

Package ‘antedep’

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Title Antependence Models for Longitudinal Data

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Description Provides functions for fitting, simulating, and inference for antependence models for longitudinal data. Supports integer-valued antependence (INAD) models for count data with thinning operators (binomial, Poisson, negative binomial) and flexible innovation distributions (Poisson, Bell, negative binomial), as well as Gaussian antependence (AD) models for continuous data. Implements maximum likelihood estimation via time-separable optimization and block coordinate descent, with confidence intervals based on Louis' identity and profile likelihood.

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aic_ad

Akaike information criterion for fitted Gaussian AD models

Description

Computes AIC using the fitted log likelihood and a parameter count that respects identifiability constraints for the Gaussian antedependence parameters.

Usage

```
aic_ad(fit)
```

Arguments

`fit` A fitted model object returned by `fit_ad`.

Details

The AIC is computed as:

$$AIC = -2 \times \ell + 2k$$

where ℓ is the log-likelihood and k is the number of free parameters.

This function applies to Gaussian AD fits from `fit_ad`.

Value

A numeric scalar AIC value.

aic_cat	<i>Compute AIC for a categorical antedependence model</i>
---------	---

Description

Calculates the Akaike Information Criterion for a fitted AD(p) model.

Usage

```
aic_cat(fit)
```

Arguments

`fit` A fitted model object of class "cat_fit" from `fit_cat()`.

Details

The AIC is computed as:

$$AIC = -2 \times \ell + 2k$$

where ℓ is the log-likelihood and k is the number of free parameters.

Value

Scalar AIC value.

Examples

```
## Not run:
y <- simulate_cat(100, 5, order = 1, n_categories = 2)
fit <- fit_cat(y, order = 1)
aic_cat(fit)

## End(Not run)
```

aic_gau	<i>Compute AIC for Gaussian AD model (alias of aic_ad)</i>
---------	--

Description

Convenience alias for [aic_ad](#).

Usage

```
aic_gau(...)
```

Arguments

... Passed through to [aic_ad](#).

Value

See [aic_ad](#).

See Also

[aic_ad](#), [aic_cat](#), [aic_inad](#)

aic_inad	<i>Akaike information criterion for fitted INAD models</i>
----------	--

Description

Computes AIC using the fitted log likelihood and a parameter count that respects structural zeros and identifiability constraints.

Usage

```
aic_inad(fit)
```

Arguments

fit A fitted model object returned by [fit_inad](#).

Details

The AIC is computed as:

$$AIC = -2 \times \ell + 2k$$

where ℓ is the log-likelihood and k is the number of free parameters.

Value

A numeric scalar AIC value.

Bell

*The Bell distribution***Description**

Density, distribution function, quantile function and random generation for the Bell distribution with parameter `theta`.

Usage

```
dbell(x, theta, log = FALSE)
```

```
pbell(x, theta)
```

```
rbell(n, theta, max_z = 100L)
```

```
qbell(p, theta, max_z = 100L)
```

Arguments

<code>x</code>	vector of nonnegative integers (for <code>dbell</code> and <code>pbell</code>).
<code>theta</code>	scalar real parameter.
<code>log</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>n</code>	number of observations to generate (for <code>rbell</code>).
<code>max_z</code>	maximum support value used for approximation in <code>rbell</code> and <code>qbell</code> .
<code>p</code>	numeric vector of probabilities between 0 and 1 inclusive (for <code>qbell</code>).

Details

Let B_x denote the x th Bell number. The Bell distribution has probability mass function

$$P(X = x) = \theta^x \exp(-\exp(\theta) + 1) \frac{B_x}{x!},$$

for nonnegative integers x and real θ .

The functions follow the standard naming used in base R: `dbell` for the density, `pbell` for the distribution function, `qbell` for the quantile function and `rbell` for random generation.

Value

For `dbell`, a numeric vector of probabilities. For `pbell`, a numeric vector of cumulative probabilities. For `qbell`, an integer vector of quantiles. For `rbell`, an integer vector of random values.

Examples

```
dbell(0:5, theta = 1)
pbell(0:5, theta = 1)
qbell(c(0.25, 0.5, 0.9), theta = 1)
set.seed(1)
rbell(10, theta = 1)
```

bic_ad	<i>Bayesian information criterion for fitted Gaussian AD models</i>
--------	---

Description

Computes BIC using the fitted log likelihood and a parameter count that respects identifiability constraints for the Gaussian antedependence parameters.

Usage

```
bic_ad(fit, n_subjects = NULL)
```

Arguments

fit	A fitted model object returned by fit_ad .
n_subjects	Number of subjects, typically <code>nrow(y)</code> . If <code>NULL</code> , inferred from <code>fit\$settings\$n_subjects</code> .

Details

The BIC is computed as:

$$BIC = -2 \times \ell + k \times \log(N)$$

where ℓ is the log-likelihood, k is the number of free parameters, and N is the number of subjects.

This function applies to Gaussian AD fits from [fit_ad](#). For categorical and INAD models, use [bic_cat](#) and [bic_inad](#).

Value

A numeric scalar BIC value.

bic_cat	<i>Compute BIC for a categorical antedependence model</i>
---------	---

Description

Calculates the Bayesian Information Criterion for a fitted AD(p) model for categorical longitudinal data.

Usage

```
bic_cat(fit, n_subjects = NULL)
```

Arguments

fit	A fitted model object of class "cat_fit" from <code>fit_cat()</code> .
n_subjects	Number of subjects. If <code>NULL</code> , extracted from <code>fit</code> .

Details

The BIC is computed as:

$$BIC = -2 \times \ell + k \times \log(N)$$

where ℓ is the log-likelihood, k is the number of free parameters, and N is the number of subjects.

Value

A numeric scalar BIC value.

Examples

```
## Not run:
# Simulate data
y <- simulate_cat(100, 5, order = 1, n_categories = 2)

# Fit models of different orders
fit0 <- fit_cat(y, order = 0)
fit1 <- fit_cat(y, order = 1)
fit2 <- fit_cat(y, order = 2)

# Compare BIC
c(BIC_0 = bic_cat(fit0), BIC_1 = bic_cat(fit1), BIC_2 = bic_cat(fit2))

## End(Not run)
```

bic_gau

Compute BIC for Gaussian AD model (alias of bic_ad)

Description

Convenience alias for [bic_ad](#).

Usage

```
bic_gau(...)
```

Arguments

... Passed through to [bic_ad](#).

Value

See [bic_ad](#).

See Also

[bic_ad](#), [bic_cat](#), [bic_inad](#)

bic_inad	<i>Bayesian information criterion for fitted INAD models</i>
----------	--

Description

Computes BIC using the fitted log likelihood and a parameter count that respects structural zeros and identifiability constraints.

Usage

```
bic_inad(fit, n_subjects = NULL)
```

Arguments

fit	A fitted model object returned by fit_inad .
n_subjects	Number of subjects, typically <code>nrow(y)</code> . If <code>NULL</code> , inferred from <code>fit\$settings\$n_subjects</code> or legacy <code>length(fit\$settings\$blocks)</code> when available (with a warning).

Details

The BIC is computed as:

$$BIC = -2 \times \ell + k \times \log(N)$$

where ℓ is the log-likelihood, k is the number of free parameters, and N is the number of subjects.

Value

A numeric scalar BIC value.

bic_order_ad	<i>BIC-based order selection for Gaussian AD models</i>
--------------	---

Description

Fits AD models of increasing orders and selects the best by BIC.

Usage

```
bic_order_ad(y, max_order = 2L, ...)
```

Arguments

y	Numeric matrix with <code>n_subjects</code> rows and <code>n_time</code> columns.
max_order	Maximum order to consider.
...	Additional arguments passed to fit_ad .

Value

A list with class `ad_bic_order` containing:

fits List of fitted models

bic BIC values for each order

best_order Order with lowest BIC

table Summary table

See Also

[bic_order_gau](#), [bic_order_cat](#), [bic_order_inad](#)

<code>bic_order_cat</code>	<i>Compare models across orders using BIC</i>
----------------------------	---

Description

Fits AD models of orders 0, 1, ..., `max_order` and compares them using BIC.

Usage

```
bic_order_cat(
  y,
  max_order = 2,
  blocks = NULL,
  homogeneous = TRUE,
  n_categories = NULL,
  criterion = "bic"
)
```

Arguments

<code>y</code>	Integer matrix of categorical data (<code>n_subjects</code> x <code>n_time</code>).
<code>max_order</code>	Maximum order to consider. Default is 2.
<code>blocks</code>	Optional block membership vector.
<code>homogeneous</code>	Whether to use homogeneous parameters across blocks.
<code>n_categories</code>	Number of categories (inferred if <code>NULL</code>).
<code>criterion</code>	Which criterion to use: "bic" (default) or "aic".

Value

A list containing:

<code>table</code>	Data frame with <code>order</code> , <code>log_l</code> , <code>n_params</code> , <code>aic</code> , <code>bic</code>
<code>best_order</code>	Order with lowest criterion value
<code>fits</code>	List of fitted models

Examples

```
## Not run:
y <- simulate_cat(100, 5, order = 1, n_categories = 2)
result <- bic_order_cat(y, max_order = 2)
print(result$table)
print(result$best_order)

## End(Not run)
```

bic_order_gau	<i>Compare Gaussian AD orders by BIC (alias of bic_order_ad)</i>
---------------	--

Description

Convenience alias for [bic_order_ad](#).

Usage

```
bic_order_gau(...)
```

Arguments

... Passed through to [bic_order_ad](#).

Value

See [bic_order_ad](#).

See Also

[bic_order_ad](#), [bic_order_cat](#), [bic_order_inad](#)

bic_order_inad	<i>BIC Model Order Comparison</i>
----------------	-----------------------------------

Description

BIC Model Order Comparison

Usage

```
bic_order_inad(
  y,
  max_order = 2,
  thinning = "binom",
  innovation = "pois",
  blocks = NULL,
  ...
)
```

Arguments

<code>y</code>	Integer matrix.
<code>max_order</code>	Maximum order (1 or 2).
<code>thinning</code>	Thinning operator.
<code>innovation</code>	Innovation distribution.
<code>blocks</code>	Optional block assignments.
<code>...</code>	Additional arguments.

Value

A list with class "bic_order_inad".

<code>bolus_inad</code>	<i>Morphine bolus analgesia counts</i>
-------------------------	--

Description

Morphine bolus self administration counts for two treatment groups recorded at 12 four hour time points. The data are stored in matrix form to facilitate use with antedependence models.

Usage

```
bolus_inad
```

Format

A list with four components:

y integer matrix of dimension N by n_time containing all subjects and time points

y_2mg integer matrix with rows corresponding to the 2 mg treatment group

y_1mg integer matrix with rows corresponding to the 1 mg treatment group

blocks integer vector of length N giving the block or treatment group indicator, 1 for 2 mg and 2 for 1 mg

Source

Dataset bolus from the **cold** package, converted to matrix form and grouped by treatment.

cattle_growth	<i>Cattle growth data (Treatments A and B)</i>
---------------	--

Description

Longitudinal cattle growth measurements for two treatment groups from Zimmerman and Nunez-Anton antedependence book companion data. This dataset is continuous-response data suitable for Gaussian AD modeling.

