

# Package: birp (via r-universe)

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**Title** Testing for Population Trends Using Low-Cost Ecological Count Data

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**Description** A Bayesian tool to test for population trends and changes in trends under arbitrary designs, including before-after (BA), control-intervention (CI) and before-after-control-intervention (BACI) designs commonly used to assess conservation impact. It infers changes in trends jointly from data obtained with multiple survey methods, as well as from limited and noisy data not necessarily collected in standardized ecological surveys. Observed counts can be modeled as following either a Poisson or a negative binomial model, and both deterministic and stochastic trend models are available. For more details on the model see Singer et al. (2025) <[doi:10.1101/2025.01.08.631844](https://doi.org/10.1101/2025.01.08.631844)>, and the file 'AUTHORS' for a list of copyright holders and contributors.

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**Author** Madleina Caduff [aut], Andreas Füglistaler [aut, cre], Daniel Wegmann [aut], Liam Singer [aut], Raphael Eckel [ctb], Conrad Sanderson [cph] (Author of Armadillo), Ryan Curtin [cph]

(Author of Armadillo), Daniel Lemire [cph] (Author of fast\_float), João Paulo Magalhaes [cph] (Author of fast\_float), Victor Zverovich [cph] (Author of {fmt}), Rene Brun [cph] (Author of FindR.cmake (CERN ROOT)), Fons Rademakers [cph] (Author of FindR.cmake (CERN ROOT))

**Maintainer** Andreas Füglistaler <andreas.fueglistaler@unifr.ch>

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**Description**

A Bayesian tool to test for population trends and changes in trends under arbitrary designs, including before-after (BA), control-intervention (CI) and before-after-control-intervention (BACI) designs commonly used to assess conservation impact. It infers changes in trends jointly from data obtained with multiple survey methods, as well as from limited and noisy data not necessarily collected in standardized ecological surveys. Observed counts can be modeled as following either a Poisson or a negative binomial model, and both deterministic and stochastic trend models are available. For more details on the model see Singer et al. (2025) <doi:10.1101/2025.01.08.631844>, and the file 'AUTHORS' for a list of copyright holders and contributors.

**Package Content**

Index of help topics:

|                           |                                                                                                                                                                                                                |
|---------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| assess_NB                 | Assess whether a Poisson model can replace the Negative Binomial model                                                                                                                                         |
| birp                      | Create a 'birp' Object                                                                                                                                                                                         |
| birp-package              | Testing for Population Trends Using Low-Cost Ecological Count Data                                                                                                                                             |
| birp_data                 | Create a birp_data Object from Count and Effort Matrices                                                                                                                                                       |
| birp_data_from_data_frame | Create a 'birp_data' Object from a Data Frame or List of Data Frames                                                                                                                                           |
| birp_data_from_file       | Create a birp_data Object from File(s)                                                                                                                                                                         |
| birp_from_command_line    | Create a birp Object from Command-Line Output Files                                                                                                                                                            |
| plot.birp                 | Plot posterior distributions of rate and/or step change parameters                                                                                                                                             |
| plot.birp_data            | Plot a birp_data Object                                                                                                                                                                                        |
| plot_epoch_pair           | Plot joint posterior of two gamma parameters                                                                                                                                                                   |
| plot_mcmc                 | Plot MCMC Traces and Posterior Densities                                                                                                                                                                       |
| plot_trend                | Plot Posterior Trend Estimates                                                                                                                                                                                 |
| print.birp                | Print a birp object                                                                                                                                                                                            |
| print.birp_data           | Print a birp_data object Prints a summary of a 'birp_data' object, including the number of methods, locations, control-intervention (CI) groups, and timepoints, as well as the names or identifiers for each. |
| prob_step                 | Posterior probability of a step change                                                                                                                                                                         |
| prob_trend                | Posterior probability of a population trend                                                                                                                                                                    |
| prob_trend_diff           | Pairwise posterior comparisons of population                                                                                                                                                                   |

|                            |                                                                                                                                                                                 |
|----------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
|                            | trends                                                                                                                                                                          |
| simulate_birp              | Simulate Data for BIRP Models Generates simulated count data using the BIRP model framework with user-defined parameters.                                                       |
| simulate_birp_from_results | This function simulates a birp_data object using all parameter estimates, dimensionality (methods, locations, timepoints) and the total number of counts nu_ij of a birp object |
| summary.birp               | Summary method for birp objects                                                                                                                                                 |
| summary.birp_data          | Summarize a birp_data object                                                                                                                                                    |

### Maintainer

Andreas Füglistaler <andreas.fueglistaler@unifr.ch>

### Author(s)

Madleina Caduff [aut], Andreas Füglistaler [aut, cre], Daniel Wegmann [aut], Liam Singer [aut], Raphael Eckel [ctb], Conrad Sanderson [cph] (Author of Armadillo), Ryan Curtin [cph] (Author of Armadillo), Daniel Lemire [cph] (Author of fast\_float), João Paulo Magalhaes [cph] (Author of fast\_float), Victor Zverovich [cph] (Author of {fmt}), Rene Brun [cph] (Author of FindR.cmake (CERN ROOT)), Fons Rademakers [cph] (Author of FindR.cmake (CERN ROOT))

---

|           |                                                                               |
|-----------|-------------------------------------------------------------------------------|
| assess_NB | <i>Assess whether a Poisson model can replace the Negative Binomial model</i> |
|-----------|-------------------------------------------------------------------------------|

---

### Description

This function tests if the Poisson model is appropriate by simulating replicate datasets under the Poisson assumption and comparing the overdispersion parameter estimates with those obtained from the Negative Binomial (NB) model fit to the original data.

