim

.interfaceSidebar *Creates the "sidebar" UI element*

Description

Creates the "sidebar" UI element

Usage

```
.interfaceSidebar(output)
```

Value

`bslib::sidebar()`

Author(s)

Seung J. Kim

.interfaceTableNavPanel *Create the "Table" nav panel*

Description

Create the "Table" nav panel

Usage

```
.interfaceTableNavPanel()
```

Value

`bslib::nav_panel()`

Author(s)

Seung J. Kim

.interfaceVolcanoNavPanel *Create the "Volcano" nav panel*

Description

Create the "Volcano" nav panel

Usage

```
.interfaceVolcanoNavPanel()
```

Value

`bslib::nav_panel()`

Author(s)

Seung J. Kim

.onAttach *Helper function that exposes .png assets to the Shiny package*

Description

Helper function that exposes .png assets to the Shiny package

Usage

```
.onAttach(libname, pkgname)
```

Arguments

libname	libname
pkgname	pkgname

Value

`shiny::addResourcePath()`

`.PCAFunction` *PCA plotting function with ggplot2*

Description

PCA plotting function with ggplot2

Usage

```
.PCAFunction(
  spe,
  precomputed,
  colourShapeBy,
  selectedVar,
  ROIshapes,
  ROIcolours
)
```

Arguments

`spe`	A SpatialExperiment::SpatialExperiment output from `standR::readGeoMx()`
`precomputed`	Output from `SingleCellExperiment::reducedDim()`
`colourShapeBy`	From input$selected_types
`selectedVar`	Either "Type" or input$selected_batch
`ROIshapes`	User input shapes from .PCA_customization() function OR PCA_customization_batch()
`ROIcolours`	User input colours from .PCA_customization() function OR PCA_customization_batch()

Value

A ggplot2::ggplot2 object

Author(s)

Seung J. Kim

`.volcanoFunction` *Volcano plot plotting function with ggplot2*

Description

Volcano plot plotting function with ggplot2

Usage

```
.volcanoFunction(
  volcano,
  delabSize,
  maxOverlap,
  title,
  logFCcutoff,
  PvalCutoff,
  DnCol,
  notDEcol,
  UpCol
)
```

Arguments

`volcano`	a data.frame
`delabSize`	from input$delabSize
`maxOverlap`	from input$maxOverlap
`title`	Contrasts title
`logFCcutoff`	from input$logFCcutoff
`PvalCutoff`	from input$PvalCutoff
`DnCol`	from input$DnCol. Determines the colour of downregulated genes.
`notDEcol`	from input$notDEcol.
`UpCol`	from input$UpCol. Determines the colour of upregulated genes.

Value

A `ggplot2::geom_point()` object

Author(s)

Seung J. Kim

shinyDSP *Creates the shiny app, ready to be loaded*

Description

Creates the shiny app, ready to be loaded

Usage

```
shinyDSP()
```

Value

A `shiny::shinyApp()` object

Author(s)

Seung J. Kim

Examples

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

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