

Package ‘bsocialv2’

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Title Analysis of Microbial Social Behavior in Bacterial Consortia

Version 0.1.1

Description Provides an S4 class and methods for analyzing microbial social behavior in bacterial consortia. Includes growth parameter extraction, social behavior classification (cooperators/cheaters/neutrals), diversity effect analysis, consortium assembly path finding, and stability analysis via coefficient of variation. Methods are described in Purswani et al. (2017) <[doi:10.3389/fmicb.2017.00919](https://doi.org/10.3389/fmicb.2017.00919)>.

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URL <https://github.com/Juane99/bsocialv2>

BugReports <https://github.com/Juane99/bsocialv2/issues>

Encoding UTF-8

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Depends R (>= 4.0), methods

Imports dplyr, ggplot2, grDevices, growthcurver, igraph, magrittr, reshape2, rlang, stats, tidyr, viridis

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'transform-raw-data.R' 'transform-curated-data.R'
'calculate-growth-params.R' 'plot-processed-curves.R'
'analyze-growth.R' 'analyze-social-behavior.R'
'summarize-social-behavior.R' 'analyze-diversity.R'
'analyze-biofilm-sequence.R' 'analyze-stability.R'

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analyze_biofilm_sequence
Analyze Biofilm Assembly Sequences

Description

Analyze Biofilm Assembly Sequences

Usage

```
analyze_biofilm_sequence(.Object)
```

Arguments

.Object A `bsocial` object.

Value

The modified `bsocial` object with assembly path lists in `resultados_analisis$biofilm_gen_paths` and `resultados_analisis$biofilm_gr_paths`, and plot functions in `graficos`.

analyze_biofilm_sequence,bsocial-method
Analyze Biofilm Assembly Sequences

Description

Builds a directed graph of possible consortium assembly paths based on strain subset relationships. Uses `igraph` to find shortest paths between simpler and more complex consortia.

Usage

```
## S4 method for signature 'bsocial'
analyze_biofilm_sequence(.Object)
```

Arguments

`.Object` A `bsocial` object after `analyze_social_behavior()` has been called.

Value

The modified `bsocial` object with biofilm paths and plot functions.

analyze_diversity *Analyze Diversity Effect on Fitness*

Description

Analyze Diversity Effect on Fitness

Usage

```
analyze_diversity(.Object)
```

Arguments

`.Object` A `bsocial` object.

Value

The modified `bsocial` object with diversity boxplots in `graficos` and relative fitness tables in `resultados_analisis` (keyed by diversity level and top-k strain ranking).

```
analyze_diversity,bsocial-method
```

Analyze Diversity Effect on Fitness

Description

Analyzes the relationship between consortium diversity (number of strains) and fitness. Compares fitness across diversity levels and identifies effects of including top-ranked strains.

Usage

```
## S4 method for signature 'bsocial'
analyze_diversity(.Object)
```

Arguments

.Object A `bsocial` object after `analyze_social_behavior()` has been called.

Value

The modified `bsocial` object with diversity analysis in `graficos` and `resultados_analisis`.

```
analyze_growth            Analyze Growth Metrics
```

Description

Analyze Growth Metrics

Usage

```
analyze_growth(.Object)
```

Arguments

.Object A `bsocial` object.

Value

The modified `bsocial` object with a scatter plot stored in `graficos$growth_scatter` and top-10 ranking tables in `resultados_analisis$best_10_ngen` and `resultados_analisis$best_10_gr`.

analyze_growth,bsocial-method
Analyze Growth Metrics

Description

Creates a scatter plot of LogPhase vs NGen colored by consortium diversity, and generates top-10 tables ranked by NGen and GR.

Usage

```
## S4 method for signature 'bsocial'  
analyze_growth(.Object)
```

Arguments

.Object A **bsocial** object with datos_procesados populated.

Value

The modified **bsocial** object with growth analysis in graficos and resultados_analisis.

analyze_social_behavior
Analyze Social Behavior (Fitness Effects)

Description

Analyze Social Behavior (Fitness Effects)

Usage

```
analyze_social_behavior(.Object)
```

Arguments

.Object A **bsocial** object.

Value

The modified **bsocial** object with resultados_analisis\$social_behavior containing fitness comparison data, boxplot objects for NGen and GR, and a success flag.

```
analyze_social_behavior,bsocial-method
      Analyze Social Behavior (Fitness Effects)
```

Description

Compares the fitness of each strain in consortia vs its monoculture baseline. Generates boxplots showing relative fitness for each strain across all consortia.

Usage

```
## S4 method for signature 'bsocial'
analyze_social_behavior(.Object)
```

Arguments

.Object A `bsocial` object with `datos_procesados` populated.

Value

The modified `bsocial` object with `resultados_analisis$social_behavior`.

```
analyze_stability        Analyze Consortium Stability
```

Description

Analyze Consortium Stability

Usage

```
analyze_stability(.Object)
```

Arguments

.Object A `bsocial` object.

Value

The modified `bsocial` object with coefficient of variation data in `resultados_analisis$stability_cv_data` and violin plots in `graficos$stability_ngen_plot` and `graficos$stability_gr_plot`.

analyze_stability,bsocial-method
Analyze Consortium Stability

Description

Calculates the coefficient of variation (CV) for growth metrics across replicates or diversity levels. Creates violin plots with Spearman correlation, p-value, and R-squared displayed as subtitles.

Usage

```
## S4 method for signature 'bsocial'  
analyze_stability(.Object)
```

Arguments

.Object A [bsocial](#) object with datos_procesados populated.