### Usage

```
assess_NB(
  x,
  stochastic = FALSE,
  numRep = 100,
  cutoff = 0.05,
  plot = TRUE,
  verbose = TRUE
)
```

**Arguments**

|                         |                                                                                                                                 |
|-------------------------|---------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>          | A birp object estimated under a negative binomial model.                                                                        |
| <code>stochastic</code> | Logical; if TRUE, use a stochastic trend model, otherwise deterministic (default).                                              |
| <code>numRep</code>     | Integer; number of replicate datasets to simulate (default 100).                                                                |
| <code>cutoff</code>     | Numeric; significance threshold for the fraction of replicates where NB overdispersion exceeds Poisson estimate (default 0.05). |
| <code>plot</code>       | Logical; if TRUE, plot the distributions of overdispersion parameters from simulated Poisson replicates (default TRUE).         |
| <code>verbose</code>    | Logical; if FALSE, suppress console output (default TRUE).                                                                      |

**Value**

A list containing:

|                                 |                                                                                                                                                     |
|---------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>keep_NB</code>            | Logical scalar, TRUE if NB model should be kept (data shows overdispersion). If FALSE, birp should be re-run using the Poisson model to gain power. |
| <code>keep_NB_per_method</code> | Logical vector indicating whether NB should be kept for each method.                                                                                |
| <code>frac</code>               | Numeric vector with fractions of replicates where Poisson simulated overdispersion exceeded observed NB overdispersion.                             |
| <code>b_Pois</code>             | Matrix of overdispersion parameter estimates from Poisson-simulated replicates.                                                                     |
| <code>b_x</code>                | Numeric vector of overdispersion parameter estimates from the original NB fit.                                                                      |

**Examples**

```
data <- simulate_birp()
est <- birp(data, negativeBinomial = TRUE)
res_assess <- assess_NB(est, numRep = 5)
```

---

|                   |                             |
|-------------------|-----------------------------|
| <code>birp</code> | <i>Create a birp Object</i> |
|-------------------|-----------------------------|

---

**Description**

This function runs the Markov Chain Monte Carlo (MCMC) algorithm on a `birp_data` object to estimate model parameters and returns a fitted birp object.

**Usage**

```
birp(
  data,
  change = "rate",
  timesOfChange = c(),
  negativeBinomial = FALSE,
  stochastic = FALSE,
```

```

    rate_design = NULL,
    step_design = NULL,
    assumeTrueDetectionProbability = FALSE,
    iterations = 1e+05,
    numBurnin = 10,
    burnin = 1000,
    thinning = 10,
    verbose = TRUE
)

```

### Arguments

|                                             |                                                                                                                                                                                                               |
|---------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>data</code>                           | A <a href="#">birp_data</a> object containing the input data.                                                                                                                                                 |
| <code>change</code>                         | A string indicating the type of change to infer. Options are 'rate' (infer exponential rates of change), 'step' (infer step changes) or 'both' (infer both rate and step change). By default, 'rate' is used. |
| <code>timesOfChange</code>                  | Numeric or integer vector specifying the times of change (change points) for the model.                                                                                                                       |
| <code>negativeBinomial</code>               | Logical; if TRUE, fits a negative binomial model instead of the default Poisson model.                                                                                                                        |
| <code>stochastic</code>                     | Logical; if TRUE, fits a stochastic trend model instead of the default deterministic trend model.                                                                                                             |
| <code>rate_design</code>                    | Optional matrix specifying the BACI (Before-After-Control-Impact) design for the rates of change (gamma, see Details). Only applies if <code>change="rate"</code> or <code>change="both"</code> .             |
| <code>step_design</code>                    | Optional matrix specifying the BACI (Before-After-Control-Impact) design for the step changes (Delta, see Details). Only applies if <code>change="step"</code> or <code>change="both"</code> .                |
| <code>assumeTrueDetectionProbability</code> | Logical; if TRUE, provided detection probabilities are treated as true probabilities (logit-transformed without standardization).                                                                             |
| <code>iterations</code>                     | Integer; total number of MCMC iterations to run.                                                                                                                                                              |
| <code>numBurnin</code>                      | Integer; number of burn-in cycles to run.                                                                                                                                                                     |
| <code>burnin</code>                         | Integer; number of MCMC iterations per burn-in cycle.                                                                                                                                                         |
| <code>thinning</code>                       | Integer; thinning interval for saving MCMC samples. Only every thinningth iteration is retained.                                                                                                              |
| <code>verbose</code>                        | Logical; if FALSE, suppresses console output.                                                                                                                                                                 |

### Details

The 'rate\_design' and 'step\_design' matrices define a Before-After Control-Impact experimental design for the rates of change (gamma) and the step changes (Delta), respectively, with the following format: - Each **row** represents a group (e.g., Control or Intervention). The **first column** specifies the group name (e.g. 'Control' or 'Intervention'). - Each **column after the first** represents a different epoch. The numbers in these columns indicate which change parameter ( $\gamma$  or  $\Delta$ ) to assign for each group and epoch. For example, `BACI = matrix(c("A", "B", 1, 1, 1, 2), nrow =`

2) corresponds to a canonical BACI design where the first row represents the control group (A) and the second row represents the intervention group (B). Please see the vignette for more examples.

