

Package ‘dovar’

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Title Dynamic Copula VAR Models for Time-Varying Dependence

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Description Fits Bayesian copula vector autoregressive models for bivariate time series with dynamic, regime-switching, and constant dependence structures. The package includes simulation, data preparation, estimation with 'Stan' through 'rstan' or 'cmdstanr', posterior summaries, diagnostics, trajectory extraction, fitted and predictive summaries, and approximate leave-one-out cross-validation model comparison for supported fits. For Bayesian computation and model comparison, see Carpenter et al. (2017) [<doi:10.18637/jss.v076.i01>](https://doi.org/10.18637/jss.v076.i01) and Vehtari, Gelman and Gabry (2017) [<doi:10.1007/s11222-016-9696-4>](https://doi.org/10.1007/s11222-016-9696-4).

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aggregate_metrics *Aggregate metrics across simulation replications*

Description

Aggregate metrics across simulation replications

Usage

aggregate_metrics(metrics_list)

Arguments

metrics_list A list of metric lists (one per replication), each containing a \$rho element as returned by `compute_rho_metrics()`.

Value

A named list with:

- rho: data frame of aggregated rho metrics (mean, SD, quantiles) for every field in the per-replication rho metric list
- n_reps: number of replications

```
as.data.frame.dcvar_model_fit
```

Convert a dcvar fit summary to a data frame

Description

Returns the full parameter summary as a tidy data frame with correct 2.5%/97.5% quantiles.

Usage

```
## S3 method for class 'dcvar_model_fit'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

x	A fitted model object (dcvar_fit, dcvar_hmm_fit, or dcvar_constant_fit).
row.names	Ignored.
optional	Ignored.
...	Additional arguments (unused).

Value

A data frame with columns variable, mean, sd, q2.5, q97.5, rhat, ess_bulk, ess_tail.

```
compute_param_metrics Compute scalar parameter recovery metrics
```

Description

Compute scalar parameter recovery metrics

Usage

```
compute_param_metrics(true_value, est_mean, est_lower, est_upper)
```

Arguments

true_value	True parameter value.
est_mean	Estimated posterior mean.
est_lower	Lower CI bound (2.5%).
est_upper	Upper CI bound (97.5%).

Value

A named list with bias, relative_bias, covered, interval_width.

compute_rho_metrics *Compute rho trajectory recovery metrics*

Description

Evaluates how well the estimated rho trajectory recovers the true values.

Usage

```
compute_rho_metrics(rho_true, rho_est, rho_lower, rho_upper)
```

Arguments

rho_true	Numeric vector of true rho values (length T-1).
rho_est	Numeric vector of estimated rho (posterior mean).
rho_lower	Numeric vector of lower CI bounds (2.5%).
rho_upper	Numeric vector of upper CI bounds (97.5%).

Value

A named list with:

- bias: mean bias
- relative_bias: mean relative bias (%)
- coverage: proportion of CIs containing true value
- interval_width: mean CI width
- correlation: Pearson correlation between true and estimated
- bias_start, bias_end: bias at first/last time point
- coverage_start, coverage_end: coverage at endpoints

covariate_effects	<i>Extract covariate effect summaries</i>
-------------------	---

Description

Returns posterior summaries for the Fisher-z intercept and covariate effects. The residual random-walk innovation scale σ_{ω} is reported separately by `var_params()` for `drift = TRUE` fits.

Usage

```
covariate_effects(object, ...)

## Default S3 method:
covariate_effects(object, ...)

## S3 method for class 'dcvar_covariate_fit'
covariate_effects(object, probs = c(0.025, 0.5, 0.975), ...)
```

Arguments

object	A <code>dcvar_covariate_fit</code> object.
...	Additional arguments (unused).
probs	Numeric vector of quantile probabilities (default: <code>c(0.025, 0.5, 0.975)</code>).

Value

A data frame with one row per effect and columns `term`, `variable`, `mean`, `sd`, and one column per requested quantile.

dcvar	<i>Fit the DC-VAR model</i>
-------	-----------------------------

Description

Fits a Dynamic Copula VAR(1) model with time-varying correlation following a random walk on the Fisher-z scale. Uses non-centered parameterisation for efficient HMC sampling.

Usage

```
dcvar(
  data,
  vars,
  time_var = "time",
  standardize = TRUE,
  margins = "normal",
```

```

    skew_direction = NULL,
    allow_gaps = FALSE,
    prior_mu_sd = 2,
    prior_phi_sd = 0.5,
    prior_sigma_eps_rate = 1,
    prior_sigma_omega_rate = 0.1,
    prior_rho_init_sd = 1,
    chains = 4,
    iter_warmup = 2000,
    iter_sampling = 4000,
    adapt_delta = 0.99,
    max_treedepth = 12,
    seed = NULL,
    cores = NULL,
    refresh = 500,
    init = NULL,
    stan_file = NULL,
    backend = getOption("dcvar.backend", "auto"),
    ...
)

```

Arguments

<code>data</code>	A data frame with time series observations.
<code>vars</code>	Character vector of two variable names to model.
<code>time_var</code>	Name of the time column (default: "time").
<code>standardize</code>	Logical; whether to z-score variables (default: TRUE).
<code>margins</code>	Character string specifying the marginal distribution. One of "normal" (default), "exponential", "skew_normal", or "gamma".
<code>skew_direction</code>	Integer vector of length D indicating skew direction for asymmetric margins. Each element must be 1 (right-skewed) or -1 (left-skewed). Required for "exponential" and "gamma" margins.
<code>allow_gaps</code>	Logical; if FALSE (default), interior missing values cause an error because they break VAR(1) time series adjacency. Set to TRUE to allow fitting with a warning instead.
<code>prior_mu_sd</code>	Prior SD for intercepts: $\mu \sim \text{normal}(\theta, \text{prior_mu_sd})$.
<code>prior_phi_sd</code>	Prior SD for VAR coefficients: $\Phi \sim \text{normal}(\theta, \text{prior_phi_sd})$.
<code>prior_sigma_eps_rate</code>	Prior mean for innovation SDs (see prepare_dcvar_data()).
<code>prior_sigma_omega_rate</code>	Prior mean for rho process SD (see prepare_dcvar_data()).
<code>prior_rho_init_sd</code>	Prior SD for initial rho on Fisher-z scale.
<code>chains</code>	Number of MCMC chains (default: 4).
<code>iter_warmup</code>	Warmup iterations per chain (default: 2000).

<code>iter_sampling</code>	Sampling iterations per chain (default: 4000).
<code>adapt_delta</code>	Target acceptance rate (default: 0.99). The DC-VAR model uses a lower default than <code>dcvar_constant()</code> (0.999) because the non-centered parameterisation already handles posterior geometry well.
<code>max_treedepth</code>	Maximum tree depth (default: 12).
<code>seed</code>	Random seed.
<code>cores</code>	Number of parallel chains. NULL uses all available cores.
<code>refresh</code>	How often to print progress (default: 500). Set to 0 for silent operation.
<code>init</code>	Custom init function or NULL for smart defaults.
<code>stan_file</code>	Path to a custom Stan file, or NULL to use the bundled model.
<code>backend</code>	Character: "auto" (default, uses rstan), "rstan", or "cmdstanr". Can also be set globally via <code>options(dcvar.backend = "cmdstanr")</code> .
<code>...</code>	Additional backend-specific sampling arguments.

Value

A `dcvar_fit` object.

See Also

[dcvar_constant\(\)](#) for the time-invariant baseline, [dcvar_hmm\(\)](#) for the regime-switching model, [dcvar_compare\(\)](#) for LOO-CV model comparison, [rho_trajectory\(\)](#) and [plot_rho\(\)](#) for inspecting results.

Examples

```
sim <- simulate_dcvar(
  n_time = 12,
  rho_trajectory = rho_decreasing(12),
  seed = 1
)
fit <- dcvar(
  sim$Y_df,
  vars = c("y1", "y2"),
  chains = 1,
  iter_warmup = 10,
  iter_sampling = 10,
  refresh = 0,
  seed = 1
)
print(fit)
summary(fit)
plot(fit)
```

`dcvar_compare`*Compare multiple fitted models using LOO-CV*

Description

Convenience wrapper around `loo::loo_compare()` that accepts named dcvar model fits.

Usage

