Package: omicplotR (via r-universe)

November 9, 2026

Title Visual Exploration of Omic Datasets Using a Shiny App

Version 1.32.0

Date 2019-11-12

biocViews Software, DifferentialExpression, GeneExpression, GUI, RNASeq, DNASeq, Metagenomics, Transcriptomics, Bayesian, Microbiome, Visualization, Sequencing, ImmunoOncology

Description A Shiny app for visual exploration of omic datasets as compositions, and differential abundance analysis using ALDEx2. Useful for exploring RNA-seq, meta-RNA-seq, 16s rRNA gene sequencing with visualizations such as principal component analysis biplots (coloured using metadata for visualizing each variable), dendrograms and stacked bar plots, and effect plots (ALDEx2). Input is a table of counts and metadata file (if metadata exists), with options to filter data by count or by metadata to remove low counts, or to visualize select samples according to selected metadata.

Imports compositions, DT, grDevices, knitr, jsonlite, matrixStats, rmarkdown, shiny, stats, vegan, zCompositions

VignetteBuilder knitr

Depends R (>= 3.6), ALDEx2 (>= 1.18.0)

License MIT + file LICENSE

LazyData true

Encoding UTF-8

RoxygenNote 6.0.1

Config/pak/sysreqs cmake make libjpeg-dev libpng-dev libuv1-dev zlib1g-dev

Repository Bioconductor 3.23

Date/Publication 2026-04-28 12:47:14 UTC

RemoteUrl https://github.com/bioc/omicplotR

RemoteRef RELEASE_3_23

RemoteSha 95307fd270c61bff93ceefe9c91eb6ba857908bc

Contents

omicplotR-package 2
internal 2
metadata 3
omicplotr.run 3
otu_table 4

Index **5**

`omicplotR-package` `omicplotR`

Description

A Shiny app for visual exploration of omic datasets as compositions, and differential abundance analysis using ALDEx2. Useful for exploring RNA-seq, meta-RNA-seq, 16s rRNA gene sequencing and more with visualizations such as principal component analysis biplot (coloured using metadata for visualizing each variable), association plots (igraph), dendrograms and stacked bar plots, and effect plots (ALDEx2). Input is a table of counts and metadata file (if metadata exists), with options to filter data by count or by metadata to remove low counts, or to visualize select samples according to selected metadata. The Shiny app's graphical user interface facilitates visual exploration for new and experienced users of R alike.

Details

To launch the `shiny` app in your default browser, type `omicplotr.run()`.

Author(s)

Daniel Giguere, Jean Macklaim, Greg Gloor

See Also

`omicplotr.run`.

`internal` *Internal omicplotR functions.*

Description

Internal functions for the app which are not intended to be called by the user. Please refer to omicplotr.run.

Author(s)

Daniel Giguere, Greg Gloor.

Examples

```
# These functions are not meant to be called by the user. However, some
# functions can be useful.

data(otu_table)
# Filter out your OTU table to remove rows that sum to less than 10.

d <- omicplotr.filter(otu_table, min.reads = 10)
```

`metadata` *Vaginal microbiome OTU table metadata*

Description

Associated metadata to `otu_table`.

Usage

```
data(metadata)
```

Format

A data frame with 297 rows and 35 columns, where rows are samples and columns are collected metadata.

References

Macklaim et al (2014). Microb Ecol Health Dis. doi: http://dx.doi.org/10.3402/mehd.v26.27799

See Also

`otu_table`

`omicplotr.run` *Run* `omicplotR` `Shiny` *app.*

Description

Launches `Shiny` for `omicplotR` in default browser. This graphical user interface facilitates visual exploration of datasets for both new and experienced R users alike.

Usage

```
omicplotr.run()
```

Value

There is no value!

Author(s)

Daniel Giguere

Examples

```
# To run omicplotR, use `omicplotr.run()` function. This will open the shiny
# app in your default browser.

# omicplotr.run()

# After running omicplotr.run(), you can filter your data and make a PCA
# biplot. Internal functions are not mean to be called by the user.

data(otu_table)
d.filt <- omicplotr.filter(otu_table)
```

---

otu_table *Vaginal microbiome OTU table*

Description

This dataset contains a count table of operational taxonomic units (OTUs) from a 16s rRNA gene sequencing experiment characterising changes in bacterial microbiota from oral antimicrobial or probiotic treatments. Associated metadata is contained in `metadata`.

Usage

```
data(otu_table)
```

Format

A data frame with 77 rows and 298 columns. The last column contains taxonomic information for each OTU. Samples are columns, OTUs are rows.

References

Macklaim et al (2014). Microb Ecol Health Dis. doi: http://dx.doi.org/10.3402/mehd.v26.27799

Index

internal, 2

metadata, 3, *4*

omicplotR *(*omicplotR-package*)*, 2
omicplotR-package, 2
omicplotr.anosim *(*internal*)*, 2
omicplotr.clr *(*internal*)*, 2
omicplotr.colouredPCA *(*internal*)*, 2
omicplotr.colvec *(*internal*)*, 2
omicplotr.filter *(*internal*)*, 2
omicplotr.getRemovedFeatures
*(*internal*)*, 2
omicplotr.getRemovedSamples *(*internal*)*,
2
omicplotr.metadataFilter *(*internal*)*, 2
omicplotr.permanova *(*internal*)*, 2
omicplotr.report *(*internal*)*, 2
omicplotr.run, *2*, 3
otu_table, *3*, 4