### Value

An object of type birp containing MCMC results and model estimates.

### Examples

```
data <- simulate_birp()
est <- birp(data)
```

---

`birp_data`

*Create a birp\_data Object from Count and Effort Matrices*

---

### Description

Constructs a 'birp\_data' object from matrices of observed counts and corresponding efforts for a single method.

### Usage

```
birp_data(counts, efforts, times, CI_groups = NULL, location_names = NULL)
```

### Arguments

|                             |                                                                                                                                                |
|-----------------------------|------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>counts</code>         | A matrix of observed counts (J locations $\times$ K timepoints). Each row corresponds to a location and each column to a timepoint.            |
| <code>efforts</code>        | A matrix of observation effort with the same dimensions as 'counts'.                                                                           |
| <code>times</code>          | A vector of length K specifying the timepoints.                                                                                                |
| <code>CI_groups</code>      | A vector of length J specifying the control-intervention (CI) group for each location. Defaults to a single group ('group_1') if not provided. |
| <code>location_names</code> | Optional names for the locations. Defaults to "Location_1", "Location_2", etc.                                                                 |

### Value

An object of type birp\_data

### Examples

```
data <- birp_data(c(10,20,30), c(100,200,300), c(1,2,5))
```

---

birp\_data\_from\_data\_frame

*Create a 'birp\_data' Object from a Data Frame or List of Data Frames*


---

### Description

Constructs a 'birp\_data' object from a single data frame or a list of data frames, with one per method.

### Usage

```
birp_data_from_data_frame(data)
```

### Arguments

|      |                                                                                                                                                                                                                                                                                                                        |
|------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| data | A data frame or a list of data frames, each representing one method. Each data frame must include the following columns: 'timepoint', 'location', 'counts', 'effort', and 'CI_group'. Each row represents a survey conducted at a specific timepoint and location, and for a specific control-intervention (CI) group. |
|------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

### Value

An object of type [birp\\_data](#)

### Examples

```
df <- data.frame(
  timepoint = 1:10,
  location = rep(1, 10),
  counts = sample(1:100, 10),
  effort = rexp(10),
  CI_group = "intervention"
)
data <- birp_data_from_data_frame(df)
```

---

birp\_data\_from\_file

*Create a birp\_data Object from File(s)*


---

### Description

Constructs a 'birp\_data' object from one or more input files, each representing data for a different method.

### Usage

```
birp_data_from_file(filenamees, method_names = NA, sep = ",")
```

**Arguments**

|              |                                                                                                                                                    |
|--------------|----------------------------------------------------------------------------------------------------------------------------------------------------|
| filenames    | A character vector of file paths. Each file must contain a data frame with the columns 'timepoint', 'location', 'counts', 'effort' and 'CI_group'. |
| method_names | Optional vector of method names corresponding to the input files. If not provided, names are inferred from the file names.                         |
| sep          | The field separator used in the files (default is comma).                                                                                          |

**Value**

An object of type `birp_data`

**Examples**

```
dir <- system.file("extdata", package = "birp")
filenames <- file.path(dir, "birp_Method_1_simulated_counts.txt")
data <- birp_data_from_file(filenames = filenames, sep = "\t")
```

---

`birp_from_command_line`

*Create a birp Object from Command-Line Output Files*

---

**Description**

This function creates a birp object by reading the output files generated by the command-line version of the birp tool.

**Usage**

```
birp_from_command_line(path)
```

**Arguments**

|      |                                                                                  |
|------|----------------------------------------------------------------------------------|
| path | Character string specifying the directory path containing all birp output files. |
|------|----------------------------------------------------------------------------------|

**Value**

An object of type birp containing MCMC results and model estimates read from files.

**Examples**

```
est <- birp_from_command_line(file.path(system.file("extdata", package = "birp")))
```

plot.birp

*Plot posterior distributions of rate and/or step change parameters***Description**

Plots the posterior densities of the rate (gamma) and/or step change (Delta) parameters estimated by a birp object.

