

# Package: zAMPEXplorer (via r-universe)

December 20, 2024

**Type** Package

**Title** A Versatile Shiny App for Microbiota Profiling in Clinical Microbiology

**Version** 0.1.0

**Description** A Shiny web application offering a user-friendly, accessible, and reproducible platform for downstream analysis of 16S rRNA-based metagenomics data. Key features include quality control visualizations (e.g., rarefaction curves), community composition plots, and statistical analyses for alpha- and beta-diversity. The app integrates advanced features like community typing with Dirichlet multinomial modeling (DMM) and metadata-driven redundancy analysis (RDA) to explore microbial associations with clinical and experimental variables.

**License** GPL-3

**URL** <https://github.com/metagenlab/zAMPEXplorer>

**BugReports** <https://github.com/metagenlab/zAMPEXplorer/issues>

**SystemRequirements** microViz (install separately from R-universe or GitHub; see INSTALL file)

**Imports** dplyr, DT, forcats, reshape2, ggplot2, ggvenn, golem, graphics, grDevices, magrittr, microbiome, MicrobiotaProcess, phyloseq, shiny, shinydashboard, shinyFiles, shinyWidgets, stats, tidyr, UpSetR, utils, vegan, writexl, fs, scales, RColorBrewer, plotly, gridExtra, tibble, htmlwidgets, ComplexHeatmap, DirichletMultinomial, InteractiveComplexHeatmap

**Suggests** config, spelling, webshot, ggside, grid, testthat (>= 3.0.0), knitr, rmarkdown, shinytest2

**biocViews** ShinyApps, StatisticalMethod, Metagenomics, Visualization, Sequencing, Microbiome

**Config/ci-settings** lint\_free: true

**Config/ci-tools** testthat

**Config/testthat/edition** 3

**Encoding** UTF-8**Language** en-US**LazyData** false**Roxygen** list(markdown = TRUE)**RoxygenNote** 7.3.2**VignetteBuilder** knitr**Config/pak/sysreqs** libfontconfig1-dev libfreetype6-dev libglpk-dev  
make libicu-dev libpng-dev libxml2-dev libssl-dev perl  
zlib1g-dev**Repository** https://metagenlab.r-universe.dev**RemoteUrl** https://github.com/metagenlab/zAMPExplorer**RemoteRef** main**RemoteSha** e4fc8d9d319959f76b6795adbfd7c1a9eb8ac901

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zAMPExplorer_app	<i>Launch the zAMPExplorer Application</i>
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## Description

zAMPExplorer provides an interactive interface for analyzing and visualizing microbiome sequencing data, particularly the output of the zAMP pipeline (phyloseq objects). It includes functionalities such as: compositional barplots, heatmaps, diversity metrics, beta-diversity analyses, and more.

## Usage

```
zAMPExplorer_app(
  onStart = NULL,
  options = list(),
  enableBookmarking = NULL,
  uiPattern = "/",
  ...
)
```

## Arguments

onStart	A function that will be called before the app is actually run. This is only needed for shinyAppObj, since in the shinyAppDir case, a global .R file can be used for this purpose.
options	Named options that should be passed to the runApp call (these can be any of the following: "port", "launch.browser", "host", "quiet", "display.mode" and "test.mode"). You can also specify width and height parameters which provide a hint to the embedding environment about the ideal height/width for the app.
enableBookmarking	Can be one of "url", "server", or "disable". The default value, NULL, will respect the setting from any previous calls to <a href="#">enableBookmarking()</a> . See <a href="#">enableBookmarking()</a> for more information on bookmarking your app.
uiPattern	A regular expression that will be applied to each GET request to determine whether the ui should be used to handle the request. Note that the entire request path must match the regular expression in order for the match to be considered successful.
...	Arguments to pass to golem options. See <a href="#">get_golem_options</a> for more details.

## Value

A shiny.appobj object representing the running Shiny application.

## Features

- Read QC, Taxa overviews.
- Compositional barplots, relative abundance heatmaps.
- Alpha and beta diversity visualizations.
- Differential abundance testing using MaAsLin2.
- Community typing using Dirichlet Multinomial Mixtures.
- Interactive RDA ordination plots.

## See Also

Useful links:

- Documentation: <https://github.com/metagenlab/zAMPExplorer>
- zAMP pipeline: <https://zamp.readthedocs.io/en/latest/>

## Examples

```
if (interactive()) {  
  zAMPExplorer_app()  
}
```

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