Package: bsocialv2 (via r-universe)

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Title Analysis of Microbial Social Behavior in Bacterial Consortia

Version 0.2.1

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>.

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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

Suggests readr, testthat (>= 3.0.0), knitr, rmarkdown

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VignetteBuilder knitr

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Contents

`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).

`analyze_diversity,bsocial-method` *Analyze Diversity Effect on Fitness*

Description

Analyzes the relationship between consortium diversity (number of strains) and fitness. Computes relative fitness by comparing each consortium's metric against the best monoculture reference.

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 `transform_raw_data()` has been called.
`method`	Character. Fitting algorithm: `"growthcurver"` (default) or `"grofit"`.

Value

The modified bsocial object with `datos_procesados` populated.

`plot_growth_scatter` *Plot Growth Scatter (LogPhase vs NGen)*

Description

Renders the scatter of LogPhase against Number of Generations coloured by consortium richness, with optional IQR-based outlier hiding for visualization. The underlying `datos_procesados` is not modified.

Usage

```
plot_growth_scatter(.Object, remove_outliers = FALSE, outlier_coef = 1.5)

## S4 method for signature 'bsocial'
plot_growth_scatter(.Object, remove_outliers = FALSE, outlier_coef = 1.5)
```

Arguments

`.Object`	A bsocial object with `datos_procesados` populated.
`remove_outliers`	Logical; if `TRUE`, hides points where LogPhase or NGen fall above the Q3 + coef * IQR threshold (Tukey boxplot rule).
`outlier_coef`	Numeric multiplier for the IQR rule (default 1.5).

Value

A ggplot2 object.

`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. Writes `resultados_analisis$summary_gen` and `$summary_gr` (lists with positives/negatives/neutrals), `resultados_analisis$stats_gen` and `$stats_gr` (per-strain medians, pairwise p-values, and classification string), and rebuilds the classification-annotated plots inside `resultados_analisis$social_behavior`.

`transform_curated_data`
Import Pre-processed (Curated) Data

Description

Import Pre-processed (Curated) Data

Usage

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

Arguments

`.Object`	A bsocial object.
`...`	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

`.Object`	A bsocial object with `datos_crudos$curated` populated.

Value

The modified bsocial object with `datos_procesados` populated.

`transform_raw_data` *Preprocess Raw Plate Reader Data*

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`

Preprocess Raw Plate Reader Data

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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