**Usage**

```
## S3 method for class 'birp'
plot(
  x,
  change = if (x$post_gamma$exists && x$post_Delta$exists) "both" else if
    (x$post_gamma$exists) "rate" else "step",
  shadingIncrease = NA,
  shadingDecrease = "#f2c7c7",
  col = "black",
  lwd = 1,
  lty = NULL,
  xlim = NA,
  ylim = NA,
  add = FALSE,
  xlab = NULL,
  ylab = "Posterior density",
  legend = NULL,
  lineAtZero = TRUE,
  ...
)
```

**Arguments**

|                 |                                                                                                                                                    |
|-----------------|----------------------------------------------------------------------------------------------------------------------------------------------------|
| x               | A birp object.                                                                                                                                     |
| change          | Character; which parameters to plot. One of "rate", "step", or "both". Default is "both" if both exist, otherwise whichever exists.                |
| shadingIncrease | Character or color specification; Shading color for the range where the parameter is greater than 0. If NA, shading is omitted. Default is NA.     |
| shadingDecrease | Character or color specification; Shading color for the range where the parameter is less than 0. If NA, shading is omitted. Default is "#f2c7c7". |
| col             | Character vector or color values; Line color(s) for the density plots. Recycled per parameter type. Default is "black".                            |
| lwd             | Numeric vector; Line width(s) for the density plots. Recycled per parameter type. Default is 1.                                                    |

|            |                                                                                                                                                                                                                                             |
|------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| lty        | Numeric or character vector; Line type(s) for the density plots. If a single value is provided, it is recycled. Default cycles through 1:n within each parameter type.                                                                      |
| xlim       | Numeric vector of length 2; Optional x-axis limits applied to all panels. If NA, limits are determined automatically. Default is NA.                                                                                                        |
| ylim       | Numeric vector of length 2; Optional y-axis limits applied to all panels. If NA, limits are determined automatically. Default is NA.                                                                                                        |
| add        | Logical; If TRUE, adds the densities to an existing plot (only valid when change is "gamma" or "Delta"). Default is FALSE.                                                                                                                  |
| xlab       | Character (or expression) vector of length 1 or 2; Label(s) for the x-axis. When change = "both", provide two labels (one per panel) or a single value recycled for both. Defaults to expression(gamma) / expression(Delta) as appropriate. |
| ylab       | Character; Label for the y-axis. Default is "Posterior density".                                                                                                                                                                            |
| legend     | Character vector of legend labels, or NA to suppress the legend. Defaults to the names stored in the respective post_* object.                                                                                                              |
| lineAtZero | Logical; If TRUE, adds a vertical line at x = 0. Default is TRUE.                                                                                                                                                                           |
| ...        | Additional graphical parameters passed to <a href="#">lines</a> and <a href="#">plot</a> .                                                                                                                                                  |

**Value**

No return value, called for side effects.

**See Also**

[birp](#)

**Examples**

```
data <- simulate_birp(timepoints = 1:5)
est <- birp(data, change = "both")
plot(est)
plot(est, change = "rate")
plot(est, change = "step")
```

---

plot.birp\_data

---

*Plot a birp\_data Object*


---

**Description**

This function plots observed counts per unit of effort over time, for each method-location combination in a birp\_data object.

**Usage**

```
## S3 method for class 'birp_data'
plot(
  x,
  col = 1:length(x$locations),
  lwd = 1,
  lty = 1:length(x$method_names),
  pch = 1:length(x$CI_groups),
  xlab = "time",
  ylab = "counts per unit of effort",
  legend.x = "topright",
  legend.y = NULL,
  legend.bty = "o",
  xlim = range(as.numeric(x$times)),
  ylim = NA,
  ...
)
```

**Arguments**

|            |                                                                                                    |
|------------|----------------------------------------------------------------------------------------------------|
| x          | A birp_data object to be plotted.                                                                  |
| col        | A vector of colors, recycled to match the number of locations.                                     |
| lwd        | A vector of line widths, recycled to match the number of method-location combinations.             |
| lty        | A vector of line types, recycled to match the number of methods.                                   |
| pch        | A vector of plotting characters, recycled to match the number of control-intervention (CI) groups. |
| xlab       | Label for the x-axis.                                                                              |
| ylab       | Label for the y-axis.                                                                              |
| legend.x   | The x-position for the legend. Use NA to omit the legend.                                          |
| legend.y   | The y-position for the legend.                                                                     |
| legend.bty | Box type for the legend; either "o" (default) or "n".                                              |
| xlim       | Numeric vector specifying the x-axis limits.                                                       |
| ylim       | Numeric vector specifying the y-axis limits. If NA, limits are computed automatically.             |
| ...        | Additional graphical parameters passed to plot() or lines().                                       |

**Value**

No return value. Called for side effects.

**Examples**

```
data <- simulate_birp()
plot(data)
```

---

|                 |                                                     |
|-----------------|-----------------------------------------------------|
| plot_epoch_pair | <i>Plot joint posterior of two gamma parameters</i> |
|-----------------|-----------------------------------------------------|

---

## Description

Plots a 2D density contour for the joint posterior of two gamma parameters from a birp object.

## Usage

```
plot_epoch_pair(
  x,
  gamma1 = which(!x$post_gamma$is_fix)[1],
  gamma2 = which(!x$post_gamma$is_fix)[2],
  xlab = .getLabelGamma.birp(x, gamma1),
  ylab = .getLabelGamma.birp(x, gamma2),
  xlim = range(x$post_gamma$trace[, c(gamma1, gamma2)]),
  ylim = xlim,
  col = "deeppink",
  diag.col = "black",
  diag.lwd = 1,
  diag.lty = 1,
  zero.col = "black",
  zero.lwd = 1,
  zero.lty = 2,
  print.p = TRUE,
  add = FALSE,
  ...
)
```