Usage

```
cattle_growth
```

Format

A list with five components:

y numeric matrix of dimension N by n_time containing all subjects

y_A numeric matrix for Treatment A subjects

y_B numeric matrix for Treatment B subjects

blocks integer vector of length N (1 = Treatment A, 2 = Treatment B)

time integer vector of measurement occasions

Source

https://www.stat.uiowa.edu/~dzimmer/Data-for-AD/cattle_growth_data_Treatment%20A.txt and https://www.stat.uiowa.edu/~dzimmer/Data-for-AD/cattle_growth_data_Treatment%20B.txt

ci_ad	<i>Confidence intervals for fitted Gaussian AD models</i>
-------	---

Description

Computes approximate Wald confidence intervals for selected parameters from a fitted Gaussian AD model.

Usage

```
ci_ad(fit, level = 0.95, parameters = "all")
```

Arguments

fit A fitted model object returned by `fit_ad`.

level Confidence level between 0 and 1.

parameters Which parameters to include: "all" (default), "mu", "phi", or "sigma".

Details

This helper currently supports complete-data Gaussian AD fits.

Standard errors are based on large-sample approximations:

- $SE(\hat{\mu}_t) \approx \hat{\sigma}_t / \sqrt{n}$
- $SE(\hat{\sigma}_t) \approx \hat{\sigma}_t / \sqrt{2n}$
- $SE(\hat{\phi}) \approx \sqrt{(1 - \hat{\phi}^2)/n}$ for free ϕ entries

Value

An object of class `ad_ci`, a list with elements `settings`, `level`, `mu`, `phi`, and `sigma`. Each non-NULL element is a data frame with columns `param`, `est`, `se`, `lower`, `upper`, and `level`.

See Also

`fit_ad`, `ci_cat`, `ci_inad`

Examples

```
## Not run:
y <- simulate_ad(n_subjects = 80, n_time = 6, order = 1, phi = 0.4)
fit <- fit_ad(y, order = 1)
ci <- ci_ad(fit)
ci$mu
ci$phi
ci$sigma

## End(Not run)
```

ci_cat

Confidence intervals for categorical AD model parameters

Description

Computes Wald-based confidence intervals for the transition probability parameters of a fitted categorical antedependence model.

Usage

```
ci_cat(fit, y = NULL, level = 0.95, parameters = "all")
```

Arguments

<code>fit</code>	A fitted model object of class <code>"cat_fit"</code> from <code>fit_cat()</code> .
<code>y</code>	Optional data matrix. If NULL, <code>fit\$cell_counts</code> is used (observed counts for closed-form fits; expected counts for EM fits).
<code>level</code>	Confidence level (default 0.95).
<code>parameters</code>	Which parameters to compute CIs for: <code>"all"</code> (default), <code>"marginal"</code> , or <code>"transition"</code> .

Details

Confidence intervals are computed using the Wald method based on the asymptotic normality of maximum likelihood estimators.

For a probability estimate $\hat{\pi}$ based on count N , the standard error is:

$$SE(\hat{\pi}) = \sqrt{\frac{\hat{\pi}(1 - \hat{\pi})}{N}}$$

For conditional probabilities $\hat{\pi}_{j|i}$ based on conditioning count N_i , the standard error is:

$$SE(\hat{\pi}_{j|i}) = \sqrt{\frac{\hat{\pi}_{j|i}(1 - \hat{\pi}_{j|i})}{N_i}}$$

The confidence interval is then:

$$\hat{\pi} \pm z_{\alpha/2} \times SE(\hat{\pi})$$

Note: CIs are truncated to the interval from 0 to 1 when they exceed these bounds.

Missing-data fits with `na_action = "marginalize"` are not currently supported because observed cell counts are not stored for that path.

Value

A list of class "cat_ci" containing:

<code>marginal</code>	Data frame of CIs for marginal parameters (if requested)
<code>transition</code>	List of data frames of CIs for transition parameters (if requested)
<code>level</code>	Confidence level used
<code>settings</code>	Model settings from fit

References

Agresti, A. (2013). Categorical Data Analysis (3rd ed.). Wiley.

See Also

[fit_cat](#)

Examples

```
## Not run:
# Fit a model
set.seed(123)
y <- simulate_cat(200, 5, order = 1, n_categories = 2)
fit <- fit_cat(y, order = 1)

# Compute confidence intervals
ci <- ci_cat(fit)
print(ci)

# Just marginal CIs
ci_marg <- ci_cat(fit, parameters = "marginal")

## End(Not run)
```

ci_gau

Confidence intervals for Gaussian AD model (alias of ci_ad)

Description

Convenience alias for [ci_ad](#).

Usage

```
ci_gau(...)
```

Arguments

... Passed through to [ci_ad](#).

Value

See [ci_ad](#).

See Also

[ci_ad](#), [ci_cat](#), [ci_inad](#)

ci_inad

Confidence intervals for fitted INAD models

Description

Computes confidence intervals for selected parameters from a fitted INAD model. For the fixed effect case, Wald intervals for time varying alpha and theta are computed via Louis identity for supported thinning-innovation combinations. For block effects tau, profile likelihood intervals are computed by fixing one component of tau and re maximizing the log likelihood over nuisance parameters. For negative binomial innovations, Wald intervals for the innovation size parameter are computed using a one dimensional observed information approximation per time point, holding other parameters fixed at their fitted values.

Usage

```
ci_inad(
  y,
  fit,
  blocks = NULL,
  level = 0.95,
  idx_time = NULL,
  ridge = 0,
  profile_maxeval = 2500,
  profile_xtol_rel = 1e-06
)
```


Arguments

<code>y</code>	Integer matrix with <code>n_subjects</code> rows and <code>n_time</code> columns.
<code>fit</code>	A fitted model object returned by <code>fit_inad</code> .
<code>blocks</code>	Optional integer vector of length <code>n_subjects</code> . Required for block effect intervals. If provided, should match <code>fit\$settings\$blocks</code> .
<code>level</code>	Confidence level between 0 and 1.
<code>idx_time</code>	Optional integer vector of time indices for which to compute intervals. Default is all time points.
<code>ridge</code>	Nonnegative ridge value added to the observed information matrix used for Louis based Wald intervals.
<code>profile_maxeval</code>	Maximum number of function evaluations used in the profile likelihood refits.
<code>profile_xtol_rel</code>	Relative tolerance used in the profile likelihood refits.

Value

An object of class `inad_ci`, a list with elements `settings`, `level`, `alpha`, `theta`, `nb_inno_size`, and `tau`. Each non NULL interval element is a data frame with columns `param`, `est`, `lower`, `upper`, and possibly `se` and `width`.

Examples

```
## Not run:
fit <- fit_inad(y, order = 1, thinning = "nbinom", innovation = "bell", blocks = blocks)
ci <- ci_inad(y, fit, blocks = blocks)
ci$alpha
ci$theta
ci$tau

## End(Not run)
```

cochlear_implant

Cochlear implant speech recognition data

Description

Longitudinal speech recognition outcomes for two groups (A/B), including incomplete records, from Zimmerman and Nunez-Anton antedependence book companion data. This dataset is continuous-response data suitable for Gaussian AD modeling.

Usage

```
cochlear_implant
```

Format

A list with six components:

y numeric matrix of dimension N by n_time containing all subjects

y_A numeric matrix for Group A subjects

y_B numeric matrix for Group B subjects

blocks integer vector of length N (1 = Group A, 2 = Group B)

group character vector of group labels ("A"/"B")

time integer vector of measurement occasions

Source

https://www.stat.uiowa.edu/~dzimmer/Data-for-AD/speech_recognition_data.txt

cochlear_implant_cat	<i>Cochlear implant categorical outcomes (derived)</i>
----------------------	--

Description

Categorical version of the cochlear implant speech recognition data, created by mapping percentage scores to ordered 10-point bins (1..11). This dataset is intended for categorical AD examples related to the cochlear application discussed by Xie and Zimmerman (2013).

Usage

```
cochlear_implant_cat
```

Format

A list with seven components:

y integer matrix of dimension N by n_time containing all subjects

y_A integer matrix for Group A subjects

y_B integer matrix for Group B subjects

blocks integer vector of length N (1 = Group A, 2 = Group B)

group character vector of group labels ("A"/"B")

n_categories number of categories (11)

category_breaks numeric cut points used for categorization

Source

Raw percentages from https://www.stat.uiowa.edu/~dzimmer/Data-for-AD/speech_recognition_data.txt; categorical mapping performed in data-raw/cochlear_implant_cat.R.

em_ad

*EM algorithm for Gaussian AD model estimation***Description**

Convenience wrapper around [fit_ad](#) with `na_action = "em"` to provide a parallel entry point to [em_inad](#).

Usage

```
em_ad(
  y,
  order = 1,
  blocks = NULL,
  estimate_mu = TRUE,
  max_iter = 100,
  tol = 1e-06,
  verbose = FALSE,
  ...
)
```

Arguments

<code>y</code>	Numeric matrix (n_subjects x n_time), may contain NA.
<code>order</code>	Integer 0, 1, or 2.
<code>blocks</code>	Optional vector of block membership (length n_subjects).
<code>estimate_mu</code>	Logical, whether to estimate mu (default TRUE).
<code>max_iter</code>	Maximum EM iterations.
<code>tol</code>	EM convergence tolerance.
<code>verbose</code>	Logical, print EM progress.
<code>...</code>	Additional arguments passed to fit_ad .

Details

This is an alias-style helper for users who prefer explicit `em_*` entry points across model families.

Value

An `ad_fit` object as returned by [fit_ad](#).

See Also

[fit_ad](#), [em_inad](#), [em_cat](#), [fit_cat](#)

em_cat

*EM algorithm for categorical AD model estimation***Description**

Fits categorical antedependence models with missing outcomes using the Expectation-Maximization (EM) algorithm for orders 0 and 1.

Usage

```
em_cat(
  y,
  order = 1,
  blocks = NULL,
  homogeneous = TRUE,
  n_categories = NULL,
  max_iter = 100,
  tol = 1e-06,
  epsilon = 1e-08,
  safeguard = TRUE,
  verbose = FALSE
)
```

Arguments

y	Integer matrix with <code>n_subjects</code> rows and <code>n_time</code> columns. Values are category codes in 1, ..., <code>n_categories</code> ; NA is allowed.
order	Antedependence order. Supported values are 0 and 1. Order 2 is not yet implemented in <code>em_cat()</code> .
blocks	Optional block/group vector of length <code>n_subjects</code> . Any coding is accepted (e.g., non-sequential integers or factor levels).
homogeneous	Logical. If TRUE, a single parameter set is fitted across blocks. If FALSE, separate parameters are fitted by block.
n_categories	Number of categories. If NULL, inferred from observed data.
max_iter	Maximum number of EM iterations.
tol	Convergence tolerance on absolute log-likelihood change.
epsilon	Small positive constant used for smoothing and numerical stability.
safeguard	Logical; if TRUE, apply step-halving when an M-step update decreases observed-data log-likelihood.
verbose	Logical; if TRUE, print EM progress.

Details

For complete data (no missing values), this function defers to [fit_cat](#) with closed-form MLEs.

For missing data and orders 0/1, each EM iteration computes expected sufficient statistics with a forward-backward E-step, then updates probabilities by normalized expected counts in the M-step. If `safeguard = TRUE`, a step-halving line search is applied to the M-step update whenever the observed-data likelihood decreases.

A final E-step is run before returning so that $\log_{-1}/\text{AIC}/\text{BIC}$ and expected cell counts correspond exactly to the returned parameter values.

Value

A `cat_fit` object with fields matching `fit_cat`. In EM mode, `cell_counts` stores expected counts from the final E-step, with `settings$cell_counts_type = "expected"`.