```
dcvar_compare(...)
```

Arguments

... Named fitted model objects (e.g., `dcvar = fit1`, `hmm = fit2`).

Value

A `loo_compare` matrix.

See Also

[loo::loo_compare\(\)](#) for details on the comparison method, [dcvar\(\)](#), [dcvar_hmm\(\)](#), [dcvar_constant\(\)](#) for fitting models.

Examples

```
sim <- simulate_dcvar(  
  n_time = 12,  
  rho_trajectory = rho_decreasing(12),  
  seed = 1  
)  
fit_dcvar <- dcvar(  
  sim$Y_df,  
  vars = c("y1", "y2"),  
  chains = 1,  
  iter_warmup = 10,  
  iter_sampling = 10,  
  refresh = 0,  
  seed = 1  
)  
fit_constant <- dcvar_constant(  
  sim$Y_df,  
  vars = c("y1", "y2"),  
  chains = 1,  
  iter_warmup = 10,  
  iter_sampling = 10,  
  refresh = 0,  
  seed = 1  
)
```

```
dcvar_compare(dcvar = fit_dcvar, constant = fit_constant)
```

dcvar_constant	<i>Fit the constant copula model</i>
----------------	--------------------------------------

Description

Fits a copula VAR(1) model with a single time-invariant correlation parameter. This serves as a baseline for comparison with the DC-VAR and HMM copula models.

Usage

```
dcvar_constant(
  data,
  vars,
  time_var = "time",
  standardize = TRUE,
  margins = "normal",
  copula = "gaussian",
  skew_direction = NULL,
  allow_gaps = FALSE,
  prior_mu_sd = 2,
  prior_phi_sd = 0.5,
  prior_sigma_eps_rate = 1,
  prior_z_rho_sd = 1,
  chains = 4,
  iter_warmup = 2000,
  iter_sampling = 4000,
  adapt_delta = 0.999,
  max_treedepth = 12,
  seed = NULL,
  cores = NULL,
  refresh = 500,
  init = NULL,
  stan_file = NULL,
  backend = getOption("dcvar.backend", "auto"),
  ...
)
```

Arguments

data	A data frame with time series observations.
vars	Character vector of two variable names to model.
time_var	Name of the time column (default: "time").
standardize	Logical; whether to z-score variables (default: TRUE).

margins	Character string specifying the marginal distribution. One of "normal" (default), "exponential", "skew_normal", or "gamma".
copula	Character string specifying the copula family. One of "gaussian" (default) or "clayton". Clayton is currently available only with normal margins.
skew_direction	Integer vector of length D indicating skew direction for asymmetric margins. Each element must be 1 (right-skewed) or -1 (left-skewed). Required for "exponential" and "gamma" margins.
allow_gaps	Logical; if FALSE (default), interior missing values cause an error because they break VAR(1) time series adjacency. Set to TRUE to allow fitting with a warning instead.
prior_mu_sd	Prior SD for intercepts: $\mu \sim \text{normal}(\theta, \text{prior_mu_sd})$.
prior_phi_sd	Prior SD for VAR coefficients: $\Phi \sim \text{normal}(\theta, \text{prior_phi_sd})$.
prior_sigma_eps_rate	Prior mean for innovation SDs (see prepare_dvar_data()).
prior_z_rho_sd	Prior SD for rho on Fisher-z scale (default: 1.0).
chains	Number of MCMC chains (default: 4).
iter_warmup	Warmup iterations per chain (default: 2000).
iter_sampling	Sampling iterations per chain (default: 4000).
adapt_delta	Target acceptance rate (default: 0.999). The constant model uses a higher default than DC-VAR (0.99) because its simpler posterior geometry benefits from tighter step-size adaptation without significant cost, reducing occasional divergences near the rho boundary.
max_treedepth	Maximum tree depth (default: 12).
seed	Random seed.
cores	Number of parallel chains. NULL uses all available cores.
refresh	How often to print progress (default: 500). Set to 0 for silent operation.
init	Custom init function or NULL for smart defaults.
stan_file	Path to a custom Stan file, or NULL to use the bundled model.
backend	Character: "auto" (default, uses rstan), "rstan", or "cmdstanr". Can also be set globally via <code>options(dvar.backend = "cmdstanr")</code> .
...	Additional backend-specific sampling arguments.

Details

`adapt_delta` defaults to 0.999 because the constant-rho model has a simpler correlation structure that benefits from tighter step-size adaptation without significant computational cost, reducing occasional divergences near the rho boundary.

Value

A `dvar_constant_fit` object.

See Also

[dcvar\(\)](#) for the time-varying model, [dcvar_hmm\(\)](#) for the regime-switching model, [dcvar_compare\(\)](#) for LOO-CV model comparison.

Examples

```
sim <- simulate_dcvar(  
  n_time = 12,  
  rho_trajectory = rho_constant(12, rho = 0.5),  
  seed = 1  
)  
fit <- dcvar_constant(  
  sim$Y_df,  
  vars = c("y1", "y2"),  
  chains = 1,  
  iter_warmup = 10,  
  iter_sampling = 10,  
  refresh = 0,  
  seed = 1  
)  
print(fit)
```

dcvar_constant_fit-methods

S3 methods for dcvar_constant_fit objects

Description

S3 methods for dcvar_constant_fit objects

Usage

```
## S3 method for class 'dcvar_constant_fit'  
print(x, ...)  
  
## S3 method for class 'dcvar_constant_fit'  
summary(object, probs = c(0.025, 0.5, 0.975), ...)  
  
## S3 method for class 'dcvar_constant_fit'  
coef(object, ...)  
  
## S3 method for class 'dcvar_constant_fit'  
plot(x, type = c("rho", "phi", "diagnostics", "ppc", "pit"), ...)
```

Arguments

x, object	A dcvar_constant_fit object.
...	Additional arguments (unused).
probs	Numeric vector of quantile probabilities for the rho estimate (default: c(0.025, 0.5, 0.975)).
type	Character; one of "rho", "phi", "diagnostics", "ppc", "pit".

Value

Invisibly returns x.

A dcvar_constant_summary object (a list).

A named list with elements mu, Phi, sigma_eps, and rho.

A ggplot object.

Functions

- `print(dcvar_constant_fit)`: Print a concise overview of the constant copula fit.
- `summary(dcvar_constant_fit)`: Produce a detailed summary including constant rho, VAR parameters, and diagnostics.
- `coef(dcvar_constant_fit)`: Extract posterior means of model coefficients.
- `plot(dcvar_constant_fit)`: Dispatch to a plot type: "rho", "phi", "diagnostics", "ppc", or "pit".

dcvar_covariate	<i>Fit the covariate DC-VAR model</i>
-----------------	---------------------------------------

Description

Fits a Gaussian Dynamic Copula VAR(1) model in which contemporaneous innovation dependence varies on the Fisher-z scale as a function of observed covariates. With `drift = TRUE`, the model adds residual random-walk drift: $zeta_i = \beta_0 + x_{i+1}' \beta + \eta_i$. With `drift = FALSE`, the dependence trajectory is explained entirely by the covariates.

Usage

```
dcvar_covariate(
  data,
  vars,
  covariates,
  time_var = "time",
  standardize = TRUE,
  standardize_covariates = FALSE,
  drift = TRUE,
  zero_init_eta = TRUE,
```