## Arguments

|          |                                                                                                           |
|----------|-----------------------------------------------------------------------------------------------------------|
| x        | A birp object.                                                                                            |
| gamma1   | Integer; Index of the first gamma parameter to plot on the x-axis. Default is the first inferred gamma.   |
| gamma2   | Integer; Index of the second gamma parameter to plot on the y-axis. Default is the second inferred gamma. |
| xlab     | Character; Label for the x-axis. Default is dynamically set based on gamma1.                              |
| ylab     | Character; Label for the y-axis. Default is dynamically set based on gamma2.                              |
| xlim     | Numeric vector of length 2; Optional x-axis limits. Default is the range of gamma1 and gamma2 values.     |
| ylim     | Numeric vector of length 2; Optional y-axis limits. Default is the same as xlim.                          |
| col      | Character or color specification; Color for contour lines. Default is "deeppink".                         |
| diag.col | Character or NA; Color of the diagonal line (y=x). Use NA to omit. Default is "black".                    |

|          |                                                                                                                                                                                  |
|----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| diag.lwd | Numeric; Line width of the diagonal line. Default is 1.                                                                                                                          |
| diag.lty | Numeric or character; Line type of the diagonal line. Default is 1 (solid).                                                                                                      |
| zero.col | Character or NA; Color of the zero reference lines (at $x=0$ and $y=0$ ). Use NA to omit. Default is "black".                                                                    |
| zero.lwd | Numeric; Line width of the zero reference lines. Default is 1.                                                                                                                   |
| zero.lty | Numeric or character; Line type of the zero reference lines. Default is 2 (dashed).                                                                                              |
| print.p  | Logical; If TRUE, adds an annotation showing the posterior probability $P(\gamma_1 < \gamma_2 \mid \text{data})$ or $P(\gamma_1 > \gamma_2 \mid \text{data})$ . Default is TRUE. |
| add      | Logical; If TRUE, adds the contour plot to an existing plot. Default is FALSE.                                                                                                   |
| ...      | Additional graphical parameters passed to <a href="#">contour</a> .                                                                                                              |

**Value**

No return value; called for side effects (plotting).

**See Also**

[birp](#)

**Examples**

```
data <- simulate_birp(timesOfChange = 2)
est <- birp(data, timesOfChange = 2)
plot_epoch_pair(est)
```

---

plot\_mcmc

---

*Plot MCMC Traces and Posterior Densities*


---

**Description**

Visualizes the MCMC trace plots and posterior densities of the gamma and Delta parameters from a birp object.

**Usage**

```
plot_mcmc(x, col = c("black", "blue"))
```

**Arguments**

|     |                                                                                      |
|-----|--------------------------------------------------------------------------------------|
| x   | A birp object containing posterior samples.                                          |
| col | Character vector; Colors for trace and density plots. Default is c("black", "blue"). |

**Value**

No return value; the function is called for its side effects (plotting).

**See Also**[birp](#)**Examples**

```
data <- simulate_birp()
est <- birp(data)
plot_mcmc(est)
```

plot\_trend

*Plot Posterior Trend Estimates***Description**

Visualizes posterior trends from a birp object by plotting the median and quantile intervals of the estimated relative densities over time. Optionally, vertical lines can be added to mark epoch boundaries and survey timepoints.

**Usage**

```
plot_trend(
  x,
  CI_group = 1,
  n_points = 1000,
  quantiles = c(0.99, 0.9, 0.5, 0.25),
  quantile.col = gray(seq(1, 0, length.out = length(quantiles) + 2)[2:(length(quantiles)
    + 1)]),
  quantile.border = NA,
  median.col = "deeppink",
  median.lwd = 2,
  median.lty = 1,
  epoch.col = "black",
  epoch.lwd = 1,
  epoch.lty = 1,
  times.col = "black",
  times.lwd = 1,
  times.lty = 2,
  log = FALSE,
  xlab = "Time",
  ylab = paste(c("log", "Relative Density")[c(log, TRUE)], collapse = " "),
  main = x$CI_groups[CI_group],
  ...
)
```

**Arguments**

|                              |                                                                                                                             |
|------------------------------|-----------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>               | A birp object containing MCMC trace and model outputs.                                                                      |
| <code>CI_group</code>        | Integer; Index of the control-intervention group to plot. Default is 1.                                                     |
| <code>n_points</code>        | Integer; Number of points to evaluate the trend over time. Default is 1000.                                                 |
| <code>quantiles</code>       | Numeric vector; Quantiles to plot as shaded intervals. Must be in (0, 1). Default is <code>c(0.99, 0.9, 0.5, 0.25)</code> . |
| <code>quantile.col</code>    | Character vector or color values; Fill colors for quantile polygons. Default is shades of gray.                             |
| <code>quantile.border</code> | Character or NA; Border color for quantile polygons. Use NA to omit borders. Default is NA.                                 |
| <code>median.col</code>      | Character; Color of the median trend line. Default is "deeppink".                                                           |
| <code>median.lwd</code>      | Numeric; Line width for the median trend. Default is 1.                                                                     |
| <code>median.lty</code>      | Numeric or character; Line type for the median trend line. Default is 1 (solid).                                            |
| <code>epoch.col</code>       | Character or color specification; Color for lines representing epoch boundaries. Default is "black".                        |
| <code>epoch.lwd</code>       | Numeric; Line width for epoch boundary lines. Default is 1.                                                                 |
| <code>epoch.lty</code>       | Numeric or character; Line type for epoch boundary lines. Default is 1 (solid).                                             |
| <code>times.col</code>       | Character or color specification; Color for vertical lines representing measurement times. Default is "black".              |
| <code>times.lwd</code>       | Numeric; Line width for measurement time lines. Default is 1.                                                               |
| <code>times.lty</code>       | Numeric or character scalar; Line type for measurement time lines. Default is 2 (dashed).                                   |
| <code>log</code>             | Logical; If TRUE, plot relative densities on a logarithmic scale; otherwise plot on the original scale. Default is FALSE.   |
| <code>xlab</code>            | Character; Label for the x-axis. Default is "Time".                                                                         |
| <code>ylab</code>            | Character; Label for the y-axis. Default dynamically set to either "log Relative Density" or "Relative Density".            |
| <code>main</code>            | Character; Main title of the plot. Defaults to the name of the selected CI group.                                           |
| <code>...</code>             | Additional graphical parameters passed to the base plot function.                                                           |

