

# Package ‘bsocialv2’

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

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'transform-raw-data.R' 'transform-curved-data.R'  
'calculate-growth-params.R' 'plot-processed-curves.R'  
'plot-growth-scatter.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).

---

```
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_nngen` 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 <a href="#">bsocial</a> 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 <a href="#">bsocial</a> 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\_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  $Q3 + \text{coef} * \text{IQR}$  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**

<code>.Object</code>	A <a href="#">bsocial</a> object with <code>datos_crudos\$plates</code> populated.
<code>groups</code>	Numeric vector defining replicate group assignments for each plate.
<code>bg_type</code>	Character. Background correction method: "blank" or "threshold".
<code>bg_param</code>	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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