# Package ‘shinyDSP’

May 9, 2026

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

**Version** 1.5.0

**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.

**License** MIT + file LICENSE

**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** fed273c

**git_last_commit_date** 2026-04-28

**Repository** Bioconductor 3.24

**Date/Publication** 2026-05-08

**Author** Seung J. Kim [aut, cre] (ORCID:
<`https://orcid.org/0000-0001-5263-0758`>),
Marco Mura [aut, fnd]

**Maintainer** Seung J. Kim <`skim823@uwo.ca`>

# 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.

### Author(s)

**Maintainer**: Seung J. Kim <`skim823@uwo.ca`> (ORCID)

Other contributors:

- Marco Mura <`marco.mura@lhsc.on.ca`> [funder]

### 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)
}
```

# Index