**Value**

No return value, called for side effects.

**See Also**

[birp](#)

**Examples**

```
data <- simulate_birp()
est <- birp(data)
plot_trend(est)
```

---

|            |                            |
|------------|----------------------------|
| print.birp | <i>Print a birp object</i> |
|------------|----------------------------|

---

**Description**

Prints a summary of the estimated parameters from a birp model.

**Usage**

```
## S3 method for class 'birp'
print(x, ...)
```

**Arguments**

|     |                                                                     |
|-----|---------------------------------------------------------------------|
| x   | A birp object.                                                      |
| ... | Additional arguments passed to internal methods (currently unused). |

**Value**

Invisibly returns the input x, called for side effects.

**See Also**

[birp](#)

**Examples**

```
data <- simulate_birp()
est <- birp(data)
print(est)
```

---

|                 |                                                                                                                                                                                                                     |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| print.birp_data | <i>Print a birp_data object Prints a summary of a birp_data object, including the number of methods, locations, control-intervention (CI) groups, and timepoints, as well as the names or identifiers for each.</i> |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

**Description**

Print a birp\_data object Prints a summary of a birp\_data object, including the number of methods, locations, control-intervention (CI) groups, and timepoints, as well as the names or identifiers for each.

**Usage**

```
## S3 method for class 'birp_data'
print(x, ...)
```

**Arguments**

`x`                      A `birp_data` object to be printed.  
`...`                    Additional arguments passed to function.

**Value**

No return value; this function is called for its side effects (printing to console).

**Examples**

```
data <- simulate_birp()
print(data)
```

---

|                        |                                               |
|------------------------|-----------------------------------------------|
| <code>prob_step</code> | <i>Posterior probability of a step change</i> |
|------------------------|-----------------------------------------------|

---

**Description**

Computes the posterior probability that a step change is increasing (positive) or decreasing (negative)

**Usage**

```
prob_step(x, positive = TRUE, Delta = NULL)
```

**Arguments**

`x`                      A 'birp' object.  
`positive`              Logical. If 'TRUE' (default), returns the posterior probability of an increasing (positive) step change,  $P(\Delta_m > 0 \mid y)$ . If 'FALSE', returns the posterior probability of a decreasing (negative) step change,  $P(\Delta_m < 0 \mid y)$ .  
`Delta`                 Integer. Index of the Delta parameter for which to return the posterior probability. If 'NULL' (default), posterior probabilities for all Delta parameters are returned.

**Value**

If 'Delta = NULL', a numeric vector containing posterior probabilities for all step change parameters. Otherwise, a single numeric value.

**See Also**

[`birp()`]

**Examples**

```

data <- simulate_birp()
est <- birp(data, change = "step")

# Posterior probabilities of positive step changes
prob_step(est)

# Posterior probability for a specific Delta
prob_step(est, Delta = 1)

# Posterior probabilities of negative step changes
prob_step(est, positive = FALSE)

```

---

|            |                                                    |
|------------|----------------------------------------------------|
| prob_trend | <i>Posterior probability of a population trend</i> |
|------------|----------------------------------------------------|

---

**Description**

Computes the posterior probability that a population trend is increasing or decreasing.

**Usage**

```
prob_trend(x, positive = TRUE, gamma = NULL)
```

**Arguments**

|          |                                                                                                                                                                                                                                          |
|----------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x        | A 'birp' object.                                                                                                                                                                                                                         |
| positive | Logical. If 'TRUE' (default), returns the posterior probability of an increasing (positive) trend, $P(\gamma_m > 0 \mid y)$ . If 'FALSE', returns the posterior probability of a decreasing (negative) trend, $P(\gamma_m < 0 \mid y)$ . |
| gamma    | Integer. Index of the gamma parameter for which to return the posterior probability. If 'NULL' (default), posterior probabilities for all gamma parameters are returned.                                                                 |

**Value**

If 'gamma = NULL', a numeric vector containing posterior probabilities for all rate parameters. Otherwise, a single numeric value.

