

# Package ‘shinyDSP’

June 20, 2025

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

**Version** 1.1.2

**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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|                  |                                                                        |
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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.

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

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|                   |                                         |
|-------------------|-----------------------------------------|
| .interfaceSidebar | <i>Creates the "sidebar" UI element</i> |
|-------------------|-----------------------------------------|

---

### Description

Creates the "sidebar" UI element

### Usage

```
.interfaceSidebar(output)
```

### Value

```
bslib::sidebar()
```

### Author(s)

Seung J. Kim

---

|                         |                                     |
|-------------------------|-------------------------------------|
| .interfaceTableNavPanel | <i>Create the "Table" nav panel</i> |
|-------------------------|-------------------------------------|

---

### 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 | <i>PCA plotting function with ggplot2</i> |
|--------------|-------------------------------------------|

---

### 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

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|                  |                                                    |
|------------------|----------------------------------------------------|
| .volcanoFunction | <i>Volcano plot plotting function with ggplot2</i> |
|------------------|----------------------------------------------------|

---

### 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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