```

allow_gaps = FALSE,
prior_mu_sd = 2,
prior_phi_sd = 0.5,
prior_sigma_eps_rate = 1,
prior_sigma_omega_rate = 0.1,
prior_rho_init_sd = 1,
prior_beta_sd = 1,
chains = 4,
iter_warmup = 2000,
iter_sampling = 4000,
adapt_delta = 0.99,
max_treedepth = 12,
seed = NULL,
cores = NULL,
refresh = 500,
init = NULL,
stan_file = NULL,
backend = getOption("dcvar.backend", "auto"),
...
)

```

Arguments

<code>data</code>	A data frame with time series observations.
<code>vars</code>	Character vector of two variable names to model.
<code>covariates</code>	Character vector of covariate column names.
<code>time_var</code>	Name of the time column (default: "time").
<code>standardize</code>	Logical; whether to z-score variables (default: TRUE).
<code>standardize_covariates</code>	Logical; whether to z-score covariates (default: FALSE).
<code>drift</code>	Logical; if TRUE (default), include residual random-walk drift after the covariate effect. If FALSE, fit the no-drift sensitivity model.
<code>zero_init_eta</code>	Logical; if TRUE (default), fixes $\eta[1] = 0$ in the residual-drift model.
<code>allow_gaps</code>	Logical; if FALSE (default), interior missing values cause an error because they break VAR(1) time series adjacency. Set to TRUE to allow fitting with a warning instead.
<code>prior_mu_sd</code>	Prior SD for intercepts: $\mu \sim \text{normal}(0, \text{prior_mu_sd})$.
<code>prior_phi_sd</code>	Prior SD for VAR coefficients: $\Phi \sim \text{normal}(0, \text{prior_phi_sd})$.
<code>prior_sigma_eps_rate</code>	Prior mean for innovation SDs (see prepare_dcvar_data()).
<code>prior_sigma_omega_rate</code>	Prior mean for rho process SD (see prepare_dcvar_data()).
<code>prior_rho_init_sd</code>	Prior SD for initial rho on Fisher-z scale.
<code>prior_beta_sd</code>	Prior SD for covariate effects.

chains	Number of MCMC chains (default: 4).
iter_warmup	Warmup iterations per chain (default: 2000).
iter_sampling	Sampling iterations per chain (default: 4000).
adapt_delta	Target acceptance rate (default: 0.99). The DC-VAR model uses a lower default than <code>dcvar_constant()</code> (0.999) because the non-centered parameterisation already handles posterior geometry well.
max_treedepth	Maximum tree depth (default: 12).
seed	Random seed.
cores	Number of parallel chains. NULL uses all available cores.
refresh	How often to print progress (default: 500). Set to 0 for silent operation.
init	Custom init function or NULL for smart defaults.
stan_file	Path to a custom Stan file, or NULL to use the bundled model.
backend	Character: "auto" (default, uses rstan), "rstan", or "cmdstanr". Can also be set globally via <code>options(dcvar.backend = "cmdstanr")</code> .
...	Additional backend-specific sampling arguments.

Value

A `dcvar_covariate_fit` object.

See Also

[prepare_dcvar_covariate_data\(\)](#), [covariate_effects\(\)](#), [rho_trajectory\(\)](#), and [dcvar\(\)](#) for the covariate-free random-walk model.

Examples

```
sim <- simulate_dcvar(
  n_time = 12,
  rho_trajectory = rho_step(12),
  seed = 1
)
sim$Y_df$phase <- as.numeric(sim$Y_df$time > 6)
fit <- dcvar_covariate(
  sim$Y_df,
  vars = c("y1", "y2"),
  covariates = "phase",
  chains = 1,
  iter_warmup = 10,
  iter_sampling = 10,
  refresh = 0,
  seed = 1
)
covariate_effects(fit)

fit_nodrift <- dcvar_covariate(
  sim$Y_df,
```

```

vars = c("y1", "y2"),
covariates = "phase",
drift = FALSE,
chains = 1,
iter_warmup = 10,
iter_sampling = 10,
refresh = 0,
seed = 1
)
rho_trajectory(fit_nodrift)

```

dcvar_covariate_fit-methods

S3 methods for covariate DC-VAR fits

Description

S3 methods for covariate DC-VAR fits

Usage

```

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

## S3 method for class 'dcvar_covariate_fit'
summary(object, probs = c(0.025, 0.5, 0.975), ...)

## S3 method for class 'dcvar_covariate_fit'
coef(object, ...)

## S3 method for class 'dcvar_covariate_fit'
plot(x, type = c("rho", "phi", "diagnostics", "ppc", "pit"), ...)

```

Arguments

x, object	A dcvar_covariate_fit object.
...	Additional arguments (unused).
probs	Numeric vector of quantile probabilities (default: c(0.025, 0.5, 0.975)).
type	Character; one of "rho", "phi", "diagnostics", "ppc", or "pit".

Value

Invisibly returns x.

A dcvar_covariate_summary object (a list).

A named list with elements mu, Phi, sigma_eps, beta_0, beta, and, when drift = TRUE, sigma_omega.

A ggplot object.

Functions

- `print(dcvar_covariate_fit)`: Print a concise overview of the covariate DC-VAR fit.
- `summary(dcvar_covariate_fit)`: Produce a detailed summary including rho trajectory, VAR parameters, covariate effects, and diagnostics.
- `coef(dcvar_covariate_fit)`: Extract posterior means of model coefficients.
- `plot(dcvar_covariate_fit)`: Dispatch to a plot type: "rho", "phi", "diagnostics", "ppc", or "pit".

<code>dcvar_diagnostics</code>	<i>Extract MCMC diagnostics</i>
--------------------------------	---------------------------------

Description

Returns a summary of sampling diagnostics including divergences, tree depth warnings, Rhat, and effective sample size. The convergence headline is computed from sampled parameters only and excludes generated quantities and deterministic transformed outputs.

Usage

```
dcvar_diagnostics(object, ...)

## Default S3 method:
dcvar_diagnostics(object, ...)

## S3 method for class 'dcvar_model_fit'
dcvar_diagnostics(object, ...)
```

Arguments

<code>object</code>	A fitted model object.
<code>...</code>	Additional arguments (unused).

Value

A named list with:

- `n_divergent`: total number of divergent transitions
- `n_max_treedepth`: transitions hitting max tree depth
- `max_rhat`: worst (highest) Rhat across sampled parameters
- `min_ess_bulk`: smallest bulk ESS among sampled parameters
- `min_ess_tail`: smallest tail ESS among sampled parameters
- `mean_accept_prob`: mean acceptance probability

dcvar_fit-methods *S3 methods for dcvar_fit objects*

Description

S3 methods for dcvar_fit objects

Usage

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

## S3 method for class 'dcvar_fit'
summary(object, probs = c(0.025, 0.5, 0.975), ...)

## S3 method for class 'dcvar_fit'
coef(object, ...)

## S3 method for class 'dcvar_fit'
plot(x, type = c("rho", "phi", "diagnostics", "ppc", "pit"), ...)
```

Arguments

x, object	A dcvar_fit object.
...	Additional arguments (unused).
probs	Numeric vector of quantile probabilities for the rho trajectory (default: c(0.025, 0.5, 0.975)).
type	Character; one of "rho", "phi", "diagnostics", "ppc", or "pit".

Value

Invisibly returns x.
 A dcvar_summary object (a list).
 A named list with elements mu, Phi, sigma_eps, and sigma_omega.
 A ggplot object.

Functions

- `print(dcvar_fit)`: Print a concise overview of the DC-VAR fit.
- `summary(dcvar_fit)`: Produce a detailed summary including rho trajectory, VAR parameters, and diagnostics.
- `coef(dcvar_fit)`: Extract posterior means of model coefficients.
- `plot(dcvar_fit)`: Dispatch to a plot type: "rho", "phi", "diagnostics", "ppc", or "pit".

dcvar_hmm

Fit the HMM copula model

Description

Fits a Hidden Markov Model copula VAR(1) with K discrete states and state-specific correlations. Uses ordered z_rho constraint to prevent label switching and a sticky Dirichlet prior to encourage state persistence.