**See Also**

[birp()]

**Examples**

```
data <- simulate_birp()
est <- birp(data)

# Posterior probabilities of increasing trends
prob_trend(est)

# Posterior probability for a specific gamma
prob_trend(est, gamma = 1)

# Posterior probabilities of decreasing trends
prob_trend(est, positive = FALSE)
```

---

|                 |                                                            |
|-----------------|------------------------------------------------------------|
| prob_trend_diff | <i>Pairwise posterior comparisons of population trends</i> |
|-----------------|------------------------------------------------------------|

---

**Description**

Computes pairwise posterior probabilities that one population trend exceeds another.

**Usage**

```
prob_trend_diff(x)
```

**Arguments**

x                      A ‘birp’ object.

**Details**

Element  $[i, j]$  of the returned matrix equals  $P(\gamma_i > \gamma_j \mid y)$ , the posterior probability that the trend associated with row  $i$  is greater than the trend associated with column  $j$ .

Values close to 1 indicate strong evidence that  $\gamma_i > \gamma_j$ , values close to 0 indicate strong evidence that  $\gamma_i < \gamma_j$ , and values near 0.5 indicate little evidence for either comparison

**Value**

A square matrix of pairwise posterior probabilities. Element  $[i, j]$  gives  $P(\gamma_i > \gamma_j \mid y)$ .

**See Also**

[birp()], [prob\_trend()]

**Examples**

```
data <- simulate_birp(timepoints = 1:5)
est <- birp(data, timesOfChange = c(2,4))

prob_trend_diff(est)
```

---

|               |                                                                                                                                  |
|---------------|----------------------------------------------------------------------------------------------------------------------------------|
| simulate_birp | <i>Simulate Data for BIRP Models Generates simulated count data using the BIRP model framework with user-defined parameters.</i> |
|---------------|----------------------------------------------------------------------------------------------------------------------------------|

---

**Description**

Simulate Data for BIRP Models Generates simulated count data using the BIRP model framework with user-defined parameters.

**Usage**

```
simulate_birp(
  timepoints = c(1, 2, 3),
  timesOfChange = c(),
  change = "rate",
  gamma = NULL,
  Delta = NULL,
  negativeBinomial = FALSE,
  stochastic = FALSE,
  numLocations = 2,
  numMethods = 1,
  numCIGroups = 1,
  numCovariatesEffort = 1,
  numCovariatesDetection = 0,
  rate_design = NULL,
  step_design = NULL,
  n_bar = 1000,
  N_0 = NULL,
  a = NULL,
  logSigma = NULL,
  logZeta = NULL,
  logPhi = NULL,
  covariatesEffort = "gamma(1, 2)",
  covariatesDetection = "normal(0, 1)",
  proportionZeroEffort = 0,
  verbose = TRUE
)
```

**Arguments**

|                        |                                                                                                                                                                                                                                                                                                                                                                  |
|------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| timepoints             | Integer vector specifying time points.                                                                                                                                                                                                                                                                                                                           |
| timesOfChange          | Integer vector indicating time points at which change in growth rate (gamma) occurs.                                                                                                                                                                                                                                                                             |
| change                 | A string indicating the type of change to infer. Options are 'rate' (infer exponential rates of change), 'step' (infer step changes) or 'both' (infer both rate and step change). By default, 'rate' is used.                                                                                                                                                    |
| gamma                  | Numeric vector denoting the values of gamma (rate of change) to simulate. If NULL, all gamma will be set to zero.                                                                                                                                                                                                                                                |
| Delta                  | Numeric vector denoting the values of Delta (step change) to simulate. If NULL, all Delta will be set to zero.                                                                                                                                                                                                                                                   |
| negativeBinomial       | Logical; if TRUE, use negative binomial instead of Poisson.                                                                                                                                                                                                                                                                                                      |
| stochastic             | Logical; if TRUE, simulate abundance as a stochastic process instead of deterministic.                                                                                                                                                                                                                                                                           |
| numLocations           | Integer; number of spatial locations.                                                                                                                                                                                                                                                                                                                            |
| numMethods             | Integer; number of sampling methods.                                                                                                                                                                                                                                                                                                                             |
| numCIGroups            | Integer; number of control–intervention groups.                                                                                                                                                                                                                                                                                                                  |
| numCovariatesEffort    | Integer; number of effort covariates.                                                                                                                                                                                                                                                                                                                            |
| numCovariatesDetection | Integer; number of detection covariates.                                                                                                                                                                                                                                                                                                                         |
| rate_design            | Optional matrix specifying BACI design for the rates of change (gamma, see Details).                                                                                                                                                                                                                                                                             |
| step_design            | Optional matrix specifying BACI design for the step changes (Delta, see Details).                                                                                                                                                                                                                                                                                |
| n_bar                  | Expected average total observations per time point (across all locations).                                                                                                                                                                                                                                                                                       |
| N_0                    | Optional numeric; initial abundance. If NULL, n_bar will be used instead.                                                                                                                                                                                                                                                                                        |
| a                      | A numeric value or vector; detection parameter(s) for the negative binomial distribution. Can be a single value (shared across methods) or a vector of values (one per method).                                                                                                                                                                                  |
| logSigma               | Optional numeric; log standard deviation in the stochastic model. If NULL, logSigma will be set to -1.                                                                                                                                                                                                                                                           |
| logZeta                | Optional numeric; log scaling factors of stochastic volatility in the stochastic model. If NULL, logZeta will be set to 0.                                                                                                                                                                                                                                       |
| logPhi                 | Optional numeric; log standard deviation of detection process in the stochastic model. If NULL, logPhi will be simulated according to the model assumptions.                                                                                                                                                                                                     |
| covariatesEffort       | Specifies how effort is calculated for covariates. Accepts: (1) a single number used for all covariates and locations; (2) a numeric vector with one value per covariate (applied to all locations); (3) a distribution string to simulate effort from, e.g., "gamma(a, b)" or "uniform(a, b)"; or (4) a vector of such distribution strings, one per covariate. |

