Package 'birp'

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Contents

birp-package . . . 2
assess_NB . . . 4
birp . . . 5
birp_data . . . 7
birp_data_from_data_frame . . . 7
birp_data_from_file . . . 8
birp_from_command_line . . . 9
plot.birp . . . 9
plot.birp_data . . . 11
plot_epoch_pair . . . 12
plot_mcmc . . . 14
plot_trend . . . 15
print.birp . . . 17
print.birp_data . . . 17
prob_step . . . 18
prob_trend . . . 19
prob_trend_diff . . . 20
simulate_birp . . . 21
simulate_birp_from_results . . . 23
summary.birp . . . 24
summary.birp_data . . . 25

Index **26**

`birp-package` *Testing for Population Trends Using Low-Cost Ecological Count Data*

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

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`assess_NB` *Assess whether a Poisson model can replace the Negative Binomial model*

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

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

Value

A list containing:

`keep_NB`	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.

keep_NB_per_method
: Logical vector indicating whether NB should be kept for each method.

frac
: Numeric vector with fractions of replicates where Poisson simulated overdispersion exceeded observed NB overdispersion.

b_Pois
: Matrix of overdispersion parameter estimates from Poisson-simulated replicates.

b_x
: 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)
```

---

birp *Create a* birp *Object*

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

data
: A birp_data object containing the input data.

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.

timesOfChange
: Numeric or integer vector specifying the times of change (change points) for the model.

`negativeBinomial`
: Logical; if `TRUE`, fits a negative binomial model instead of the default Poisson model.

`stochastic`
: Logical; if `TRUE`, fits a stochastic trend model instead of the default deterministic trend model.

`rate_design`
: Optional matrix specifying the BACI (Before-After-Control-Impact) design for the rates of change (gamma, see Details). Only applies if `change="rate"` or `change="both"`.

`step_design`
: Optional matrix specifying the BACI (Before-After-Control-Impact) design for the step changes (Delta, see Details). Only applies if `change="step"` or `change="both"`.

`assumeTrueDetectionProbability`
: Logical; if `TRUE`, provided detection probabilities are treated as true probabilities (logit-transformed without standardization).

`iterations`
: Integer; total number of MCMC iterations to run.

`numBurnin`
: Integer; number of burn-in cycles to run.

`burnin`
: Integer; number of MCMC iterations per burn-in cycle.

`thinning`
: Integer; thinning interval for saving MCMC samples. Only every `thinning`th iteration is retained.

`verbose`
: 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 (γ or Δ) 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

counts	A matrix of observed counts (J locations × K timepoints). Each row corresponds to a location and each column to a timepoint.
efforts	A matrix of observation effort with the same dimensions as ‘counts‘.
times	A vector of length K specifying the timepoints.
CI_groups	A vector of length J specifying the control-intervention (CI) group for each location. Defaults to a single group (‘group_1‘) if not provided.
location_names	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(filenames, 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 lines and plot.

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 *Plot joint posterior of two gamma parameters*

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(gamma1 < gamma2 | data) or P(gamma1 > gamma2 | data). Default is TRUE.

add	Logical; If TRUE, adds the contour plot to an existing plot. Default is FALSE.
...	Additional graphical parameters passed to contour.

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

`x`	A `birp` object containing MCMC trace and model outputs.
`CI_group`	Integer; Index of the control-intervention group to plot. Default is 1.
`n_points`	Integer; Number of points to evaluate the trend over time. Default is 1000.
`quantiles`	Numeric vector; Quantiles to plot as shaded intervals. Must be in (0, 1). Default is c(0.99, 0.9, 0.5, 0.25).
`quantile.col`	Character vector or color values; Fill colors for quantile polygons. Default is shades of gray.

quantile.border
: Character or NA; Border color for quantile polygons. Use NA to omit borders. Default is NA.

median.col
: Character; Color of the median trend line. Default is "deeppink".

median.lwd
: Numeric; Line width for the median trend. Default is 1.

median.lty
: Numeric or character; Line type for the median trend line. Default is 1 (solid).

epoch.col
: Character or color specification; Color for lines representing epoch boundaries. Default is "black".

epoch.lwd
: Numeric; Line width for epoch boundary lines. Default is 1.

epoch.lty
: Numeric or character; Line type for epoch boundary lines. Default is 1 (solid).

times.col
: Character or color specification; Color for vertical lines representing measurement times. Default is "black".

times.lwd
: Numeric; Line width for measurement time lines. Default is 1.

times.lty
: Numeric or character scalar; Line type for measurement time lines. Default is 2 (dashed).

log
: Logical; If TRUE, plot relative densities on a logarithmic scale; otherwise plot on the original scale. Default is FALSE.

xlab
: Character; Label for the x-axis. Default is "Time".

ylab
: Character; Label for the y-axis. Default dynamically set to either "log Relative Density" or "Relative Density".

main
: Character; Main title of the plot. Defaults to the name of the selected CI group.

...
: 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` *Print a birp object*

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` *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.*

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)
```

---

prob_step *Posterior probability of a step change*

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` *Posterior probability of a population trend*

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 *Pairwise posterior comparisons of population trends*

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

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 (γ or Δ) 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 μ for the negative binomial model, with one value per method-location combination. If NULL, μ_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 *Summarize a birp_data object*

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)
```

Index

∗ **package**
birp-package, 2

assess_NB, 4

birp, 5, *11*, *14*, *16, 17*, *25*
birp-package, 2
birp_data, *5*, 7, *8*, *23, 24*
birp_data_from_data_frame, 7
birp_data_from_file, 8
birp_from_command_line, 9

contour, *14*

lines, *11*

plot, *11*
plot.birp, 9
plot.birp_data, 11
plot_epoch_pair, 12
plot_mcmc, 14
plot_trend, 15
print.birp, 17
print.birp_data, 17
prob_step, 18
prob_trend, 19
prob_trend_diff, 20

simulate_birp, 21
simulate_birp_from_results, 23
summary.birp, 24
summary.birp_data, 25