

Package ‘shinyDSP’

September 15, 2025

Title A Shiny App For Visualizing Nanostring GeoMx DSP Data

Version 1.0.3

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, scatter, 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_21
git_last_commit 12362c3
git_last_commit_date 2025-06-16
Repository Bioconductor 3.21
Date/Publication 2025-09-14
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shinyDSP-package	<i>shinyDSP: A Shiny App For Visualizing Nanostring GeoMx DSP Data</i>
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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()
```

<i>.PCAFunction</i>	<i>PCA plotting function with ggplot2</i>
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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

<code>.volcanoFunction</code>	<i>Volcano plot plotting function with ggplot2</i>
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Description

Volcano plot plotting function with ggplot2

Usage

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

Arguments

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

Value

A `ggplot2::geom_point()` object

Author(s)

Seung J. Kim

shinyDSP	<i>Creates the shiny app, ready to be loaded</i>
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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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