See Also

`fit_cat`, `logL_cat`

em_gau

EM algorithm for Gaussian AD model (alias of em_ad)

Description

Convenience alias for `em_ad`.

Usage

```
em_gau(...)
```

Arguments

... Passed through to `em_ad`.

Value

See `em_ad`.

See Also

`em_ad`, `em_inad`

em_inad

EM Algorithm for INAD Model Estimation

Description

Fits INAD models using the Expectation-Maximization algorithm. This is an alternative to direct likelihood optimization.

Usage

```
em_inad(
  y,
  order = 1,
  thinning = "binom",
  innovation = "pois",
  blocks = NULL,
  max_iter = 200,
  tol = 1e-07,
  alpha_init = NULL,
```

```

    theta_init = NULL,
    tau_init = NULL,
    nb_inno_size = NULL,
    safeguard = TRUE,
    verbose = FALSE
  )

```

Arguments

y	Integer matrix with n_subjects rows and n_time columns.
order	Model order (1 or 2). Order 0 does not require EM.
thinning	Thinning operator: "binom", "pois", or "nbinom".
innovation	Innovation distribution: "pois", "bell", or "nbinom".
blocks	Optional integer vector of length n_subjects for block effects.
max_iter	Maximum number of EM iterations.
tol	Convergence tolerance for log-likelihood change.
alpha_init	Optional initial values for alpha parameters.
theta_init	Optional initial values for theta parameters.
tau_init	Optional initial values for tau parameters.
nb_inno_size	Size parameter for negative binomial innovation (if used).
safeguard	Logical; if TRUE, use step-halving when likelihood decreases.
verbose	Logical; if TRUE, print iteration progress.

Details

For Gaussian and CAT EM entry points, see [em_ad](#) and [em_cat](#). For CAT specifically, `fit_cat()` supports `na_action = "em"` for orders 0/1 and `na_action = "marginalize"` for order 2 missing-data fits.

Value

A list with class "inad_fit" containing estimated parameters.

See Also

[em_ad](#), [em_cat](#), [fit_inad](#), [fit_cat](#)

fit_ad

Fit Gaussian antedependence model by maximum likelihood

Description

Fits an AD(0), AD(1), or AD(2) model for Gaussian longitudinal data by maximum likelihood. Missing values can be handled by complete-case deletion or by EM (see [em_ad](#) for an explicit EM wrapper).

Usage

```
fit_ad(
  y,
  order = 1,
  blocks = NULL,
  na_action = c("fail", "complete", "em"),
  estimate_mu = TRUE,
  em_max_iter = 100,
  em_tol = 1e-06,
  em_verbose = FALSE,
  ...
)
```

Arguments

<code>y</code>	Numeric matrix (n_subjects x n_time). May contain NA.
<code>order</code>	Integer 0, 1, or 2.
<code>blocks</code>	Optional vector of block membership (length n_subjects).
<code>na_action</code>	One of "fail", "complete", or "em".
<code>estimate_mu</code>	Logical, whether to estimate mu (default TRUE).
<code>em_max_iter</code>	Maximum EM iterations (only used when na_action = "em").
<code>em_tol</code>	EM convergence tolerance (only used when na_action = "em").
<code>em_verbose</code>	Logical, print EM progress (only used when na_action = "em").
<code>...</code>	Passed through to the EM fitter.

Details

For missing data with `na_action = "em"`, AD orders 0 and 1 are the primary production path. AD order 2 is available, but the current EM implementation uses simplified second-order updates and should be treated as provisional for high-stakes inference.

Value

A list with components including `mu`, `phi`, `sigma`, `tau`, `log_l`, `n_obs`, `n_missing`.

See Also

[em_ad](#), [fit_gau](#), [fit_cat](#), [fit_inad](#)

fit_cat

Fit a categorical antedependence model by maximum likelihood

Description

Computes maximum likelihood estimates for the parameters of an AD(p) model for categorical longitudinal data. The model is parameterized by transition probabilities, and MLEs are obtained in closed form.

Usage

```
fit_cat(
  y,
  order = 1,
  blocks = NULL,
  homogeneous = TRUE,
  n_categories = NULL,
  na_action = c("fail", "complete", "marginalize", "em"),
  em_max_iter = 100,
  em_tol = 1e-06,
  em_epsilon = 1e-08,
  em_safeguard = TRUE,
  em_verbose = FALSE
)
```

Arguments

y	Integer matrix with n_subjects rows and n_time columns. Each entry should be a category code from 1 to c, where c is the number of categories.
order	Antependence order p. Must be 0, 1, or 2. Default is 1.
blocks	Optional integer vector of length n_subjects specifying group membership. If NULL, all subjects are treated as one group.
homogeneous	Logical. If TRUE (default), parameters are shared across all groups (blocks are ignored for estimation). If FALSE, separate transition probabilities are estimated for each group.
n_categories	Number of categories. If NULL (default), inferred from the maximum value in y.
na_action	Handling of missing values in y. One of "fail" (default, error if any missing), "complete" (drop subjects with any missing values), or "marginalize" (maximize observed-data likelihood by integrating over missing outcomes), or "em" (use em_cat for orders 0 and 1).
em_max_iter	Maximum EM iterations used when na_action = "em".
em_tol	EM convergence tolerance used when na_action = "em".
em_epsilon	Numerical smoothing constant used when na_action = "em".
em_safeguard	Logical; if TRUE, use step-halving safeguard in em_cat when na_action = "em".
em_verbose	Logical; print EM progress when na_action = "em".

Details

For AD(p), the model decomposes as:

$$P(Y_1, \dots, Y_n) = P(Y_1, \dots, Y_p) \times \prod_{k=p+1}^n P(Y_k | Y_{k-p}, \dots, Y_{k-1})$$

MLEs are computed as empirical proportions:

- Marginal/joint probabilities: count / N
- Transition probabilities: conditional count / marginal count

Empty cells receive probability 0 (if denominator is also 0).

When `na_action = "em"`, `fit_cat()` dispatches to `em_cat`. In that case, `em_safeguard` controls step-halving protection against likelihood-decreasing updates, and returned `log_l/AIC/BIC/cell_counts` are synchronized via a final E-step under the returned parameters. For `order = 2`, `na_action = "em"` is not available and errors explicitly; use `na_action = "marginalize"`.

Value

A list of class `"cat_fit"` containing:

<code>marginal</code>	List of marginal/joint probabilities for initial time points
<code>transition</code>	List of transition probability arrays for $k = p+1$ to n
<code>log_l</code>	Log-likelihood at MLE
<code>aic</code>	Akaike Information Criterion
<code>bic</code>	Bayesian Information Criterion
<code>n_params</code>	Number of free parameters
<code>cell_counts</code>	List of cell counts: observed counts for closed-form fits (<code>na_action = "fail"/"complete"</code>), expected counts from the final E-step for EM fits (<code>na_action = "em"</code>), and NULL for <code>na_action = "marginalize"</code>
<code>convergence</code>	Optimizer convergence code (0 for closed-form solutions)
<code>settings</code>	List of model settings

References

Xie, Y. and Zimmerman, D. L. (2013). Antedependence models for nonstationary categorical longitudinal data with ignorable missingness: likelihood-based inference. *Statistics in Medicine*, 32, 3274-3289.

Examples

```
## Not run:
# Simulate binary AD(1) data
set.seed(123)
y <- simulate_cat(n_subjects = 100, n_time = 5, order = 1, n_categories = 2)

# Fit model
fit <- fit_cat(y, order = 1)
print(fit)

# Compare orders
fit0 <- fit_cat(y, order = 0)
fit1 <- fit_cat(y, order = 1)
fit2 <- fit_cat(y, order = 2)
c(AIC_0 = fit0$aic, AIC_1 = fit1$aic, AIC_2 = fit2$aic)

# EM fit with missing data
y_miss <- y
y_miss[sample(length(y_miss), size = round(0.15 * length(y_miss)))] <- NA
fit_em <- fit_cat(
  y_miss,
  order = 1,
  na_action = "em",
  em_max_iter = 80,
```

```

    em_tol = 1e-6
  )
  fit_em$settings$n_iter
  fit_em$settings$cell_counts_type

  ## End(Not run)

```

fit_gau

Fit Gaussian AD model (alias of fit_ad)

Description

Convenience alias for [fit_ad](#).

Usage

```
fit_gau(...)
```

Arguments

... Passed through to [fit_ad](#).

Value

See [fit_ad](#).

See Also

[fit_ad](#), [fit_cat](#), [fit_inad](#)

fit_inad

Fit INAD model by maximum likelihood

Description

Fits INAD models by maximum likelihood.

Usage

```

fit_inad(
  y,
  order = 1,
  thinning = c("binom", "pois", "nbinom"),
  innovation = c("pois", "bell", "nbinom"),
  blocks = NULL,
  max_iter = 50,
  tol = 1e-06,
  verbose = FALSE,
  init_alpha = NULL,
  init_theta = NULL,

```

```

    init_tau = 0.4,
    init_nb_inno_size = 1,
    na_action = c("fail", "complete", "marginalize")
  )

```

Arguments

y	Integer matrix n_sub by n_time.
order	Integer in {0, 1, 2}.
thinning	One of "binom", "pois", "nbinom".
innovation	One of "pois", "bell", "nbinom".
blocks	Optional integer vector length n_sub. Default NULL.
max_iter	Max iterations for FE coordinate descent.
tol	Tolerance for FE log likelihood stopping.
verbose	Logical.
init_alpha	Optional initial alpha. For order 1 numeric length 1 or n_time. For order 2 matrix n_time by 2 or list(alpha1, alpha2).
init_theta	Optional initial theta numeric length 1 or n_time.
init_tau	Optional initial tau. Scalar expands to c(0, x, ..., x). Vector forces first to 0.
init_nb_inno_size	Optional initial size for innovation nbinom, length 1 or n_time.
na_action	How to handle missing values: <ul style="list-style-type: none"> • "fail": stop if any NA is present. • "complete": fit using complete-case subjects only. • "marginalize": maximize observed-data likelihood under MAR.

Details

No fixed effect: time separable optimization using logL_inad_i with theta eliminated by moment equations for order 1 and 2.

Fixed effect: block coordinate descent using nloptr BOBYQA, updating tau, alpha, theta, and nb_inno_size if needed.

Value

A list with estimators, log likelihood, and settings.

logL_ad

Log-likelihood for Gaussian AD models (with missing data support)

Description

Computes the log-likelihood for Gaussian antedependence models of order 0, 1, or 2. Supports missing data under MAR assumption via na_action parameter.

Usage

```
logL_ad(
  y,
  order,
  mu = NULL,
  phi = NULL,
  sigma = NULL,
  blocks = NULL,
  tau = 0,
  na_action = c("marginalize", "complete", "fail")
)
```

Arguments

y	Numeric matrix with n_subjects rows and n_time columns. May contain NA.
order	Antedependence order, one of 0, 1, or 2.
mu	Mean vector (length n_time).
phi	Dependence coefficient(s). For order 1: vector of length n_time-1. For order 2: matrix with 2 columns or vector of length 2*(n_time-2).
sigma	Innovation standard deviations (length n_time).
blocks	Integer vector of block membership (length n_subjects), or NULL.
tau	Block effects, first element constrained to zero
na_action	How to handle missing values: <ul style="list-style-type: none"> • marginalize: Compute observed-data likelihood (default) • complete: Use only complete cases • fail: Error if any NA present

Details

For complete data (no NA), all three na_action options give the same result.