`covariatesDetection`  
 Specifies how detection probabilities are calculated for covariates. Accepts: (1) a single number for all covariates and locations; (2) a numeric vector with one value per covariate (applied to all locations); (3) a distribution string, e.g., "normal(a, b)" or "uniform(a, b)"; or (4) a vector of such distribution strings, one per covariate.

`proportionZeroEffort`  
 Proportion of time–location–method combinations with zero effort (0 to 1).

`verbose`  
 Logical; if TRUE, print progress messages.

### Details

The ‘rate\_design’ and ‘step\_design’ matrices define a Before-After Control-Impact experimental design for the rates of change ( $\gamma$ ) and the step changes ( $\Delta$ ), respectively, with the following format: - Each **row** represents a group (e.g., Control or Intervention). The **first column** specifies the group name (e.g. ‘Control’ or ‘Intervention’). - Each **column after the first** represents a different epoch. The numbers in these columns indicate which change parameter ( $\gamma$  or  $\Delta$ ) to assign for each group and epoch. For example, `BACI = matrix(c("A", "B", 1, 1, 1, 2), nrow = 2)` corresponds to a canonical BACI design where the first row represents the control group (A) and the second row represents the intervention group (B). Please see the vignette for examples.

### Value

An object of type `birp_data` containing the simulated dataset.

### Examples

```
data <- simulate_birp()
```

---

```
simulate_birp_from_results
```

*This function simulates a birp\_data object using all parameter estimates, dimensionality (methods, locations, timepoints) and the total number of counts nu\_ij of a birp object*

---

### Description

This function simulates a `birp_data` object using all parameter estimates, dimensionality (methods, locations, timepoints) and the total number of counts `nu_ij` of a birp object

### Usage

```
simulate_birp_from_results(
  x,
  negativeBinomial = FALSE,
  stochastic = FALSE,
  mu = NULL,
```

```

    b = NULL,
    logSigma = NULL,
    logZeta = NULL,
    logPhi = NULL,
    verbose = TRUE
  )

```

### Arguments

|                  |                                                                                                                                                                                               |
|------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| x                | An object of type birp.                                                                                                                                                                       |
| negativeBinomial | Logical; if TRUE, simulate counts using a negative binomial distribution instead of Poisson.                                                                                                  |
| stochastic       | Logical; if TRUE, use a stochastic model with log-normal fluctuations.                                                                                                                        |
| mu               | A numeric vector specifying values of $\mu$ for the negative binomial model, with one value per method-location combination. If NULL, $\mu_i$ for method $i$ is set to 1/number of locations. |
| b                | A numeric vector specifying values of $b$ for the negative binomial model (one per method). If NULL, all $b_i$ are set to 1.                                                                  |
| logSigma         | A single numeric value specifying logSigma for the stochastic model. If NULL, logSigma is set to -1.                                                                                          |
| logZeta          | A numeric vector specifying values of logZeta for the stochastic model. If NULL, logZeta is set to 0.                                                                                         |
| logPhi           | A numeric vector specifying values of logPhi for the stochastic model. If NULL, values are simulated according to the model assumptions.                                                      |
| verbose          | Logical; if FALSE, suppresses console output.                                                                                                                                                 |

### Value

An object of type `birp_data`

### Examples

```

data <- simulate_birp()
x <- birp(data)
data2 <- simulate_birp_from_results(x)

```

---

summary.birp

*Summary method for birp objects*


---

### Description

Provides a printed summary of model estimates for a birp object.

**Usage**

```
## S3 method for class 'birp'  
summary(object, ...)
```

**Arguments**

|        |                                            |
|--------|--------------------------------------------|
| object | A birp object.                             |
| ...    | Additional arguments passed to print.birp. |

**Value**

Invisibly returns the input object, called for side effects.

**See Also**

[birp](#)

**Examples**

```
data <- simulate_birp()  
est <- birp(data)  
summary(est)
```

---

|                   |                                     |
|-------------------|-------------------------------------|
| summary.birp_data | <i>Summarize a birp_data object</i> |
|-------------------|-------------------------------------|

---

**Description**

Provides a printed summary of the contents of a birp\_data object.

**Usage**

```
## S3 method for class 'birp_data'  
summary(object, ...)
```

**Arguments**

|        |                                      |
|--------|--------------------------------------|
| object | A birp_data object to be summarized. |
| ...    | Additional arguments.                |

**Value**

No return value; this function is called for its side effects (printing to console).

**Examples**

```
data <- simulate_birp()  
summary(data)
```

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