Usage

```
dcvar_hmm(
  data,
  vars,
  K = 2,
  time_var = "time",
  standardize = TRUE,
  margins = "normal",
  skew_direction = NULL,
  allow_gaps = FALSE,
  prior_mu_sd = 2,
  prior_phi_sd = 0.5,
  prior_sigma_eps_rate = 1,
  prior_kappa = 10,
  prior_alpha_off = 1,
  prior_z_rho_sd = 1,
  chains = 4,
  iter_warmup = 2000,
  iter_sampling = 4000,
  adapt_delta = 0.99,
  max_treedepth = 12,
  seed = NULL,
  cores = NULL,
  refresh = 500,
  init = NULL,
  stan_file = NULL,
  backend = getOption("dcvar.backend", "auto"),
  ...
)
```

Arguments

data	A data frame with time series observations.
vars	Character vector of two variable names to model.
K	Number of hidden states (default: 2).
time_var	Name of the time column (default: "time").

standardize	Logical; whether to z-score variables (default: TRUE).
margins	Character string specifying the marginal distribution. One of "normal" (default), "exponential", "skew_normal", or "gamma".
skew_direction	Integer vector of length D indicating skew direction for asymmetric margins. Each element must be 1 (right-skewed) or -1 (left-skewed). Required for "exponential" and "gamma" margins.
allow_gaps	Logical; if FALSE (default), interior missing values cause an error because they break VAR(1) time series adjacency. Set to TRUE to allow fitting with a warning instead.
prior_mu_sd	Prior SD for intercepts: $\mu \sim \text{normal}(\theta, \text{prior_mu_sd})$.
prior_phi_sd	Prior SD for VAR coefficients: $\Phi \sim \text{normal}(\theta, \text{prior_phi_sd})$.
prior_sigma_eps_rate	Prior mean for innovation SDs (see prepare_dcvar_data()).
prior_kappa	Sticky Dirichlet self-transition concentration (default: 10).
prior_alpha_off	Sticky Dirichlet off-diagonal concentration (default: 1).
prior_z_rho_sd	Prior SD for state-specific z_rho (default: 1.0).
chains	Number of MCMC chains (default: 4).
iter_warmup	Warmup iterations per chain (default: 2000).
iter_sampling	Sampling iterations per chain (default: 4000).
adapt_delta	Target acceptance rate (default: 0.99). The DC-VAR model uses a lower default than dcvar_constant() (0.999) because the non-centered parameterisation already handles posterior geometry well.
max_treedepth	Maximum tree depth (default: 12).
seed	Random seed.
cores	Number of parallel chains. NULL uses all available cores.
refresh	How often to print progress (default: 500). Set to 0 for silent operation.
init	Custom init function or NULL for smart defaults.
stan_file	Path to a custom Stan file, or NULL to use the bundled model.
backend	Character: "auto" (default, uses rstan), "rstan", or "cmdstanr". Can also be set globally via <code>options(dcvar.backend = "cmdstanr")</code> .
...	Additional backend-specific sampling arguments.

Value

A `dcvar_hmm_fit` object.

See Also

[dcvar\(\)](#) for the smooth time-varying model, [dcvar_constant\(\)](#) for the time-invariant baseline, [hmm_states\(\)](#) for state extraction, [plot_hmm_states\(\)](#) for visualisation, [dcvar_compare\(\)](#) for LOO-CV model comparison.

Examples

```
sim <- simulate_dcvar(  
  n_time = 12,  
  rho_trajectory = rho_step(12),  
  seed = 1  
)  
fit <- dcvar_hmm(  
  sim$Y_df,  
  vars = c("y1", "y2"),  
  K = 2,  
  chains = 1,  
  iter_warmup = 10,  
  iter_sampling = 10,  
  refresh = 0,  
  seed = 1  
)  
print(fit)  
hmm_states(fit)
```

dcvar_hmm_fit-methods *S3 methods for dcvar_hmm_fit objects*

Description

S3 methods for dcvar_hmm_fit objects

Usage

```
## S3 method for class 'dcvar_hmm_fit'  
print(x, ...)  
  
## S3 method for class 'dcvar_hmm_fit'  
summary(object, probs = c(0.025, 0.5, 0.975), ...)  
  
## S3 method for class 'dcvar_hmm_fit'  
coef(object, ...)  
  
## S3 method for class 'dcvar_hmm_fit'  
plot(  
  x,  
  type = c("rho", "states", "transition", "phi", "diagnostics", "ppc", "pit"),  
  ...  
)
```

Arguments

x, object	A <code>dcvar_hmm_fit</code> object.
...	Additional arguments (unused).
probs	Numeric vector of quantile probabilities for the rho trajectory (default: <code>c(0.025, 0.5, 0.975)</code>).
type	Character; one of "rho", "states", "transition", "phi", "diagnostics", "ppc", or "pit".

Value

Invisibly returns x.

A `dcvar_hmm_summary` object (a list).

A named list with elements `mu`, `Phi`, `sigma_eps`, `z_rho`, and `rho_state`.

A `ggplot` object.

Functions

- `print(dcvar_hmm_fit)`: Print a concise overview of the HMM fit.
- `summary(dcvar_hmm_fit)`: Produce a detailed summary including state information, VAR parameters, and diagnostics.
- `coef(dcvar_hmm_fit)`: Extract posterior means of model coefficients including state-specific rho values.
- `plot(dcvar_hmm_fit)`: Dispatch to a plot type: "rho", "states", "transition", "phi", "diagnostics", "ppc", or "pit".

`dcvar_multilevel`
Fit an experimental multilevel copula VAR(1) model

Description

Fits a hierarchical copula VAR(1) model with unit-specific VAR coefficients (random effects) and a global copula correlation. Uses non-centered parameterization for the random Phi coefficients.

Usage

```
dcvar_multilevel(
  data,
  vars,
  id_var = "id",
  time_var = "time",
  center = TRUE,
  margins = "normal",
  skew_direction = NULL,
  prior_phi_bar_sd = 0.5,
```

```

    prior_tau_phi_scale = 0.2,
    prior_sigma_sd = 1,
    prior_rho_sd = 0.5,
    chains = 4,
    iter_warmup = 2000,
    iter_sampling = 4000,
    adapt_delta = 0.9,
    max_treedepth = 14,
    seed = NULL,
    cores = NULL,
    refresh = 500,
    init = NULL,
    stan_file = NULL,
    backend = getOption("dcvar.backend", "auto"),
    ...
)

```

Arguments

<code>data</code>	A data frame in long (panel) format with columns for unit ID, time, and two outcome variables.
<code>vars</code>	Character vector of two variable names to model.
<code>id_var</code>	Name of the unit/person ID column (default: "id").
<code>time_var</code>	Name of the time column (default: "time").
<code>center</code>	Logical; whether to person-mean center the data (default: TRUE). The bundled multilevel Stan model requires <code>center = TRUE</code> ; set <code>center = FALSE</code> only with a custom <code>stan_file</code> that includes intercept terms.
<code>margins</code>	Character string specifying the marginal distribution. One of "normal" (default) or "exponential".
<code>skew_direction</code>	Integer vector of length 2 indicating skew direction for exponential margins. Required when <code>margins = "exponential"</code> .
<code>prior_phi_bar_sd</code>	Prior SD for population-mean VAR coefficients.
<code>prior_tau_phi_scale</code>	Prior scale for half-t(3) on <code>tau_phi</code> .
<code>prior_sigma_sd</code>	Prior SD for half-normal on innovation SDs.
<code>prior_rho_sd</code>	Prior SD for normal on rho.
<code>chains</code>	Number of MCMC chains.
<code>iter_warmup</code>	Warmup iterations per chain.
<code>iter_sampling</code>	Sampling iterations per chain.
<code>adapt_delta</code>	Target acceptance rate.
<code>max_treedepth</code>	Maximum tree depth.
<code>seed</code>	Random seed.
<code>cores</code>	Number of parallel chains.

refresh	How often to print progress.
init	Custom init function or NULL.
stan_file	Custom Stan file path or NULL.
backend	Character: "auto" (default, uses rstan), "rstan", or "cmdstanr". Can also be set globally via <code>options(dcvar.backend = "cmdstanr")</code> .
...	Additional backend-specific sampling arguments.

Details

Experimental extension. This multilevel variant supports `fitted()` and `predict()`. PSIS-LOO is available for exponential-margin multilevel fits. PIT diagnostics are not yet implemented.

`adapt_delta` defaults to 0.90 and `max_treedepth` to 14 because the hierarchical structure with random effects benefits from deeper trees but does not require aggressive step-size adaptation.

Value

A `dcvar_multilevel_fit` object.

Note

This model currently supports normal and exponential margins.