For missing data:

- marginalize: Uses MVN marginalization to compute $P(Y_{\text{obs}})$. This is the correct observed-data likelihood for MAR missing data.
- complete: Removes subjects with any missing values. May lose information.
- fail: Stops with error. Useful to ensure no missing data present.

Value

Scalar log-likelihood value.

logL_cat

*Compute log-likelihood for a categorical antedependence model***Description**

Evaluates the log-likelihood of an AD(p) model for categorical longitudinal data at given parameter values.

Usage

```
logL_cat(
  y,
  order,
  marginal,
  transition = NULL,
  blocks = NULL,
  homogeneous = TRUE,
  n_categories = NULL,
  na_action = c("fail", "complete", "marginalize")
)
```

Arguments

y	Integer matrix with n_subjects rows and n_time columns. Each entry should be a category code from 1 to c.
order	Antedependence order p. Must be 0, 1, or 2.
marginal	List of marginal/joint probabilities for initial time points. Structure depends on order (see Details).
transition	List of transition probability arrays for time points k = p+1 to n. Each element should be an array of dimension $c^p \times c$ where the last dimension corresponds to the current time point.
blocks	Optional integer vector of length n_subjects specifying group membership. Required if homogeneous = FALSE.
homogeneous	Logical. If TRUE (default), same parameters used for all subjects. If FALSE, marginal and transition should be lists indexed by block.
n_categories	Number of categories. If NULL, inferred from data.
na_action	Handling of missing values in y. One of "fail" (default, error if any missing), "complete" (drop subjects with any missing values), or "marginalize" (integrate over missing categorical outcomes under the AD model).

Details

The log-likelihood for AD(p) decomposes into contributions from initial time points and transition time points.

For order 0 (independence), the log-likelihood is the sum of log marginal probabilities at each time point.

Parameter structure for marginal:

- Order 0: List with elements t1, t2, ..., tn, each a vector of length c

- Order 1: List with element t1 (vector of length c)
- Order 2: List with t1 (vector), t2_given_1to1 (c x c matrix)

Parameter structure for transition:

- Order 0: Not used (NULL or empty list)
- Order 1: List with elements t2, t3, ..., tn, each c x c matrix
- Order 2: List with elements t3, t4, ..., tn, each c x c x c array

Value

Scalar log-likelihood value.

References

Xie, Y. and Zimmerman, D. L. (2013). Antedependence models for nonstationary categorical longitudinal data with ignorable missingness: likelihood-based inference. *Statistics in Medicine*, 32, 3274-3289.

logL_gau	<i>Log-likelihood for Gaussian AD model (alias of logL_ad)</i>
----------	--

Description

Convenience alias for [logL_ad](#).

Usage

```
logL_gau(...)
```

Arguments

... Passed through to [logL_ad](#).

Value

See [logL_ad](#).

See Also

[logL_ad](#), [logL_cat](#), [logL_inad](#)

logL_inad	<i>INAD log likelihood (full data)</i>
-----------	--

Description

If `blocks` is `NULL`, this computes the log likelihood as the sum of per time contributions from `logL_inad_i` for computational convenience.

Usage

```
logL_inad(
  y,
  order = 1,
  thinning = c("binom", "pois", "nbinom"),
  innovation = c("pois", "bell", "nbinom"),
  alpha,
  theta,
  nb_inno_size = NULL,
  blocks = NULL,
  tau = 0,
  na_action = c("fail", "complete", "marginalize")
)
```

Arguments

<code>y</code>	Integer matrix <code>n_sub</code> by <code>n_time</code> .
<code>order</code>	Integer in <code>{0, 1, 2}</code> .
<code>thinning</code>	One of "binom", "pois", "nbinom".
<code>innovation</code>	One of "pois", "bell", "nbinom".
<code>alpha</code>	Thinning parameters. For order 1, numeric length 1 or <code>n_time</code> . For order 2, either a matrix <code>n_time</code> by 2 or a list(<code>alpha1</code> , <code>alpha2</code>).
<code>theta</code>	Innovation mean parameters. Numeric length 1 or <code>n_time</code> .
<code>nb_inno_size</code>	Size parameter for innovation "nbinom". Numeric length 1 or <code>n_time</code> .
<code>blocks</code>	Optional integer vector of length <code>n_sub</code> . If <code>NULL</code> , no fixed effect.
<code>tau</code>	Optional numeric vector. Only used if <code>blocks</code> is not <code>NULL</code> .
<code>na_action</code>	How to handle missing values: <ul style="list-style-type: none"> • "fail": error if any NA is present. • "complete": use only complete-case subjects. • "marginalize": observed-data likelihood under MAR via truncated-state recursion.

Value

A scalar log likelihood.

logL_inad_i	<i>INAD log likelihood contribution at time i (no fixed effect)</i>
-------------	---

Description

Returns the time i contribution, summed over subjects, for the no fixed effect model.

Usage

```
logL_inad_i(
  y,
  i,
  order = 1,
  thinning = c("binom", "pois", "nbinom"),
  innovation = c("pois", "bell", "nbinom"),
  alpha,
  theta,
  nb_inno_size = NULL
)
```

Arguments

y	Integer matrix n_sub by n_time.
i	Time index in 1..ncol(y).
order	Integer in {0, 1, 2}.
thinning	One of "binom", "pois", "nbinom".
innovation	One of "pois", "bell", "nbinom".
alpha	Thinning parameters. For order 1, numeric length 1 or n_time. For order 2, either a matrix n_time by 2 or a list(alpha1, alpha2).
theta	Innovation mean parameter at time i, or a vector length 1 or n_time.
nb_inno_size	Size parameter for innovation "nbinom". Numeric length 1 or n_time.

Value

A scalar log likelihood contribution for time i.

lrt_contrast_ad	<i>Test linear hypotheses on the mean under antedependence</i>
-----------------	--

Description

Tests the null hypothesis $C * \mu = c$ for a specified contrast matrix C and vector c, under an AD(p) covariance structure. This implements Theorem 7.2 of Zimmerman & Núñez-Antón (2009).

Usage

```
lrt_contrast_ad(y, C, c = NULL, p = 1L)
```


Arguments

y	Numeric matrix with <code>n_subjects</code> rows and <code>n_time</code> columns.
C	Contrast matrix with <code>c</code> rows and <code>n_time</code> columns, where <code>c</code> is the number of contrasts being tested. Rows must be linearly independent.
c	Right-hand side vector of length equal to <code>nrow(C)</code> . Default is a vector of zeros.
p	Antedependence order of the covariance structure.

Details

The Wald test statistic (Theorem 7.2) is:

$$(C\bar{Y} - c)^T (C\hat{\Sigma}C^T)^{-1} (C\bar{Y} - c)$$

where $\hat{\Sigma}$ is the REML estimator of the covariance matrix under the AD(p) model.

Common examples include:

- Testing if mean is constant: `C` is the first-difference matrix
- Testing for linear trend: `C` tests deviations from linearity

Value

A list with class `ad_contrast_test` containing:

C Contrast matrix
c Right-hand side vector
mu_hat Estimated mean vector
contrast_est Estimated value of `C * mu`
statistic Wald test statistic
df Degrees of freedom (number of contrasts)
p_value P-value from chi-square distribution

References

Zimmerman, D.L. and Núñez-Antón, V. (2009). Antedependence Models for Longitudinal Data. Chapman & Hall/CRC. Chapter 7.

Examples

```
## Not run:
y <- simulate_ad(n_subjects = 50, n_time = 5, order = 1)

# Test if mean is constant (all differences = 0)
# C is 4x5 matrix of first differences
C <- matrix(0, nrow = 4, ncol = 5)
for (i in 1:4) {
  C[i, i] <- 1
  C[i, i+1] <- -1
}
test <- lrt_contrast_ad(y, C = C, p = 1)
print(test)

## End(Not run)
```

lrt_contrast_gau	<i>Linear contrast test for Gaussian AD means (alias of lrt_contrast_ad)</i>
------------------	--

Description

Convenience alias for [lrt_contrast_ad](#).

Usage

```
lrt_contrast_gau(...)
```

Arguments

... Passed through to [lrt_contrast_ad](#).

Value

See [lrt_contrast_ad](#).

See Also

[lrt_contrast_ad](#)

lrt_homogeneity_ad	<i>Test for homogeneity of AD covariance structure across groups</i>
--------------------	--

Description

Tests the null hypothesis that G groups have the same $AD(p)$ covariance structure against the alternative that they have different $AD(p)$ structures. This implements Theorem 6.6 of Zimmerman & Núñez-Antón (2009).

Usage

```
lrt_homogeneity_ad(y, blocks, p = 1L, use_modified = TRUE)
```

Arguments

<code>y</code>	Numeric matrix with <code>n_subjects</code> rows and <code>n_time</code> columns.
<code>blocks</code>	Integer vector of length <code>n_subjects</code> indicating group membership.
<code>p</code>	Antedependence order.
<code>use_modified</code>	Logical. If TRUE (default), use modified test statistic for better small-sample approximation.

Details

The test compares:

- H0: All G groups have the same AD(p) covariance matrix $\text{Sigma}(\theta)$
- H1: Groups have different AD(p) covariance matrices $\text{Sigma}(\theta_g)$

The likelihood ratio test statistic (Theorem 6.6) involves comparing pooled and within-group RSS values. The degrees of freedom are $(G-1)(2n - p)(p + 1)/2$.

This test is useful for determining whether a common covariance structure can be assumed across treatment groups before performing mean comparisons.

Value

A list with class `ad_homogeneity_test` containing:

statistic Test statistic value

statistic_modified Modified test statistic (if `use_modified = TRUE`)

df Degrees of freedom

p_value P-value from chi-square distribution

p_value_modified P-value from modified test

G Number of groups

group_sizes Sample sizes for each group

order Antedependence order

References

Zimmerman, D.L. and Núñez-Antón, V. (2009). Antedependence Models for Longitudinal Data. Chapman & Hall/CRC. Section 6.4.

Kenward, M.G. (1987). A method for comparing profiles of repeated measurements. *Applied Statistics*, 36, 296-308.

See Also

[lrt_order_ad](#), [lrt_two_sample_ad](#)

Examples

```
## Not run:
# Simulate data from two groups with same covariance
n1 <- 30
n2 <- 35
y1 <- simulate_ad(n1, n_time = 6, order = 1, phi = 0.5, sigma = 1)
y2 <- simulate_ad(n2, n_time = 6, order = 1, phi = 0.5, sigma = 1)
y <- rbind(y1, y2)
blocks <- c(rep(1, n1), rep(2, n2))

# Test homogeneity
test <- lrt_homogeneity_ad(y, blocks, p = 1)
print(test)

## End(Not run)
```

lrt_homogeneity_cat *Likelihood ratio test for homogeneity across groups (categorical data)*

Description

Tests whether multiple groups share the same transition probability parameters in a categorical antedependence model.

Usage

```
lrt_homogeneity_cat(
  y = NULL,
  blocks = NULL,
  order = 1,
  n_categories = NULL,
  fit_null = NULL,
  fit_alt = NULL
)
```

Arguments

y	Integer matrix with n_subjects rows and n_time columns. Each entry should be a category code from 1 to c. Can be NULL if both fit_null and fit_alt are provided.
blocks	Integer vector of length n_subjects specifying group membership. Required unless pre-fitted models are provided.
order	Antedependence order p. Default is 1.
n_categories	Number of categories. If NULL, inferred from data.
fit_null	Optional pre-fitted homogeneous model (class "cat_fit" with homogeneous = TRUE). If provided, y is not required for fitting under H0.
fit_alt	Optional pre-fitted heterogeneous model (class "cat_fit" with homogeneous = FALSE). If provided, y is not required for fitting under H1.

