

Package ‘shinyDSP’

April 24, 2025

Title A Shiny App For Visualizing Nanostring GeoMx DSP Data

Version 1.0.0

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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biocViews DifferentialExpression, GeneExpression, ShinyApps, Spatial, Transcriptomics

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

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

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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 outputs 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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