

# Package ‘shinyDSP’

April 24, 2025

**Title** A Shiny App For Visualizing Nanostring GeoMx DSP Data

**Version** 1.1.0

**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

**git\_url** <https://git.bioconductor.org/packages/shinyDSP>

**git\_branch** devel

**git\_last\_commit** 759133d

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-04-23

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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.

## Author(s)

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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 <a href="#">SpatialExperiment::SpatialExperiment</a> output from <a href="#">standR::readGeoMx()</a>
precomputed	Output from <a href="#">SingleCellExperiment::reducedDim()</a>
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

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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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