Details

The null hypothesis is that all G groups share the same transition probability parameters:

$$H_0 : \pi^{(1)} = \pi^{(2)} = \dots = \pi^{(G)}$$

The alternative hypothesis allows each group to have its own parameters.

The degrees of freedom are:

$$df = (G - 1) \times k$$

where G is the number of groups and k is the number of free parameters per population.

Value

A list of class "cat_lrt" containing:

lrt_stat	Likelihood ratio test statistic
df	Degrees of freedom
p_value	P-value from chi-square distribution
fit_null	Fitted homogeneous model (H0)
fit_alt	Fitted heterogeneous model (H1)
n_groups	Number of groups
table	Summary data frame

References

Xie, Y. and Zimmerman, D. L. (2013). Antedependence models for nonstationary categorical longitudinal data with ignorable missingness: likelihood-based inference. *Statistics in Medicine*, 32, 3274-3289.

See Also

[fit_cat](#), [lrt_order_cat](#)

Examples

```
## Not run:
# Simulate data with different transition probabilities for two groups
set.seed(123)
marg1 <- list(t1 = c(0.7, 0.3))
marg2 <- list(t1 = c(0.4, 0.6))
trans1 <- list(t2 = matrix(c(0.9, 0.1, 0.2, 0.8), 2, byrow = TRUE),
               t3 = matrix(c(0.9, 0.1, 0.2, 0.8), 2, byrow = TRUE))
trans2 <- list(t2 = matrix(c(0.5, 0.5, 0.5, 0.5), 2, byrow = TRUE),
               t3 = matrix(c(0.5, 0.5, 0.5, 0.5), 2, byrow = TRUE))

y1 <- simulate_cat(100, 3, order = 1, n_categories = 2,
                  marginal = marg1, transition = trans1)
y2 <- simulate_cat(100, 3, order = 1, n_categories = 2,
                  marginal = marg2, transition = trans2)
y <- rbind(y1, y2)
blocks <- c(rep(1, 100), rep(2, 100))

# Test homogeneity
test <- lrt_homogeneity_cat(y, blocks, order = 1)
print(test)

## End(Not run)
```

lrt_homogeneity_gau	<i>Covariance homogeneity test for Gaussian AD (alias of lrt_homogeneity_ad)</i>
---------------------	--

Description

Convenience alias for [lrt_homogeneity_ad](#).

Usage

```
lrt_homogeneity_gau(...)
```

Arguments

... Passed through to [lrt_homogeneity_ad](#).

Value

See [lrt_homogeneity_ad](#).

See Also

[lrt_homogeneity_ad](#), [lrt_homogeneity_cat](#), [lrt_homogeneity_inad](#)

lrt_homogeneity_inad	<i>Likelihood Ratio Test for Homogeneity in INAD Models</i>
----------------------	---

Description

Tests hypotheses about parameter equality across treatment or grouping factors in integer-valued antedependence models. Implements the homogeneity testing framework from Section 3.7 of Li & Zimmerman (2026).

Usage

```
lrt_homogeneity_inad(
  y,
  blocks,
  order = 1,
  thinning = "binom",
  innovation = "pois",
  test = c("all", "mean", "dependence"),
  fit_pooled = NULL,
  fit_inadfe = NULL,
  fit_hetero = NULL,
  ...
)
```

Arguments

<code>y</code>	Integer matrix with <code>n_subjects</code> rows and <code>n_time</code> columns.
<code>blocks</code>	Integer vector of length <code>n_subjects</code> specifying group membership.
<code>order</code>	Antedependence order (0, 1, or 2).
<code>thinning</code>	Thinning operator: "binom", "pois", or "nbinom".
<code>innovation</code>	Innovation distribution: "pois", "bell", or "nbinom".
<code>test</code>	Type of homogeneity test: <ul style="list-style-type: none"> "all": Tests M1 (pooled) vs M3 (fully heterogeneous) "mean": Tests M1 (pooled) vs M2 (shared dependence, different means) "dependence": Tests M2 (INADFE) vs M3 (fully heterogeneous)
<code>fit_pooled</code>	Optional pre-computed pooled fit (M1).
<code>fit_inadfe</code>	Optional pre-computed INADFE fit (M2).
<code>fit_hetero</code>	Optional pre-computed heterogeneous fit (M3).
<code>...</code>	Additional arguments passed to <code>fit_inad</code> .

Details

The function supports three nested model comparisons as described in the paper:

M1 (Pooled): All parameters are common across groups. This corresponds to fitting `fit_inad(y, blocks = NULL)`.

M2 (INADFE): The thinning parameters α are shared across groups, but innovation means differ via block effects τ . This is the standard INADFE model fitted via `fit_inad(y, blocks = blocks)`.

M3 (Fully Heterogeneous): Both α and θ parameters can differ across groups. This is fitted by running separate `fit_inad` calls for each group.

The three test types correspond to:

- "all": H0: M1 vs H1: M3 (complete homogeneity vs complete heterogeneity)
- "mean": H0: M1 vs H1: M2 (test for group differences in means only)
- "dependence": H0: M2 vs H1: M3 (test for group differences in dependence)

Degrees of freedom are computed as the difference in free parameters between the null and alternative models.

Value

A list with class "lrt_homogeneity_inad" containing:

lrt_stat Likelihood ratio test statistic

df Degrees of freedom

p_value P-value from chi-square distribution

test Type of test performed

fit_null Fitted model under H0

fit_alt Fitted model under H1

bic_null BIC under H0

bic_alt BIC under H1

bic_selected Which model BIC prefers

table Summary data frame

References

Li, C. and Zimmerman, D.L. (2026). Integer-valued antedependence models for longitudinal count data. *Biostatistics*. Section 3.7.

See Also

[fit_inad](#), [lrt_order_inad](#), [lrt_stationarity_inad](#)

Examples

```
## Not run:
data("bolus_inad")
y <- bolus_inad$y
blocks <- bolus_inad$blocks

# Test for any group differences (M1 vs M3)
test_all <- lrt_homogeneity_inad(y, blocks, order = 1,
                                thinning = "nbinom", innovation = "bell",
                                test = "all")

print(test_all)

# Test only for mean differences (M1 vs M2)
test_mean <- lrt_homogeneity_inad(y, blocks, order = 1,
                                  thinning = "nbinom", innovation = "bell",
                                  test = "mean")

print(test_mean)

# Test for dependence differences given different means (M2 vs M3)
test_dep <- lrt_homogeneity_inad(y, blocks, order = 1,
                                 thinning = "nbinom", innovation = "bell",
                                 test = "dependence")

print(test_dep)

## End(Not run)
```

lrt_one_sample_ad

One-sample test for mean structure under antedependence

Description

Tests the null hypothesis that the mean vector equals a specified value $\mu = \mu_0$ against the alternative $\mu \neq \mu_0$, under an AD(p) covariance structure. This implements Theorem 7.1 of Zimmerman & Núñez-Antón (2009).

Usage

```
lrt_one_sample_ad(y, mu0, p = 1L, use_modified = TRUE)
```


Arguments

<code>y</code>	Numeric matrix with <code>n_subjects</code> rows and <code>n_time</code> columns.
<code>mu0</code>	Hypothesized mean vector under the null (length <code>n_time</code>).
<code>p</code>	Antedependence order of the covariance structure.
<code>use_modified</code>	Logical. If TRUE (default), use the modified test statistic (formula 7.7) for better small-sample approximation.

Details

The test exploits the AD structure to gain power over tests that don't assume any covariance structure. The likelihood ratio test statistic (Theorem 7.1) is:

$$N \sum_{i=1}^n [\log RSS_i(\mu_0) - \log RSS_i(\hat{\mu})]$$

where $RSS_i(\mu)$ is the residual sum of squares from the regression of $Y_i - \mu_i$ on its p predecessors $Y_{(i-1)} - \mu_{(i-1)}$, ..., $Y_{(i-p)} - \mu_{(i-p)}$.

The test has n degrees of freedom (one for each component of μ).

Value

A list with class `ad_mean_test` containing:

test_type "one-sample"
mu0 Hypothesized mean under null
mu_hat MLE of mean (sample mean)
statistic Test statistic value
statistic_modified Modified test statistic (if `use_modified = TRUE`)
df Degrees of freedom (`n_time`)
p_value P-value from chi-square distribution
p_value_modified P-value from modified test
order Antedependence order used

References

Zimmerman, D.L. and Núñez-Antón, V. (2009). Antedependence Models for Longitudinal Data. Chapman & Hall/CRC. Chapter 7.

See Also

[lrt_two_sample_ad](#), [lrt_order_ad](#)

Examples

```
## Not run:
# Simulate data with known mean
mu_true <- c(10, 11, 12, 13, 14, 15)
y <- simulate_ad(n_subjects = 50, n_time = 6, order = 1, mu = mu_true)

# Test if mean is zero
```

```
test <- lrt_one_sample_ad(y, mu0 = rep(0, 6), p = 1)
print(test)

# Test if mean equals true value (should not reject)
test2 <- lrt_one_sample_ad(y, mu0 = mu_true, p = 1)
print(test2)

## End(Not run)
```

lrt_one_sample_gau	<i>One-sample mean test for Gaussian AD (alias of lrt_one_sample_ad)</i>
--------------------	--

Description

Convenience alias for [lrt_one_sample_ad](#).

Usage

```
lrt_one_sample_gau(...)
```

Arguments

... Passed through to [lrt_one_sample_ad](#).

Value

See [lrt_one_sample_ad](#).

See Also

[lrt_one_sample_ad](#), [lrt_two_sample_ad](#)

lrt_order_ad	<i>Likelihood ratio test for antedependence order</i>
--------------	---

Description

Tests the null hypothesis that the data follow an AD(p) model against the alternative that they follow an AD(p+q) model, using the likelihood ratio test described in Theorem 6.4 and 6.5 of Zimmerman & Núñez-Antón (2009).

Usage

```
lrt_order_ad(y, p = 0L, q = 1L, mu = NULL, use_modified = TRUE)
```

Arguments

y	Numeric matrix with n_subjects rows and n_time columns.
p	Order under the null hypothesis (default 0).
q	Order increment under the alternative (default 1, so alternative is AD(p+q)).
mu	Optional mean vector. If NULL, the saturated mean (sample means) is used.
use_modified	Logical. If TRUE (default), use the modified test statistic (formula 6.9) which has better small-sample properties.

Details

The test is based on the intervenor-adjusted sample partial correlations. Under the null hypothesis AD(p), the partial correlations $r_{(i,i-k|(i-k+1:i-1))}$ should be zero for $k > p$.

The likelihood ratio test statistic (Theorem 6.4) is:

$$-N \sum_{j=1}^q \sum_{i=p+j+1}^n \log(1 - r_{i,i-p-j \cdot (i-p-j+1:i-1)}^2)$$

which is asymptotically chi-square with $(2n - 2p - q - 1)(q/2)$ degrees of freedom.

The modified test (formula 6.9) adjusts for small-sample bias using Kenward's (1987) correction.

Value

A list with class `ad_order_test` containing:

- p** Order under null hypothesis
- q** Order increment
- statistic** Test statistic value
- statistic_modified** Modified test statistic (if `use_modified = TRUE`)
- df** Degrees of freedom
- p_value** P-value from chi-square distribution
- p_value_modified** P-value from modified test (if `use_modified = TRUE`)
- n_subjects** Number of subjects
- n_time** Number of time points

References

- Zimmerman, D.L. and Núñez-Antón, V. (2009). Antedependence Models for Longitudinal Data. Chapman & Hall/CRC. Chapter 6.
- Kenward, M.G. (1987). A method for comparing profiles of repeated measurements. Applied Statistics, 36, 296-308.

