Package ‘shinyDSP’

April 22, 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 ouputs 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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Contents

`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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