The bundled multilevel Stan program is defined for person-mean centered data and omits intercept terms. With the bundled model, `center = FALSE` is therefore not supported.

See Also

[random_effects\(\)](#) for extracting unit-specific coefficients, [simulate_dcvar_multilevel\(\)](#) for data generation.

dcvar_multilevel_fit-methods

S3 methods for dcvar_multilevel_fit objects

Description

S3 methods for `dcvar_multilevel_fit` objects

Usage

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

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

```
## S3 method for class 'dcvar_multilevel_fit'
```

```
coef(object, ...)

## S3 method for class 'dcvar_multilevel_fit'
plot(x, type = c("random_effects", "diagnostics"), ...)
```

Arguments

x, object	A dcvar_multilevel_fit object.
...	Additional arguments (unused).
type	Character; one of "random_effects", "diagnostics".

Details

Unlike single-level models (where `coef()` returns Φ), the multilevel model returns hierarchical parameters:

`phi_bar` Population-mean VAR coefficients (analogous to Φ in single-level models, vectorised as `phi11`, `phi12`, `phi21`, `phi22`).

`tau_phi` Between-unit SD of VAR coefficients.

`sigma` Innovation SDs.

`rho` Copula correlation (constant across units).

Use `random_effects()` to obtain unit-specific VAR coefficients.

Value

Invisibly returns x.

A `dcvar_multilevel_summary` object (a list).

A named list of posterior means.

A `ggplot` object.

Functions

- `print(dcvar_multilevel_fit)`: Print a concise overview.
- `summary(dcvar_multilevel_fit)`: Produce a detailed summary.
- `coef(dcvar_multilevel_fit)`: Extract posterior means of population-level coefficients.
- `plot(dcvar_multilevel_fit)`: Dispatch to a plot type.

dcvar_sem

*Fit an experimental SEM copula VAR(1) model***Description**

Fits a copula VAR(1) model with a fixed measurement model (factor loadings and measurement error SD are not estimated). Latent innovations are treated as parameters, making this model computationally intensive for large T.

Usage

```
dcvar_sem(
  data,
  indicators,
  J = NULL,
  lambda = NULL,
  sigma_e = NULL,
  margins = "normal",
  skew_direction = NULL,
  time_var = "time",
  method = c("indicator", "naive"),
  prior_mu_sd = 0.25,
  prior_phi_sd = 0.5,
  prior_sigma_sd = 0.5,
  prior_rho_sd = 0.75,
  chains = 4,
  iter_warmup = 2000,
  iter_sampling = 4000,
  adapt_delta = 0.95,
  max_treedepth = 13,
  seed = NULL,
  cores = NULL,
  refresh = 500,
  init = NULL,
  stan_file = NULL,
  backend = getOption("dcvar.backend", "auto"),
  ...
)
```

Arguments

data	A data frame with time series of indicator variables.
indicators	A list of two character vectors, each naming J indicator columns per latent variable. For example: <code>list(PA = c("y1_1", "y1_2", "y1_3"), NA_ = c("y2_1", "y2_2", "y2_3"))</code> .
J	Number of indicators per latent variable. If <code>method = "naive"</code> and J is NULL, it is inferred from indicators.

lambda	Numeric vector of length J with fixed factor loadings. Required when method = "indicator".
sigma_e	Fixed measurement error SD (scalar). Required when method = "indicator".
margins	Character string specifying the latent innovation margin. One of "normal" (default) or "exponential".
skew_direction	Integer vector of length 2 indicating skew direction for exponential margins. Each element must be 1 (right-skewed) or -1 (left-skewed). Required when margins = "exponential".
time_var	Name of the time column (default: "time").
method	Character string: "indicator" (default) fits the fixed measurement model; "naive" averages indicators within each latent block and fits the observed score VAR.
prior_mu_sd	Prior SD for intercepts: $\mu \sim \text{normal}(\theta, \text{prior_mu_sd})$.
prior_phi_sd	Prior SD for VAR coefficients: $\phi \sim \text{normal}(\theta, \text{prior_phi_sd})$.
prior_sigma_sd	Prior SD for the lognormal prior on the latent innovation scale parameter. For normal margins this is applied to sigma; for exponential margins it is applied to sigma_exp.
prior_rho_sd	Prior SD for rho_raw: $\rho_{\text{raw}} \sim \text{normal}(\theta, \text{prior_rho_sd})$, with $\rho = 0.97 * \tanh(\rho_{\text{raw}})$.
chains	Number of MCMC chains.
iter_warmup	Warmup iterations per chain.
iter_sampling	Sampling iterations per chain.
adapt_delta	Target acceptance rate.
max_treedepth	Maximum tree depth.
seed	Random seed.
cores	Number of parallel chains.
refresh	How often to print progress.
init	Custom init function or NULL.
stan_file	Custom Stan file path or NULL.
backend	Character: "auto" (default, uses rstan), "rstan", or "cmdstanr". Can also be set globally via options(dcvar.backend = "cmdstanr").
...	Additional backend-specific sampling arguments.

Details

Experimental extension. This SEM variant supports fitted() and predict(). PSIS-LOO is available for naive score fits. PIT diagnostics are not yet implemented.

Boundary constraints. The SEM model constrains each VAR coefficient (Phi) to the interval $[-0.99, 0.99]$, unlike other dcvar models where Phi is unconstrained. Very strong autoregressive or cross-lag dynamics near ± 1 cannot be captured by this variant.

The copula correlation ρ is constrained to $(-0.97, 0.97)$ via $\rho = 0.97 * \tanh(\rho_{\text{raw}})$ to avoid boundary singularity in the Gaussian copula density. Extremely high correlations near ± 1 are truncated.

Margins. The SEM model currently supports normal and exponential latent innovation margins. Exponential margins use the same shifted-exponential parameterization as the single-level models and therefore require `skew_direction`. Other non-normal margins are not yet available.

Post-estimation. `fitted()` and `predict()` are available for both the latent-state scale (`type = "link"`) and the observed-indicator scale (`type = "response"`). Use `latent_states()` when you specifically need the full posterior summaries of the latent trajectories.

Value

A `dcvar_sem_fit` object.

Note

This model currently supports normal and exponential latent margins. For skew-normal or gamma margins, use `dcvar()`, `dcvar_constant()`, or `dcvar_hmm()`.

See Also

`latent_states()` for extracting estimated latent states, `simulate_dcvar_sem()` for data generation.

dcvar_sem_fit-methods *S3 methods for dcvar_sem_fit objects*

Description

S3 methods for `dcvar_sem_fit` objects

Usage

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

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

## S3 method for class 'dcvar_sem_fit'
coef(object, ...)

## S3 method for class 'dcvar_sem_fit'
plot(x, type = c("latent_states", "rho", "diagnostics"), ...)
```

Arguments

<code>x</code> , object	A <code>dcvar_sem_fit</code> object.
<code>...</code>	Additional arguments (unused).
<code>type</code>	Character; one of "latent_states", "rho", "diagnostics".

Value

Invisibly returns x.

A `dcvar_sem_summary` object (a list).

A named list of posterior means.

A `ggplot` object.

Functions

- `print(dcvar_sem_fit)`: Print a concise overview.
- `summary(dcvar_sem_fit)`: Produce a detailed summary.
- `coef(dcvar_sem_fit)`: Extract posterior means of latent VAR coefficients.
- `plot(dcvar_sem_fit)`: Dispatch to a plot type.

<code>dcvar_stan_path</code>	<i>Get path to bundled Stan model file</i>
------------------------------	--

Description

Returns the file path to a Stan model file included with the package.

Usage

```
dcvar_stan_path(
  model = c("dcvar", "dcvar_covariate", "dcvar_covariate_nodrift", "hmm", "constant",
            "multilevel", "sem", "sem_naive"),
  margins = "normal",
  copula = "gaussian"
)
```

Arguments

<code>model</code>	Character string: "dcvar", "dcvar_covariate", "dcvar_covariate_nodrift", "hmm", "constant", "multilevel", "sem", or "sem_naive".
<code>margins</code>	Character string: margin type ("normal", "exponential", "skew_normal", "gamma"). Default: "normal".
<code>copula</code>	Character string: copula family ("gaussian" or "clayton"). Default: "gaussian".

Value

File path to the Stan model file.

Examples

```
dcvar_stan_path("dcvar")
dcvar_stan_path("constant", margins = "exponential")
```

dependence_summary *Extract a unified dependence summary*

Description

Returns posterior summaries for Kendall's tau, using the fitted copula family to transform the model-specific dependence parameter. For Gaussian copulas, $\tau = 2 / \pi * \arcsin(\rho)$. For Clayton copulas, $\tau = \theta / (\theta + 2)$.

Usage

```
dependence_summary(object, ...)  
  