See Also

[lrt_one_sample_ad](#), [lrt_homogeneity_ad](#)

Examples

```
## Not run:
# Simulate AD(1) data
y <- simulate_ad(n_subjects = 50, n_time = 6, order = 1, phi = 0.5)

# Test AD(0) vs AD(1)
test01 <- lrt_order_ad(y, p = 0, q = 1)
print(test01)

# Test AD(1) vs AD(2)
test12 <- lrt_order_ad(y, p = 1, q = 1)
print(test12)

## End(Not run)
```

lrt_order_cat	<i>Likelihood ratio test for antedependence order (categorical data)</i>
---------------	--

Description

Tests whether a higher-order AD model provides significantly better fit than a lower-order model for categorical longitudinal data.

Usage

```
lrt_order_cat(
  y = NULL,
  order_null = 0,
  order_alt = 1,
  blocks = NULL,
  homogeneous = TRUE,
  n_categories = NULL,
  fit_null = NULL,
  fit_alt = NULL
)
```

Arguments

y	Integer matrix with <code>n_subjects</code> rows and <code>n_time</code> columns. Each entry should be a category code from 1 to <code>c</code> . Can be <code>NULL</code> if both <code>fit_null</code> and <code>fit_alt</code> are provided.
order_null	Order under the null hypothesis (default 0).
order_alt	Order under the alternative hypothesis (default 1). Must be greater than <code>order_null</code> .
blocks	Optional integer vector of length <code>n_subjects</code> specifying group membership.
homogeneous	Logical. If <code>TRUE</code> (default), parameters are shared across all groups.
n_categories	Number of categories. If <code>NULL</code> , inferred from data.
fit_null	Optional pre-fitted model under null hypothesis (class "cat_fit"). If provided, <code>y</code> is not required for fitting under H_0 .
fit_alt	Optional pre-fitted model under alternative hypothesis. If provided, <code>y</code> is not required for fitting under H_1 .

Details

The likelihood ratio test statistic is:

$$\lambda = -2[\ell_0 - \ell_1]$$

where ℓ_0 and ℓ_1 are the maximized log-likelihoods under the null and alternative hypotheses.

Under H_0 , λ follows a chi-square distribution with degrees of freedom equal to the difference in the number of free parameters.

For testing AD(p) vs AD(p+1), the degrees of freedom are:

$$df = (c - 1) \times c^p \times (n - p - 1)$$

where c is the number of categories and n is the number of time points.

Value

A list of class "cat_lrt" containing:

lrt_stat	Likelihood ratio test statistic
df	Degrees of freedom
p_value	P-value from chi-square distribution
fit_null	Fitted model under H_0
fit_alt	Fitted model under H_1
order_null	Order under null
order_alt	Order under alternative
table	Summary data frame

References

Xie, Y. and Zimmerman, D. L. (2013). Antedependence models for nonstationary categorical longitudinal data with ignorable missingness: likelihood-based inference. *Statistics in Medicine*, 32, 3274-3289.

See Also

[fit_cat](#), [bic_order_cat](#)

Examples

```
## Not run:
# Simulate AD(1) data
set.seed(123)
y <- simulate_cat(200, 6, order = 1, n_categories = 2)

# Test AD(0) vs AD(1)
test_01 <- lrt_order_cat(y, order_null = 0, order_alt = 1)
print(test_01$table)

# Test AD(1) vs AD(2)
test_12 <- lrt_order_cat(y, order_null = 1, order_alt = 2)
print(test_12$table)

# Using pre-fitted models
fit0 <- fit_cat(y, order = 0)
```

```
fit1 <- fit_cat(y, order = 1)
test_prefitted <- lrt_order_cat(fit_null = fit0, fit_alt = fit1)

## End(Not run)
```

lrt_order_gau	<i>LRT for Gaussian AD order (alias of lrt_order_ad)</i>
---------------	--

Description

Convenience alias for [lrt_order_ad](#).

Usage

```
lrt_order_gau(...)
```

Arguments

... Passed through to [lrt_order_ad](#).

Value

See [lrt_order_ad](#).

See Also

[lrt_order_ad](#), [lrt_order_cat](#), [lrt_order_inad](#)

lrt_order_inad	<i>Likelihood Ratio Test for INAD Model Order</i>
----------------	---

Description

Performs a likelihood ratio test comparing INAD models of different orders.

Usage

```
lrt_order_inad(
  y,
  order_null = 1,
  order_alt = 2,
  thinning = "binom",
  innovation = "pois",
  blocks = NULL,
  use_chibar = TRUE,
  weights = NULL,
  fit_null = NULL,
  fit_alt = NULL,
  ...
)
```

Arguments

<code>y</code>	Integer matrix with <code>n_subjects</code> rows and <code>n_time</code> columns.
<code>order_null</code>	Order under null hypothesis (0 or 1).
<code>order_alt</code>	Order under alternative hypothesis (1 or 2). Must be <code>order_null + 1</code> .
<code>thinning</code>	Thinning operator: "binom", "pois", or "nbinom".
<code>innovation</code>	Innovation distribution: "pois", "bell", or "nbinom".
<code>blocks</code>	Optional integer vector for block effects.
<code>use_chibar</code>	Logical; if TRUE, use chi-bar-square for boundary test.
<code>weights</code>	Optional weights for chi-bar-square mixture.
<code>fit_null</code>	Optional pre-computed null fit.
<code>fit_alt</code>	Optional pre-computed alternative fit.
<code>...</code>	Additional arguments passed to <code>fit_inad</code> .

Value

A list with class "lrt_order_inad".

`lrt_stationarity_cat` *Likelihood ratio test for stationarity (categorical data)*

Description

Tests whether a categorical antedependence process is strictly stationary, meaning both the marginal distribution and transition probabilities are constant over time.

Usage

```
lrt_stationarity_cat(
  y,
  order = 1,
  blocks = NULL,
  homogeneous = TRUE,
  n_categories = NULL
)
```

Arguments

<code>y</code>	Integer matrix with <code>n_subjects</code> rows and <code>n_time</code> columns. Each entry should be a category code from 1 to <code>c</code> .
<code>order</code>	Antedependence order <code>p</code> . Default is 1.
<code>blocks</code>	Optional integer vector of length <code>n_subjects</code> specifying group membership.
<code>homogeneous</code>	Logical. If TRUE (default), parameters are shared across all groups.
<code>n_categories</code>	Number of categories. If NULL, inferred from data.

Details

Strict stationarity requires:

1. The marginal distribution $P(Y_k)$ is constant for all k
2. The transition probabilities $P(Y_k | Y(k-p), \dots, Y(k-1))$ are constant for all $k > p$

This is stronger than time-invariance, which only requires condition 2.

The null hypothesis is tested against the general (non-stationary) AD(p) model. The degrees of freedom are:

$$df = (c - 1)(n - 1) + (c - 1)c^p(n - p - 1)$$

for order $p \geq 1$, which accounts for both marginal and transition constraints.

Value

A list of class "cat_lrt" containing:

lrt_stat	Likelihood ratio test statistic
df	Degrees of freedom
p_value	P-value from chi-square distribution
fit_null	Fitted stationary model (H0)
fit_alt	Fitted non-stationary model (H1)
table	Summary data frame

References

Xie, Y. and Zimmerman, D. L. (2013). Antedependence models for nonstationary categorical longitudinal data with ignorable missingness: likelihood-based inference. *Statistics in Medicine*, 32, 3274-3289.

See Also

[lrt_timeinvariance_cat](#), [lrt_order_cat](#)

Examples

```
## Not run:
# Simulate stationary AD(1) data
set.seed(123)
y <- simulate_cat(200, 6, order = 1, n_categories = 2)

# Test stationarity
test <- lrt_stationarity_cat(y, order = 1)
print(test)

## End(Not run)
```

lrt_stationarity_inad *Likelihood Ratio Test for INAD Stationarity*

Description

Tests whether time-varying parameters can be constrained to constants.

Usage

```
lrt_stationarity_inad(
  y,
  order = 1,
  thinning = "binom",
  innovation = "pois",
  blocks = NULL,
  constrain = "both",
  fit_unconstrained = NULL,
  verbose = FALSE,
  ...
)
```

Arguments

y	Integer matrix with n_subjects rows and n_time columns.
order	Model order (1 or 2).
thinning	Thinning operator: "binom", "pois", or "nbinom".
innovation	Innovation distribution: "pois", "bell", or "nbinom".
blocks	Optional integer vector for block effects.
constrain	Which parameters to constrain: "alpha", "theta", "both" for order 1; "alpha1", "alpha2", "alpha", "theta", "all" for order 2.
fit_unconstrained	Optional pre-computed unconstrained fit.
verbose	Logical; if TRUE, print progress.
...	Additional arguments.

Value

A list with class "lrt_stationarity_inad".

lrt_timeinvariance_cat

Likelihood ratio test for time-invariance (categorical data)

Description

Tests whether transition probabilities are constant over time in a categorical antedependence model.

Usage

```
lrt_timeinvariance_cat(
  y,
  order = 1,
  blocks = NULL,
  homogeneous = TRUE,
  n_categories = NULL
)
```

Arguments

y	Integer matrix with n_subjects rows and n_time columns. Each entry should be a category code from 1 to c.
order	Antedependence order p. Default is 1.
blocks	Optional integer vector of length n_subjects specifying group membership.
homogeneous	Logical. If TRUE (default), parameters are shared across all groups.
n_categories	Number of categories. If NULL, inferred from data.

Details

The null hypothesis is that all transition probabilities (for $k > p$) are equal across time:

$$H_0 : \pi_{y_k | y_{k-p}, \dots, y_{k-1}} \text{ is constant for } k = p + 1, \dots, n$$

This reduces (n-p) separate transition matrices/arrays to a single one.

The degrees of freedom are:

$$df = (c - 1) \times c^p \times (n - p - 1)$$

Value

A list of class "cat_lrt" containing:

lrt_stat	Likelihood ratio test statistic
df	Degrees of freedom
p_value	P-value from chi-square distribution
fit_null	Fitted time-invariant model (H0)
fit_alt	Fitted time-varying model (H1)
table	Summary data frame

References

Xie, Y. and Zimmerman, D. L. (2013). Antedependence models for nonstationary categorical longitudinal data with ignorable missingness: likelihood-based inference. *Statistics in Medicine*, 32, 3274-3289.

See Also

[fit_cat](#), [lrt_order_cat](#)

Examples

```
## Not run:
# Simulate data with time-invariant transitions
set.seed(123)
y <- simulate_cat(200, 6, order = 1, n_categories = 2)

# Test time-invariance
test <- lrt_timeinvariance_cat(y, order = 1)
print(test)

## End(Not run)
```

lrt_two_sample_ad	<i>Two-sample test for equality of mean profiles under antedependence</i>
-------------------	---

Description

Tests the null hypothesis that two groups have equal mean profiles $\mu_1 = \mu_2$ against the alternative $\mu_1 \neq \mu_2$, assuming a common AD(p) covariance structure. This implements Theorem 7.3 of Zimmerman & Núñez-Antón (2009).

Usage

```
lrt_two_sample_ad(y, blocks, p = 1L, use_modified = TRUE)
```

Arguments

y	Numeric matrix with n_subjects rows and n_time columns.
blocks	Integer vector of length n_subjects indicating group membership (must contain exactly two unique values, typically 1 and 2).
p	Antedependence order of the common covariance structure.
use_modified	Logical. If TRUE (default), use modified test statistic.

