

Package: BIOSZEN (via r-universe)

September 25, 2026

Type Package

Title Biological Data Analysis and Visualization with Shiny

Version 2.1.2

Description App for data analysis and visualization from an Excel file. It can generate boxplot, barplot, violin plot, stacked plots, heatmaps, correlation plots between parameters, and concentration-response curves with IC50 estimates. It includes metadata-based reproducibility, normalized-data workflows, downloadable graphics and workbooks, normality tests such as Shapiro-Wilk, Kolmogorov-Smirnov, and Anderson-Darling, and significance tests such as ANOVA, Kruskal-Wallis, t-test, and Wilcoxon. It also extracts microbial growth curve parameters (uMax, max_percap_time, doub_time, lag_time, ODmax, max_time, AUC, OD0) from fixed-interval or irregular/discontinuous numeric time points.

License GPL-3

URL <https://github.com/bioszen/BIOSZEN>

BugReports <https://github.com/bioszen/BIOSZEN/issues>

Encoding UTF-8

ByteCompile true

Depends R (>= 4.1.0)

Imports shiny, shinyFiles, later, httpuv, shiny.i18n, ggplot2, plotly, dplyr, tidyr, readxl, openxlsx, rstatix, PMCMRplus, DescTools, digest, broom, viridis, RColorBrewer, gcplyr, patchwork, shinyjs, DT, nortest, officer (>= 0.7.4), rvg (>= 0.4.2), xml2, stringr, forcats, tibble, scales, bslib, htmlwidgets, webshot2, shinyBS, multcomp, drc, ggrepel, rlang, writexl, readr, rmarkdown, zip

Suggests knitr, doconv, ggtext, lme4, lmerTest, testthat (>= 3.0.0), shinytest2, chromote, png

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RoxygenNote 7.3.1
NeedsCompilation no
Config/pak/sysreqs libcairo2-dev chromium cmake libfontconfig1-dev libfreetype6-dev libfribidi-dev libgmp3-dev make libharfbuzz-dev libicu-dev libjpeg-dev libpng-dev libtiff-dev libuv1-dev libwebp-dev libxml2-dev libmpfr-dev libssl-dev libx11-dev zlib1g-dev
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BIOSZEN	<i>Launch BIOSZEN</i>
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Description

Starts the interactive BIOSZEN Shiny application. BIOSZEN() is the concise public launcher; run_app() remains available for backward compatibility.

Usage

```
BIOSZEN(  
  host = getOption("shiny.host", "127.0.0.1"),  
  port = getOption("shiny.port", 4321),  
  launch.browser = TRUE,  
  app_window = FALSE  
)  
  
run_app(  
  host = getOption("shiny.host", "127.0.0.1"),
```

```
port = getOption("shiny.port", 4321),
launch.browser = getOption("shiny.launch.browser", TRUE)
)
```

Arguments

host	Host interface for the local Shiny server.
port	Port for the local Shiny server.
launch.browser	Browser launcher passed to <code>shiny::runApp()</code> . The default, <code>TRUE</code> , opens the app automatically. Supply <code>FALSE</code> to disable automatic opening or a function to use a custom launcher.
app_window	Logical. When <code>FALSE</code> (the default), <code>BIOSZEN()</code> opens the operating system's configured default browser. Set it to <code>TRUE</code> to prefer a dedicated Chromium app window and fall back to the default browser. This argument is used by <code>BIOSZEN()</code> ; <code>run_app()</code> retains its original browser-launch interface.

Value

The value returned by `shiny::runApp()`, invisibly when appropriate.

bioszen_citation	<i>Cite BIOSZEN</i>
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Description

Returns the official BIOSZEN citation from the package's centralized metadata. The concept DOI always resolves to the current Zenodo record.

Usage

```
bioszen_citation(format = c("text", "bibentry", "bibtex", "doi"))
```

Arguments

format	Citation format: plain "text", a "bibentry", BibTeX, or the DOI alone.
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Value

A character value, except for `format = "bibentry"`, which returns a bibentry object.

bioszen_update	<i>Update BIOSZEN</i>
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Description

Checks R-universe for a newer BIOSZEN version, requests consent, and installs it into the library containing the current package. BIOSZEN never updates while its Shiny application is running.