## Default S3 method:  
dependence_summary(object, ...)  
  
## S3 method for class 'dcvar_fit'  
dependence_summary(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)  
  
## S3 method for class 'dcvar_covariate_fit'  
dependence_summary(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)  
  
## S3 method for class 'dcvar_hmm_fit'  
dependence_summary(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)  
  
## S3 method for class 'dcvar_constant_fit'  
dependence_summary(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)  
  
## S3 method for class 'dcvar_multilevel_fit'  
dependence_summary(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)  
  
## S3 method for class 'dcvar_sem_fit'  
dependence_summary(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)
```

Arguments

object	A fitted model object.
...	Additional arguments (unused).
probs	Numeric vector of quantile probabilities.

Value

A data frame with columns time, mean, sd, and one column per requested quantile.

draws	<i>Extract posterior draws</i>
-------	--------------------------------

Description

Extract posterior draws from a fitted model.

Usage

```
draws(object, ...)
```

```
## Default S3 method:
draws(object, ...)
```

```
## S3 method for class 'dcvar_model_fit'
draws(object, variable = NULL, format = "draws_array", ...)
```

Arguments

object	A fitted model object.
...	Additional arguments (unused).
variable	Character vector of parameter names. NULL returns all.
format	Draw format: "draws_array", "draws_matrix", or "draws_df" (default: "draws_array").

Value

A posterior draws object.

fitted.dcvar_model_fit	<i>Fitted values from a copula VAR model</i>
------------------------	--

Description

Returns the one-step-ahead fitted values (posterior mean of $y_{\hat{t}}$) from the VAR(1) component:
 $y_{\hat{t}} = \mu + \Phi * (y_{[t-1]} - \mu)$.

Usage

```
## S3 method for class 'dcvar_model_fit'
fitted(object, type = c("link", "response"), ...)
```

```
## S3 method for class 'dcvar_multilevel_fit'
fitted(object, type = c("link", "response"), ...)
```

```
## S3 method for class 'dcvar_sem_fit'
fitted(object, type = c("link", "response"), ...)
```

Arguments

object A fitted model object.

type Character; "link" (default) returns values on the model's internal scale (standardized if applicable), "response" back-transforms to the original data scale.

... Additional arguments (unused).

Details

If the model was fit with `standardize = TRUE` (the default), fitted values are on the standardized (z-scored) scale by default. Use `type = "response"` to back-transform to the original data scale.

`fitted()` and `predict()` are implemented for the public fit classes. For multilevel fits, the methods return unit-specific trajectories. For SEM fits, `type = "link"` returns latent-state summaries and `type = "response"` returns observed indicator-scale summaries.

Value

A data frame of posterior-mean fitted values. Single-level fits return columns `time` plus one column per modeled variable. Multilevel fits additionally include `unit`. SEM fits return either latent-state columns (`type = "link"`) or observed-indicator columns (`type = "response"`).

hmm_states	<i>Extract HMM state information</i>
------------	--------------------------------------

Description

Returns state posteriors, Viterbi path, state-specific rho values, and the transition matrix from an HMM copula fit.

Usage

```
hmm_states(object, ...)

## Default S3 method:
hmm_states(object, ...)

## S3 method for class 'dcvar_hmm_fit'
hmm_states(object, ...)
```

Arguments

object A `dcvar_hmm_fit` object.

... Additional arguments (unused).

Value

A named list with:

- `gamma`: $T_{\text{eff}} \times K$ matrix of posterior state probabilities
- `viterbi`: integer vector of MAP state sequence
- `rho_state`: list with mean, lower, upper for each state
- `A`: $K \times K$ posterior mean transition matrix
- `rho_hmm`: posterior-averaged rho trajectory

interpret_rho_trajectory

Interpret a rho trajectory in clinical terms

Description

Generates a human-readable interpretation of the estimated rho trajectory, describing the overall trend, magnitude of change, and key features.

Usage

```
interpret_rho_trajectory(
  object,
  threshold = 0.1,
  strength_breaks = .default_strength_breaks,
  magnitude_breaks = .default_magnitude_breaks,
  fluctuation_threshold = 0.3,
  ...
)
```

Arguments

<code>object</code>	A fitted model object (<code>dcvar_fit</code> , <code>dcvar_hmm_fit</code> , or <code>dcvar_constant_fit</code>).
<code>threshold</code>	Minimum absolute change in posterior-mean rho to be considered "meaningful" (default: 0.1).
<code>strength_breaks</code>	Named numeric vector of thresholds for classifying correlation strength (default: <code>c(strong = 0.7, moderate = 0.4, weak = 0.2)</code>). Values above the highest threshold are "strong", etc.
<code>magnitude_breaks</code>	Named numeric vector of thresholds for classifying the magnitude of trajectory range (default: <code>c(large = 0.5, moderate = 0.3, small = 0.1)</code>).
<code>fluctuation_threshold</code>	Proportion of sign changes in first differences to flag "substantial fluctuation" (default: 0.3).
<code>...</code>	Additional arguments (unused).

Value

A character string with the interpretation (invisibly). The interpretation is also printed to the console.

Examples

```
sim <- simulate_dcvar(
  n_time = 12,
  rho_trajectory = rho_decreasing(12),
  seed = 1
)
fit <- dcvar(
  sim$Y_df,
  vars = c("y1", "y2"),
  chains = 1,
  iter_warmup = 10,
  iter_sampling = 10,
  refresh = 0,
  seed = 1
)
interpret_rho_trajectory(fit)
```

 latent_states

Extract latent states from a SEM fit

Description

Returns posterior summaries for the estimated latent states at each time point.

Usage

```
latent_states(object, ...)

## Default S3 method:
latent_states(object, ...)

## S3 method for class 'dcvar_sem_fit'
latent_states(object, probs = c(0.025, 0.5, 0.975), ...)
```

Arguments

object	A <code>dcvar_sem_fit</code> object.
...	Additional arguments (unused).
probs	Numeric vector of quantile probabilities.

Value

A data frame with columns `time`, `variable`, `mean`, `sd`, and `quantile` columns.

loo.dcvr	<i>Compute LOO-CV for a fitted model</i>
----------	--

Description

Compute LOO-CV for a fitted model

Usage

```
## S3 method for class 'dcvar_fit'  
loo(x, ...)  
  
## S3 method for class 'dcvar_covariate_fit'  
loo(x, ...)  
  
## S3 method for class 'dcvar_hmm_fit'  
loo(x, ...)  
  
## S3 method for class 'dcvar_constant_fit'  
loo(x, ...)  
  
## S3 method for class 'dcvar_multilevel_fit'  
loo(x, ...)  
  
## S3 method for class 'dcvar_sem_fit'  
loo(x, ...)
```

Arguments

x	A fitted model object.
...	Additional arguments passed to <code>loo::loo()</code> .

Details

PSIS-LOO is available for Gaussian and Clayton single-level fits, covariate fits, exponential-margin multilevel fits, and naive SEM score fits. Indicator SEM fits and normal-margin multilevel fits are not supported because their stored `log_lik` quantities are not comparable pointwise predictive densities.

Value

A loo object from the loo package.

pit_test	<i>KS test for PIT uniformity</i>
----------	-----------------------------------

Description

Runs a Kolmogorov-Smirnov test per variable to assess whether PIT values are approximately uniform. This is a heuristic check on the plug-in PIT values returned by `pit_values()`, not an exact posterior predictive test.

Usage

```
pit_test(object, ...)