Details

This test is also known as a "profile comparison" test. The likelihood ratio test statistic (Theorem 7.3) compares the pooled RSS (under H0: common mean) to the sum of within-group RSS (under H1: separate means):

$$N \sum_{i=1}^n [\log RSS_i(\mu) - \log RSS_i(\mu_1, \mu_2)]$$

where $RSS_i(\mu)$ uses a common mean and $RSS_i(\mu_1, \mu_2)$ uses group-specific means.

Value

A list with class `ad_mean_test` containing:

test_type "two-sample"

mu1_hat Estimated mean for group 1

mu2_hat Estimated mean for group 2

mu_pooled Pooled mean estimate under H_0

statistic Test statistic value

statistic_modified Modified test statistic

df Degrees of freedom (n_time)

p_value P-value from chi-square distribution

p_value_modified P-value from modified test

order Antedependence order used

References

Zimmerman, D.L. and Núñez-Antón, V. (2009). Antedependence Models for Longitudinal Data. Chapman & Hall/CRC. Chapter 7.

Examples

```
## Not run:
# Simulate data from two groups with different means
n1 <- 30
n2 <- 35
y1 <- simulate_ad(n1, n_time = 6, order = 1, mu = rep(10, 6))
y2 <- simulate_ad(n2, n_time = 6, order = 1, mu = rep(12, 6))
y <- rbind(y1, y2)
blocks <- c(rep(1, n1), rep(2, n2))

# Test equality of profiles
test <- lrt_two_sample_ad(y, blocks, p = 1)
print(test)

## End(Not run)
```

lrt_two_sample_gau	<i>Two-sample mean profile test for Gaussian AD (alias of lrt_two_sample_ad)</i>
--------------------	--

Description

Convenience alias for [lrt_two_sample_ad](#).

Usage

```
lrt_two_sample_gau(...)
```

Arguments

... Passed through to [lrt_two_sample_ad](#).

Value

See [lrt_two_sample_ad](#).

See Also

[lrt_two_sample_ad](#), [lrt_one_sample_ad](#)

partial_corr	<i>Compute intervenor-adjusted partial correlation matrix</i>
--------------	---

Description

Computes the partial correlation between $Y[i]$ and $Y[j]$ adjusting for the "intervenor" variables $Y[i+1]$, ..., $Y[j-1]$. Under an antedependence model of order p , partial correlations for $|i-j| > p$ should be approximately zero.

Usage

```
partial_corr(y, test = FALSE, n_digits = 3)
```

Arguments

<code>y</code>	Numeric matrix with <code>n_subjects</code> rows and <code>n_time</code> columns.
<code>test</code>	Logical; if TRUE, returns significance flags based on approximate threshold $2/\sqrt{n_{\text{eff}}}$ where $n_{\text{eff}} = n_{\text{subjects}} - (\text{lag} - 1)$. Default FALSE.
<code>n_digits</code>	Integer; number of decimal places for rounding. Default 3.

Details

The intervenor-adjusted partial correlation between $Y[i]$ and $Y[j]$ ($i < j$) is computed as the correlation between the residuals from regressing $Y[i]$ and $Y[j]$ on the intervenor set $Y[i+1], \dots, Y[j-1]$.

For adjacent time points ($|i-j| = 1$), the partial correlation equals the ordinary correlation since there are no intervenors.

The diagonal of both returned matrices contains variances (not correlations). This keeps scale information available alongside correlation structure.

The significance test uses an approximate threshold of $2/\sqrt{n_{\text{eff}}}$, which corresponds roughly to a 95% confidence bound under normality. This is a rough screening tool, not a formal hypothesis test.

Value

A list with components:

correlation	Matrix with correlations (upper triangle) and variances (diagonal)
partial_correlation	Matrix with partial correlations (lower triangle) and variances (diagonal)
significant	(If test=TRUE) Matrix flagging significant partial correlations (1 = significant)
n_subjects	Number of subjects
n_time	Number of time points

References

Zimmerman, D. L. and Nunez-Anton, V. (2009). Antedependence Models for Longitudinal Data. CRC Press.

See Also

[plot_prism](#) for visual diagnostics

Examples

```
## Not run:
data("bolus_inad")
pc <- partial_corr(bolus_inad$y, test = TRUE)

# View partial correlations (lower triangle)
pc$partial_correlation

# Extract variances from the diagonal
variances <- diag(pc$partial_correlation)

# Check which are "significant" (rough screen for AD order)
pc$significant

## End(Not run)
```

plot_prism

*PRISM plot (Partial Residual Intervenor Scatterplot Matrix)***Description**

Creates a matrix of scatterplots for diagnosing antedependence structure. The upper triangle shows ordinary scatterplots of $Y[i]$ vs $Y[j]$. The lower triangle shows PRISM plots: residuals from regressing $Y[i]$ and $Y[j]$ on the intervenor variables $Y[i+1]$, ..., $Y[j-1]$.

Usage

```
plot_prism(
  y,
  time_labels = NULL,
  pch = 20,
  cex = 0.6,
  col_upper = "steelblue",
  col_lower = "firebrick",
  main = "PRISM Diagnostic Plot"
)
```

Arguments

<code>y</code>	Numeric matrix with <code>n_subjects</code> rows and <code>n_time</code> columns.
<code>time_labels</code>	Optional character vector of time point labels. Default uses column names or "T1", "T2", etc.
<code>pch</code>	Point character for scatterplots. Default 20 (filled circle).
<code>cex</code>	Point size. Default 0.6.
<code>col_upper</code>	Color for upper triangle plots. Default "steelblue".
<code>col_lower</code>	Color for lower triangle (PRISM) plots. Default "firebrick".
<code>main</code>	Overall title. Default "PRISM Diagnostic Plot".

Details

Under an antedependence model of order p , the partial correlation between $Y[i]$ and $Y[j]$ given the intervenors should be zero when $|i-j| > p$. This means PRISM plots in the lower triangle should show no association for lags greater than p .

Interpretation:

- Upper triangle: Shows marginal associations between time points
- Lower triangle (PRISM): Shows conditional associations after removing effects of intervenor variables
- If AD(1) holds: Only the first sub-diagonal of lower triangle should show association
- If AD(2) holds: First two sub-diagonals should show association

Value

Invisibly returns NULL. Called for side effect (plotting).

References

Zimmerman, D. L. and Nunez-Anton, V. (2009). Antedependence Models for Longitudinal Data. CRC Press. Chapter 2.

See Also

[partial_corr](#) for numerical partial correlations

Examples

```
## Not run:
data("bolus_inad")
plot_prism(bolus_inad$y)

# With custom labels
plot_prism(bolus_inad$y, time_labels = paste0("Hour ", seq(0, 44, by = 4)))

## End(Not run)
```

plot_profile

Profile plot (spaghetti plot) for longitudinal data

Description

Creates a profile plot showing individual subject trajectories with overlaid mean trajectory and standard deviation bands.

Usage

```
plot_profile(
  y,
  time_points = NULL,
  blocks = NULL,
  block_labels = NULL,
  title = "Profile Plot",
  xlab = "Time",
  ylab = "Measurement",
  ylim = NULL,
  show_sd = TRUE,
  individual_alpha = 0.3,
  individual_color = "grey50",
  mean_color = "blue",
  sd_color = "red",
  mean_lwd = 2
)
```


Arguments

<code>y</code>	Numeric matrix with <code>n_subjects</code> rows and <code>n_time</code> columns, or a data frame with measurements.
<code>time_points</code>	Optional numeric vector of time points for x-axis. Default uses <code>1:n_time</code> or attempts to extract from column names.
<code>blocks</code>	Optional integer vector of block memberships for stratified plotting. If provided, creates separate panels for each block.
<code>block_labels</code>	Optional character vector of labels for blocks.
<code>title</code>	Plot title. Default "Profile Plot".
<code>xlab</code>	X-axis label. Default "Time".
<code>ylab</code>	Y-axis label. Default "Measurement".
<code>ylim</code>	Optional y-axis limits as <code>c(min, max)</code> .
<code>show_sd</code>	Logical; if TRUE (default), show +/- 1 SD error bars.
<code>individual_alpha</code>	Alpha (transparency) for individual trajectories. Default 0.3.
<code>individual_color</code>	Color for individual trajectories. Default "grey50".
<code>mean_color</code>	Color for mean trajectory. Default "blue".
<code>sd_color</code>	Color for SD error bars. Default "red".
<code>mean_lwd</code>	Line width for mean trajectory. Default 2.

Details

This function provides a quick visual summary of longitudinal data showing:

- Individual subject trajectories (light grey lines)
- Mean trajectory across subjects (bold colored line)
- +/- 1 standard deviation bands (error bars)

When `blocks` is provided, the plot is faceted by block membership, allowing comparison of trajectories across treatment groups or other strata.

Value

A `ggplot2` object (invisibly). Called primarily for side effect (plotting).

Examples

```
## Not run:
data("bolus_inad")

# Basic profile plot
plot_profile(bolus_inad$y)

# With block stratification
plot_profile(bolus_inad$y, blocks = bolus_inad$blocks,
             block_labels = c("2mg", "1mg"))

# Customized
plot_profile(bolus_inad$y,
```

```

time_points = seq(0, 44, by = 4),
title = "Bolus Counts Over Time",
xlab = "Hours", ylab = "Count")

## End(Not run)

```

print.ad_bic_order	<i>Print method for BIC order selection</i>
--------------------	---

Description

Print method for BIC order selection

Usage

```

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

```

Arguments

x	Object of class ad_bic_order.
...	Unused.

print.ad_ci	<i>Print method for AD confidence intervals</i>
-------------	---

Description

Print method for AD confidence intervals

Usage

```

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

```

Arguments

x	An object of class ad_ci.
...	Unused.

Value

The input object, invisibly.

```
print.ad_contrast_test
```

Print method for AD contrast test

Description

Print method for AD contrast test

Usage

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

Arguments

x	Object of class ad_contrast_test.
...	Unused.

```
print.ad_homogeneity_test
```

Print method for AD homogeneity test

Description

Print method for AD homogeneity test

Usage

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

Arguments

x	Object of class ad_homogeneity_test.
...	Unused.

```
print.ad_mean_test      Print method for AD mean test
```

Description

Print method for AD mean test

Usage

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

Arguments

x	Object of class ad_mean_test.
...	Unused.

```
print.ad_order_test     Print method for AD order test
```

Description

Print method for AD order test

Usage

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

Arguments

x	Object of class ad_order_test.
...	Unused.

```
print.cat_ci            Print method for cat_ci objects
```

Description

Print method for cat_ci objects

Usage

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

Arguments

x	A cat_ci object
...	Additional arguments (ignored)

print.cat_fit	<i>Print method for cat_fit objects</i>
---------------	---

Description

Print method for cat_fit objects

Usage

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

Arguments

x	A cat_fit object
...	Additional arguments (ignored)

print.cat_lrt	<i>Print method for cat_lrt objects</i>
---------------	---

Description

Print method for cat_lrt objects

Usage

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

Arguments

x	A cat_lrt object
...	Additional arguments (ignored)

print.homogeneity_tests_inad	<i>Print method for homogeneity_tests_inad</i>
------------------------------	--

Description

Print method for homogeneity_tests_inad

Usage

```
## S3 method for class 'homogeneity_tests_inad'  
print(x, digits = 4, ...)
```

Arguments

x	Object of class homogeneity_tests_inad
digits	Number of digits for printing
...	Unused

print.inad_ci	<i>Print method for INAD confidence intervals</i>
---------------	---

Description

Print method for INAD confidence intervals

Usage

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

Arguments

x	An object of class inad_ci.
...	Unused.