Usage

```
bioszen_update(
  ask = TRUE,
  repos = .bioszen_default_repositories()
)
```

Arguments

ask	Whether to ask for interactive confirmation before installation. Set to FALSE only when prior user consent has already been obtained.
repos	Package repositories used for the check and installation.

Value

TRUE when an update was installed and FALSE when no installation was needed or the user declined.

bioszen_update_available	<i>Check for a BIOSZEN Update</i>
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Description

Checks the BIOSZEN R-universe repository without installing anything.

Usage

```
bioszen_update_available(
  repos = .bioszen_default_repositories(),
  quiet = FALSE
)
```

Arguments

repos	Package repositories to query. The BIOSZEN R-universe and CRAN are used by default.
quiet	Whether connection or repository errors should be returned silently as NA.

Value

A logical scalar. Attributes contain the installed and available versions. NA means that the check could not be completed.

growth_parameters	<i>Calculate BIOSZEN Growth Parameters</i>
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Description

Calculates microbial growth parameters with the same combined method used by the BIOSZEN Shiny application. The robust exponential-phase detector is run first; the permissive detector fills only values that the robust method could not calculate.

Usage

```
growth_parameters(
  input,
  output_dir = NULL,
  sheet = NULL,
  overwrite = FALSE,
  max_time = 48,
  time_interval = 0.5,
  time_mode = c("fixed", "irregular"),
  time_column = NULL
)
```

Arguments

input	A data frame, a supported growth file (.xlsx, .xls, or .csv), a vector of supported files, or a directory containing supported files. Data frames may be wide (Time plus well columns) or tidy (Well, Time, and Measurements).
output_dir	Optional directory for generated parameter workbooks. No files are written when this is NULL. A missing directory is created.
sheet	Optional Excel sheet name or index. The first sheet is used by default. Ignored for data frames and CSV files.
overwrite	Whether existing result workbooks may be replaced.
max_time	Maximum time used when converting the raw reader-export format supported by the Shiny growth module.
time_interval	Time interval used when converting the raw reader-export format supported by the Shiny growth module.
time_mode	Time handling mode. "fixed" preserves the historical maximum-time and interval conversion. "irregular" reads numeric time values from the input file.
time_column	Optional time-column name for irregular mode. When NULL or blank, common English and Spanish names are detected automatically.

Value

For one input, the same parameter table produced by the Shiny growth workflow, with class `bioszen_growth_parameters`. For multiple files, a named list with class `bioszen_growth_parameters_list`. Generated file paths are stored in the `output_file` attribute of each result.

Examples

```
time <- seq(0, 12, by = 0.5)
curves <- data.frame(
  Time = time,
  A1 = 0.05 + 0.9 / (1 + exp(-0.8 * (time - 5)))
)
result <- growth_parameters(curves)
```

growth_parameters_irregular

Calculate BIOSZEN Growth Parameters from Irregular Time Points

Description

A convenience variant of `growth_parameters()` for curve tables whose recorded time points are uneven or discontinuous. Numeric time values are read directly from the selected column and must be finite, unique, and strictly increasing within each well.

Usage

```
growth_parameters_irregular(
  input,
  output_dir = NULL,
  sheet = NULL,
  overwrite = FALSE,
  time_column = NULL
)
```

Arguments

<code>input</code>	A data frame, a supported growth file (<code>.xlsx</code> , <code>.xls</code> , or <code>.csv</code>), a vector of supported files, or a directory containing supported files. Data frames may be wide or tidy.
<code>output_dir</code>	Optional directory for generated parameter workbooks. No files are written when this is <code>NULL</code> .
<code>sheet</code>	Optional Excel sheet name or index. The first sheet is used by default. Ignored for data frames and CSV files.
<code>overwrite</code>	Whether existing result workbooks may be replaced.
<code>time_column</code>	Optional time-column name. When <code>NULL</code> or blank, common English and Spanish names such as <code>Time</code> , <code>Tiempo</code> , <code>Hour</code> , and <code>Hora</code> are detected automatically.

Value

The same result type and parameter columns as `growth_parameters()`.

See Also

[growth_parameters\(\)](#)

Examples

```
irregular <- data.frame(  
  Time = c(0, 0.08, 0.17, 0.5, 1, 2),  
  A1 = c(0.05, 0.051, 0.053, 0.06, 0.08, 0.16)  
)  
result <- growth_parameters_irregular(irregular)
```

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