## Default S3 method:
pit_test(object, ...)

## S3 method for class 'dcvar_model_fit'
pit_test(object, ...)
```

Arguments

object	A fitted model object.
...	Additional arguments (unused).

Details

This applies a Kolmogorov-Smirnov test to the approximate PIT values returned by `pit_values()`. The result is a heuristic check and does not account for serial dependence or full posterior uncertainty. PIT tests are currently implemented for single-level fits only.

Value

A data frame with columns `variable`, `ks_statistic`, `p_value`, `n`.

pit_values	<i>Extract PIT values from a fitted model</i>
------------	---

Description

Computes approximate Probability Integral Transform values using posterior mean residuals and posterior mean margin parameters. Large departures from uniformity can indicate model misfit, but these are not exact posterior predictive PIT values.

Usage

```
pit_values(object, ...)  
  
## Default S3 method:  
pit_values(object, ...)  
  
## S3 method for class 'dcvar_model_fit'  
pit_values(object, ...)
```

Arguments

object	A fitted model object.
...	Additional arguments (unused).

Details

PIT values are computed from posterior mean residuals and posterior mean margin parameters. Treat them as a fast plug-in diagnostic rather than an exact posterior predictive transform that integrates over full posterior uncertainty. PIT diagnostics are currently implemented for the three core single-level fit classes only.

Value

A data frame with columns time, variable, pit.

plot_diagnostics	<i>Plot MCMC diagnostics</i>
------------------	------------------------------

Description

Creates a combined panel with trace plots, Rhat, and ESS diagnostics.

Usage

```
plot_diagnostics(object, ...)
```

Arguments

object	A fitted model object.
...	Additional arguments (unused).

Value

A combined ggplot object (via patchwork).

plot_hmm_states *Plot HMM state posteriors*

Description

Plot HMM state posteriors

Usage

```
plot_hmm_states(object, show_viterbi = TRUE, ...)
```

Arguments

object A `dcvar_hmm_fit` object.
 show_viterbi Logical; overlay the Viterbi (MAP) state sequence (default: TRUE).
 ... Additional arguments (unused).

Value

A ggplot object.

plot_latent_states *Plot estimated latent states with credible intervals*

Description

Plot estimated latent states with credible intervals

Usage

```
plot_latent_states(object, true_states = NULL, ...)
```

Arguments

object A `dcvar_sem_fit` object.
 true_states Optional T x 2 matrix of true latent states for overlay.
 ... Additional arguments (unused).

Value

A ggplot object.

plot_phi	<i>Plot VAR(1) coefficient matrix as a heatmap</i>
----------	--

Description

Plot VAR(1) coefficient matrix as a heatmap

Usage

```
plot_phi(object, var_names = NULL, ...)
```

Arguments

object	A fitted model object.
var_names	Character vector of variable names for axis labels.
...	Additional arguments (unused).

Value

A ggplot object.

plot_pit	<i>Plot PIT histograms</i>
----------	----------------------------

Description

Creates faceted histograms of the approximate PIT values returned by `pit_values()`. Under good model fit, these histograms should be roughly uniform, but they remain plug-in diagnostics rather than exact posterior predictive checks.

Usage

```
plot_pit(object, bins = 20, ...)
```

Arguments

object	A fitted model object.
bins	Number of histogram bins (default: 20).
...	Additional arguments (unused).

Details

PIT histograms visualize the approximate plug-in PIT values returned by `pit_values()`. They are currently implemented for the three core single-level fit classes only.

Value

A ggplot object.

plot_ppc	<i>Posterior predictive check for residual correlations</i>
----------	---

Description

Posterior predictive check for residual correlations

Usage

```
plot_ppc(object, n_sample = 100, ...)
```

Arguments

object	A fitted model object.
n_sample	Number of posterior draws to use (default: 100).
...	Additional arguments (unused).

Details

Posterior predictive checks are currently available for normal and exponential margins. Gamma and skew-normal fits store copula-level replicated z-scores in `eps_rep`, so their replicated draws are not on the same residual scale as `eps`.

Value

A ggplot object.

plot_random_effects	<i>Plot random effects (caterpillar plot)</i>
---------------------	---

Description

Displays unit-specific VAR coefficients with credible intervals.

Usage

```
plot_random_effects(object, ...)
```

Arguments

object	A <code>dvar_multilevel_fit</code> object.
...	Additional arguments (unused).

Value

A ggplot object.

plot_rho	<i>Plot the rho trajectory with credible intervals</i>
----------	--

Description

Plot the rho trajectory with credible intervals

Usage

```
plot_rho(
  object,
  show_ci = TRUE,
  ci_level = 0.95,
  inner_level = 0.8,
  true_rho = NULL,
  title = NULL,
  ...
)
```

Arguments

object	A dcvvar_fit or dcvvar_hmm_fit object.
show_ci	Logical; show credible interval ribbons (default: TRUE).
ci_level	Credible interval level for the outer ribbon (default: 0.95).
inner_level	Credible interval level for the inner ribbon (default: 0.80). Set to NULL to disable the inner ribbon.
true_rho	Optional numeric vector of true rho values for overlay (useful for simulation studies).
title	Plot title.
...	Additional arguments (unused).

Value

A ggplot object.

plot_trajectories *Plot and compare multiple rho trajectory shapes*

Description

Visualises several named trajectory scenarios side by side for comparison.

Usage

```
plot_trajectories(
  n_time,
  scenarios = c("constant", "decreasing", "increasing", "random_walk", "single_middle",
    "large_change", "double_relapse"),
  ...
)
```

Arguments

n_time	Number of time points.
scenarios	Character vector of scenario names (see rho_scenario()). Default: all built-in scenarios.
...	Additional arguments passed to rho_scenario() .

Value

A ggplot object.

Examples

```
plot_trajectories(100)
plot_trajectories(100, scenarios = c("decreasing", "single_middle"))
```

predict.dcvr_model_fit
One-step-ahead predictions from a copula VAR model

Description

Returns point predictions and **marginal** prediction intervals by combining the VAR(1) fitted values with the estimated innovation SDs. Intervals are computed per-variable using a normal approximation and do not account for the copula dependence structure between variables.

Usage

```
## S3 method for class 'dcvar_model_fit'
predict(object, type = c("link", "response"), ci_level = 0.95, ...)

## S3 method for class 'dcvar_multilevel_fit'
predict(object, type = c("link", "response"), ci_level = 0.95, ...)

## S3 method for class 'dcvar_sem_fit'
predict(object, type = c("link", "response"), ci_level = 0.95, ...)
```

Arguments

object	A fitted model object.
type	Character; "link" (default) returns values on the model's internal scale (standardized if applicable), "response" back-transforms to the original data scale.
ci_level	Prediction interval level (default: 0.95).
...	Additional arguments (unused).

Details

predict() is implemented for the public fit classes. For multilevel fits, the methods return unit-specific trajectories. For SEM fits, type = "link" returns latent states and type = "response" returns observed indicator predictions.

Value

A data frame of marginal prediction intervals at the specified level. Single-level and SEM fits return columns time, variable, mean, lower, upper. Multilevel fits additionally include unit.

prepare_constant_data *Prepare data for the constant copula model*

Description

Transforms a data frame into a list suitable for the constant copula Stan model.

Usage

```
prepare_constant_data(
  data,
  vars,
  time_var = "time",
  standardize = TRUE,
  margins = "normal",
  skew_direction = NULL,
  prior_mu_sd = 2,
```

```

  prior_phi_sd = 0.5,
  prior_sigma_eps_rate = 1,
  prior_z_rho_sd = 1,
  allow_gaps = FALSE
)

```

Arguments

<code>data</code>	A data frame with time series observations.
<code>vars</code>	Character vector of two variable names to model.
<code>time_var</code>	Name of the time column (default: "time").
<code>standardize</code>	Logical; whether to z-score variables (default: TRUE).
<code>margins</code>	Character string specifying the marginal distribution. One of "normal" (default), "exponential", "skew_normal", or "gamma".
<code>skew_direction</code>	Integer vector of length D indicating skew direction for asymmetric margins. Each element must be 1 (right-skewed) or -1 (left-skewed). Required for "exponential" and "gamma" margins.
<code>prior_mu_sd</code>	Prior SD for intercepts: $\mu \sim \text{normal}(\theta, \text{prior_mu_sd})$.
<code>prior_phi_sd</code>	Prior SD for VAR coefficients: $\Phi \sim \text{normal}(\theta, \text{prior_phi_sd})$.
<code>prior_sigma_eps_rate</code>	Prior mean for innovation SDs: $\sigma_{\text{eps}} \sim \text{exponential}(1/\text{prior_sigma_eps_rate})$. Default 1 gives $\text{exponential}(1)$ with prior mean 1.
<code>prior_z_rho_sd</code>	Prior SD for rho on Fisher-z scale (default: 1.0).
<code>allow_gaps</code>	Logical; if FALSE (default), interior missing values cause an error. If TRUE, they produce a warning and are removed.

Value

A named list suitable as Stan data input.