Value

The modified [bsocial](#) object with stability analysis results.

bsocial-class *S4 Class for Microbial Social Behavior Analysis*

Description

The [bsocial](#) class encapsulates data and results for analyzing microbial social behavior in bacterial consortia.

Slots

id_proyecto Character. Project identifier.
cepas_seleccionadas Character vector. Names of the selected strains.
datos_crudos List. Raw input data (plates, curated, consortia).
datos_procesados Data frame. Processed metrics (NGen, GR, LogPhase).
resultados_analisis List. Analysis results from each pipeline step.
graficos List. Generated ggplot2 plots and plotting functions.

Examples

```
obj <- new("bsocial")  
obj@id_proyecto <- "my_experiment"
```

calculate_growth_params

Calculate Growth Parameters from Preprocessed Curves

Description

Calculate Growth Parameters from Preprocessed Curves

Usage

```
calculate_growth_params(.Object, ...)
```

Arguments

.Object	A bsocial object.
...	Additional arguments (method).

Value

The modified [bsocial](#) object with `datos_procesados` populated as a data frame containing consortia identifiers, strain presence/absence, and growth parameters (LogPhase, NGen, GR) fitted from the preprocessed curves.

calculate_growth_params,bsocial-method

Calculate Growth Parameters from Preprocessed Curves

Description

Fits growth curves and extracts LogPhase, number of generations (NGen), and growth rate (GR) for each consortium.

Usage

```
## S4 method for signature 'bsocial'
calculate_growth_params(.Object, method = "growthcurver")
```

Arguments

.Object	A bsocial object after <code>transform_raw_data()</code> has been called.
method	Character. Fitting algorithm: "growthcurver" (default) or "grofit".

Value

The modified [bsocial](#) object with `datos_procesados` populated.

plot_processed_curves *Plot Preprocessed Growth Curves*

Description

Plot Preprocessed Growth Curves

Usage

```
plot_processed_curves(.Object)
```

Arguments

.Object A [bsocial](#) object.

Value

A [ggplot](#) object showing faceted line plots of mean growth curves (optical density over time) grouped by experimental condition.

plot_processed_curves,bsocial-method
Plot Preprocessed Growth Curves

Description

Creates a faceted line plot of mean growth curves after preprocessing, grouped by experimental condition.

Usage

```
## S4 method for signature 'bsocial'  
plot_processed_curves(.Object)
```

Arguments

.Object A [bsocial](#) object after transform_raw_data() has been called.

Value

A ggplot2 object.

```
summarize_social_behavior
```

Classify Strains as Cooperators, Cheaters, or Neutrals

Description

Classify Strains as Cooperators, Cheaters, or Neutrals

Usage

```
summarize_social_behavior(.Object, ...)
```

Arguments

.Object	A bsocial object.
...	Additional arguments.

Value

The modified **bsocial** object with resultados_analisis\$summary_gen and resultados_analisis\$summary_gr, each a list with character vectors positives (cooperators), negatives (cheaters), and neutrals.

```
summarize_social_behavior,bsocial-method
```

Classify Strains as Cooperators, Cheaters, or Neutrals

Description

Uses pairwise t-tests and median comparisons to classify each strain based on its effect on consortium fitness.

Usage

```
## S4 method for signature 'bsocial'
summarize_social_behavior(.Object)
```

Arguments

.Object	A bsocial object after analyze_social_behavior() has been called.
---------	--

Value

The modified **bsocial** object with resultados_analisis\$summary_gen and \$summary_gr.

`transform_curated_data`*Import Pre-processed (Curated) Data*

Description

Import Pre-processed (Curated) Data

Usage

```
transform_curated_data(.Object, ...)
```

Arguments

<code>.Object</code>	A bsocial object.
<code>...</code>	Additional arguments.

Value

The modified [bsocial](#) object with `datos_procesados` populated as a data frame containing consortia identifiers, strain presence/absence, and growth parameters (LogPhase, NGen, GR).

`transform_curated_data,bsocial-method`*Import Pre-processed (Curated) Data*

Description

Imports a pre-processed CSV containing growth parameters already calculated externally. Expected columns: Consortia, LogPhase, NGen, GR, plus strain presence/absence columns matching `cepas_seleccionadas`.

Usage

```
## S4 method for signature 'bsocial'  
transform_curated_data(.Object)
```

Arguments

<code>.Object</code>	A bsocial object with <code>datos_crudos\$curated</code> populated.
----------------------	---

Value

The modified [bsocial](#) object with `datos_procesados` populated.

transform_raw_data	<i>Preprocess Raw Plate Reader Data</i>
--------------------	---

Description

Preprocess Raw Plate Reader Data

Usage

```
transform_raw_data(.Object, ...)
```

Arguments

.Object	A bsocial object.
...	Additional arguments (groups, bg_type, bg_param).

Value

The modified [bsocial](#) object with resultados_analisis populated with preprocessed growth curves, cycle times, curve mapping, and replicate statistics.

transform_raw_data,bsocial-method	<i>Preprocess Raw Plate Reader Data</i>
-----------------------------------	---

Description

Normalizes raw plate reader data by applying background correction and aggregating replicates. Supports blank-based or OD threshold correction.

Usage

```
## S4 method for signature 'bsocial'
transform_raw_data(.Object, groups, bg_type, bg_param)
```

Arguments

.Object	A bsocial object with datos_crudos\$plates populated.
groups	Numeric vector defining replicate group assignments for each plate.
bg_type	Character. Background correction method: "blank" or "threshold".
bg_param	Numeric or character. For "blank": the blank sample ID. For "threshold": the OD threshold value.

Value

The modified [bsocial](#) object with resultados_analisis populated.

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