Value

The input object, invisibly.

print.lrt_homogeneity_inad	<i>Print method for lrt_homogeneity_inad</i>
----------------------------	--

Description

Print method for lrt_homogeneity_inad

Usage

```
## S3 method for class 'lrt_homogeneity_inad'
print(x, digits = 4, ...)
```

Arguments

x	Object of class lrt_homogeneity_inad
digits	Number of digits for printing
...	Unused

run_homogeneity_tests_inad

Run all homogeneity tests for INAD

Description

Convenience function to run all three homogeneity tests at once and return a summary.

Usage

```
run_homogeneity_tests_inad(
  y,
  blocks,
  order = 1,
  thinning = "binom",
  innovation = "pois",
  ...
)
```

Arguments

y	Integer matrix with n_subjects rows and n_time columns.
blocks	Integer vector of length n_subjects specifying group membership.
order	Antedependence order (0, 1, or 2).
thinning	Thinning operator: "binom", "pois", or "nbinom".
innovation	Innovation distribution: "pois", "bell", or "nbinom".
...	Additional arguments passed to fit_inad.

Value

A list with class "homogeneity_tests_inad" containing results for all three tests and a summary table.

Examples

```
## Not run:
data("bolus_inad")
tests <- run_homogeneity_tests_inad(bolus_inad$y, bolus_inad$blocks,
                                   order = 1, thinning = "nbinom",
                                   innovation = "bell")

print(tests)

## End(Not run)
```

run_order_tests_cat	<i>Run all pairwise order tests</i>
---------------------	-------------------------------------

Description

Performs sequential likelihood ratio tests for AD orders 0 vs 1, 1 vs 2, etc.

Usage

```
run_order_tests_cat(
  y,
  max_order = 2,
  blocks = NULL,
  homogeneous = TRUE,
  n_categories = NULL
)
```

Arguments

y	Integer matrix of categorical data (n_subjects x n_time).
max_order	Maximum order to test. Default is 2.
blocks	Optional block membership vector.
homogeneous	Whether to use homogeneous parameters across blocks.
n_categories	Number of categories (inferred if NULL).

Details

This function performs forward selection: starting from order 0, it tests whether increasing the order provides significant improvement. The selected order is the highest order where the test was significant (at $\alpha = 0.05$).

Value

A list containing:

tests	List of lrt_order_cat results for each comparison
table	Summary data frame with all comparisons
fits	List of all fitted models
selected_order	Recommended order based on sequential testing at $\alpha=0.05$

Examples

```
## Not run:
y <- simulate_cat(200, 6, order = 1, n_categories = 2)
result <- run_order_tests_cat(y, max_order = 2)
print(result$table)
cat("Selected order:", result$selected_order, "\n")

## End(Not run)
```

run_stationarity_tests_cat

Run all stationarity-related tests for categorical AD

Description

Performs tests for time-invariance and strict stationarity.

Usage

```
run_stationarity_tests_cat(
  y,
  order = 1,
  blocks = NULL,
  homogeneous = TRUE,
  n_categories = NULL
)
```

Arguments

y	Integer matrix of categorical data (n_subjects x n_time).
order	Antedependence order p. Default is 1.
blocks	Optional block membership vector.
homogeneous	Whether to use homogeneous parameters across blocks.
n_categories	Number of categories (inferred if NULL).

Value

A list containing:

time_invariance	Result of lrt_timeinvariance_cat
stationarity	Result of lrt_stationarity_cat
table	Summary data frame

Examples

```
## Not run:
y <- simulate_cat(200, 6, order = 1, n_categories = 2)
result <- run_stationarity_tests_cat(y, order = 1)
print(result$table)

## End(Not run)
```

```
run_stationarity_tests_inad
```

Run All Stationarity Tests

Description

Run All Stationarity Tests

Usage

```
run_stationarity_tests_inad(
  y,
  order = 1,
  thinning = "binom",
  innovation = "pois",
  blocks = NULL,
  verbose = TRUE,
  ...
)
```

Arguments

y	Integer matrix.
order	Model order (1 or 2).
thinning	Thinning operator.
innovation	Innovation distribution.
blocks	Optional block assignments.
verbose	Logical.
...	Additional arguments.

Value

A list with class "stationarity_tests_inad".

```
simulate_ad
```

Simulate Gaussian antedependence series

Description

Generate longitudinal continuous data from a Gaussian antedependence (AD) model of order 0, 1, or 2 using a conditional regression on predecessors.

Usage

```
simulate_ad(
  n_subjects,
  n_time,
  order = 1L,
  mu = NULL,
  phi = NULL,
  sigma = NULL,
  blocks = NULL,
  tau = 0,
  seed = NULL
)
```

Arguments

n_subjects	number of subjects
n_time	number of time points
order	antependence order, 0, 1 or 2
mu	mean parameter; NULL, scalar, or length n_time
phi	dependence parameter; ignored when order = 0. For order = 1, NULL, scalar, or length n_time. For order = 2, NULL or a 2 by n_time matrix.
sigma	innovation standard deviation; NULL, scalar, or length n_time
blocks	integer vector of length n_subjects indicating block membership for each subject; if NULL, no block effect is applied
tau	group effect vector indexed by block; tau[1] is forced to 0. If scalar x, it is expanded to c(0, x, ..., x) with length equal to the number of blocks
seed	optional random seed for reproducibility

Details

For order = 0, each time point is generated independently as $Y[, t] = \mu[t] + \tau[\text{block}] + \text{eps}$, with $\text{eps} \sim N(0, \sigma[t]^2)$.

For order = 1, for $t \geq 2$: $Y[, t] = m_t + \phi[t] * (Y[, t - 1] - m_{\{t-1\}}) + \text{eps}_t$, where $m_t = \mu[t] + \tau[\text{block}]$ and $\text{eps}_t \sim N(0, \sigma[t]^2)$.

For order = 2, for $t \geq 3$: $Y[, t] = m_t + \phi[1, t] * (Y[, t - 1] - m_{\{t-1\}}) + \phi[2, t] * (Y[, t - 2] - m_{\{t-2\}}) + \text{eps}_t$.

If blocks is provided, each subject s belongs to a block and receives a mean shift $\tau[\text{blocks}[s]]$. tau[1] is forced to 0.

Value

numeric matrix with dimension n_subjects by n_time

simulate_cat

*Simulate data from a categorical antedependence model***Description**

Generates simulated longitudinal categorical data from an AD(p) model with specified transition probabilities.

Usage

```
simulate_cat(
  n_subjects,
  n_time,
  order = 1,
  n_categories = 2,
  marginal = NULL,
  transition = NULL,
  blocks = NULL,
  homogeneous = TRUE,
  seed = NULL
)
```

Arguments

n_subjects	Number of subjects to simulate.
n_time	Number of time points.
order	Antedependence order p. Must be 0, 1, or 2. Default is 1.
n_categories	Number of categories c. Default is 2 (binary).
marginal	List of marginal/joint probabilities for initial time points. If NULL, uniform probabilities are used. See Details for structure.
transition	List of transition probability arrays for time points $k = p+1$ to n . If NULL, uniform transitions are used. See Details.
blocks	Optional integer vector of length n_subjects specifying group membership. Used with homogeneous = FALSE.
homogeneous	Logical. If TRUE (default), same parameters for all subjects. If FALSE, marginal and transition should be lists indexed by block.
seed	Optional random seed for reproducibility.

Details

Data are simulated sequentially:

1. For $k = 1$: Draw $Y(1)$ from marginal distribution
2. For $k = 2$ to p : Draw $Y(k)$ conditional on $Y(1), \dots, Y(k-1)$
3. For $k = p+1$ to n : Draw $Y(k)$ conditional on $Y(k-p), \dots, Y(k-1)$

Parameter structure for marginal:

- Order 0: List with elements t_1, t_2, \dots, t_n , each a vector of length c summing to 1

- Order 1: List with element t1 (vector of length c)
- Order 2: List with t1 (vector), t2_given_1to1 (c x c matrix where rows represent conditioning values and columns represent outcomes)

Parameter structure for transition:

- Order 0: Not used (NULL)
- Order 1: List with elements t2, t3, ..., tn, each c x c matrix where rows are previous values and columns are current values (rows sum to 1)
- Order 2: List with elements t3, t4, ..., tn, each c x c x c array where first two indices are conditioning values and third is outcome

Value

Integer matrix with n_subjects rows and n_time columns, where each entry is a category code from 1 to c.

References

Xie, Y. and Zimmerman, D. L. (2013). Antedependence models for nonstationary categorical longitudinal data with ignorable missingness: likelihood-based inference. *Statistics in Medicine*, 32, 3274-3289.

simulate_gau	<i>Simulate Gaussian AD data (alias of simulate_ad)</i>
--------------	---

Description

Convenience alias for [simulate_ad](#).

Usage

```
simulate_gau(...)
```

Arguments

... Passed through to [simulate_ad](#).

Value

See [simulate_ad](#).

See Also

[simulate_ad](#), [simulate_cat](#), [simulate_inad](#)

simulate_inad

*Simulate integer valued antedependence series***Description**

Generate longitudinal count data from an INAD model using a thinning operator and an innovation distribution.

Usage

```
simulate_inad(
  n_subjects,
  n_time,
  order = 1L,
  thinning = c("binom", "pois", "nbinom"),
  innovation = c("pois", "bell", "nbinom"),
  alpha = NULL,
  theta = NULL,
  nb_inno_size = NULL,
  blocks = NULL,
  tau = 0,
  seed = NULL
)
```

Arguments

n_subjects	number of subjects
n_time	number of time points
order	antedependence order, 0, 1 or 2
thinning	thinning operator, one of "binom", "pois", "nbinom"
innovation	innovation distribution, one of "pois", "bell", "nbinom"
alpha	thinning parameter or vector or matrix; if NULL, defaults are used depending on the order
theta	innovation mean parameter or vector; if NULL, defaults are used depending on the innovation type. For negative binomial innovations, theta represents the mean of the innovation distribution.
nb_inno_size	size (dispersion) parameter for negative binomial innovations when innovation = "nbinom"; must be positive. If NULL, defaults to 1. Larger values correspond to less overdispersion (approaching Poisson as size -> Inf).
blocks	integer vector of length n_subjects indicating block membership for each subject; if NULL, no block effect is applied
tau	group effect vector indexed by block; tau[1] is forced to 0. If scalar x, it is expanded to c(0, x, ..., x) with length equal to the number of blocks
seed	optional random seed for reproducibility

Details

Time 1 observations are generated from the innovation distribution alone. For times 2 to `n_time`, counts are generated as thinning of previous counts plus independent innovations. When `order = 0`, all time points are generated from the innovation distribution and the thinning operator and `alpha` are ignored.

If `blocks` is provided, innovations include a block effect and use the parameter $\theta[t] + \tau[\text{blocks}[i]]$ for subject `i` at time `t`.

Value

integer matrix of counts with dimension `n_subjects` by `n_time`

<code>summary.cat_ci</code>	<i>Summary method for cat_ci objects</i>
-----------------------------	--

Description

Summary method for `cat_ci` objects

Usage

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

Arguments

<code>object</code>	A <code>cat_ci</code> object
<code>...</code>	Additional arguments (ignored)

Value

A data frame summarizing all CIs

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