```
prepare_dcvar_covariate_data
```

Prepare data for the covariate DC-VAR model

Description

Transforms a data frame into a list suitable for the Gaussian covariate DC-VAR Stan models. Outcome rows are sorted by `time_var`; rows with missing outcomes are removed with the same adjacency rules used by `prepare_dcvar_data()`, and covariates are filtered in the same order so $X[t + 1,]$ aligns with the outcome occasion of transition $Y[t,] \rightarrow Y[t + 1,]$.

Usage

```
prepare_dcvvar_covariate_data(
  data,
  vars,
  covariates,
  time_var = "time",
  standardize = TRUE,
  standardize_covariates = FALSE,
  allow_gaps = FALSE,
  prior_mu_sd = 2,
  prior_phi_sd = 0.5,
  prior_sigma_eps_rate = 1,
  prior_sigma_omega_rate = 0.1,
  prior_rho_init_sd = 1,
  prior_beta_sd = 1,
  zero_init_eta = TRUE
)
```

Arguments

<code>data</code>	A data frame with time series observations.
<code>vars</code>	Character vector of two variable names to model.
<code>covariates</code>	Character vector of covariate column names.
<code>time_var</code>	Name of the time column (default: "time").
<code>standardize</code>	Logical; whether to z-score variables (default: TRUE).
<code>standardize_covariates</code>	Logical; whether to z-score covariates (default: FALSE). Binary phase indicators should usually be left on their original scale.
<code>allow_gaps</code>	Logical; if FALSE (default), interior missing values cause an error. If TRUE, they produce a warning and are removed.
<code>prior_mu_sd</code>	Prior SD for intercepts: $\mu \sim \text{normal}(\theta, \text{prior_mu_sd})$.
<code>prior_phi_sd</code>	Prior SD for VAR coefficients: $\Phi \sim \text{normal}(\theta, \text{prior_phi_sd})$.
<code>prior_sigma_eps_rate</code>	Prior mean for innovation SDs: $\sigma_{\text{eps}} \sim \text{exponential}(1/\text{prior_sigma_eps_rate})$. Default 1 gives $\text{exponential}(1)$ with prior mean 1.
<code>prior_sigma_omega_rate</code>	Prior mean for rho process SD: $\sigma_{\text{omega}} \sim \text{exponential}(1/\text{prior_sigma_omega_rate})$. Default 0.1 gives $\text{exponential}(10)$ with prior mean 0.1.
<code>prior_rho_init_sd</code>	Prior SD for initial rho on Fisher-z scale.
<code>prior_beta_sd</code>	Prior SD for the covariate effects: $\beta \sim \text{normal}(\theta, \text{prior_beta_sd})$.
<code>zero_init_eta</code>	Logical; if TRUE (default), fixes the first residual drift state at zero ($\eta[1] = \emptyset$). If FALSE, the first transition can receive an immediate residual random-walk shock.

Value

A named list suitable as Stan data input.

prepare_dcvar_data	<i>Prepare data for the DC-VAR model</i>
--------------------	--

Description

Transforms a data frame into a list suitable for the DC-VAR Stan model. Handles sorting, missing values, and optional standardization.

Usage

```
prepare_dcvar_data(
  data,
  vars,
  time_var = "time",
  standardize = TRUE,
  margins = "normal",
  skew_direction = NULL,
  prior_mu_sd = 2,
  prior_phi_sd = 0.5,
  prior_sigma_eps_rate = 1,
  prior_sigma_omega_rate = 0.1,
  prior_rho_init_sd = 1,
  allow_gaps = FALSE
)
```

Arguments

data	A data frame with time series observations.
vars	Character vector of two variable names to model.
time_var	Name of the time column (default: "time").
standardize	Logical; whether to z-score variables (default: TRUE).
margins	Character string specifying the marginal distribution. One of "normal" (default), "exponential", "skew_normal", or "gamma".
skew_direction	Integer vector of length D indicating skew direction for asymmetric margins. Each element must be 1 (right-skewed) or -1 (left-skewed). Required for "exponential" and "gamma" margins.
prior_mu_sd	Prior SD for intercepts: $\mu \sim \text{normal}(\theta, \text{prior_mu_sd})$.
prior_phi_sd	Prior SD for VAR coefficients: $\Phi \sim \text{normal}(\theta, \text{prior_phi_sd})$.
prior_sigma_eps_rate	Prior mean for innovation SDs: $\sigma_{\text{eps}} \sim \text{exponential}(1/\text{prior_sigma_eps_rate})$. Default 1 gives $\text{exponential}(1)$ with prior mean 1.

prior_sigma_omega_rate	Prior mean for rho process SD: $\text{sigma_omega} \sim \text{exponential}(1/\text{prior_sigma_omega_rate})$. Default 0.1 gives $\text{exponential}(10)$ with prior mean 0.1.
prior_rho_init_sd	Prior SD for initial rho on Fisher-z scale.
allow_gaps	Logical; if FALSE (default), interior missing values cause an error. If TRUE, they produce a warning and are removed.

Value

A named list suitable as Stan data input.

Prior naming conventions

Parameters ending in `_sd` specify normal prior standard deviations (location parameters). Parameters ending in `_rate` specify exponential prior means (scale parameters), where the exponential rate is $1/\text{prior_*_rate}$. The constant and HMM models use `prior_z_rho_sd` (normal prior on the Fisher-z scale), while the DC-VAR model uses `prior_sigma_omega_rate` (exponential prior on the random-walk SD) because the two quantities have fundamentally different roles.

prepare_hmm_data	<i>Prepare data for the HMM copula model</i>
------------------	--

Description

Transforms a data frame into a list suitable for the HMM copula Stan model. Includes HMM-specific prior hyperparameters.

Usage

```
prepare_hmm_data(
  data,
  vars,
  K = 2,
  time_var = "time",
  standardize = TRUE,
  margins = "normal",
  skew_direction = NULL,
  prior_mu_sd = 2,
  prior_phi_sd = 0.5,
  prior_sigma_eps_rate = 1,
  prior_kappa = 10,
  prior_alpha_off = 1,
  prior_z_rho_sd = 1,
  allow_gaps = FALSE
)
```

Arguments

data	A data frame with time series observations.
vars	Character vector of two variable names to model.
K	Number of hidden states (default: 2).
time_var	Name of the time column (default: "time").
standardize	Logical; whether to z-score variables (default: TRUE).
margins	Character string specifying the marginal distribution. One of "normal" (default), "exponential", "skew_normal", or "gamma".
skew_direction	Integer vector of length D indicating skew direction for asymmetric margins. Each element must be 1 (right-skewed) or -1 (left-skewed). Required for "exponential" and "gamma" margins.
prior_mu_sd	Prior SD for intercepts: $\mu \sim \text{normal}(0, \text{prior_mu_sd})$.
prior_phi_sd	Prior SD for VAR coefficients: $\Phi \sim \text{normal}(0, \text{prior_phi_sd})$.
prior_sigma_eps_rate	Prior mean for innovation SDs: $\sigma_{\text{eps}} \sim \text{exponential}(1/\text{prior_sigma_eps_rate})$. Default 1 gives $\text{exponential}(1)$ with prior mean 1.
prior_kappa	Sticky Dirichlet self-transition concentration (default: 10).
prior_alpha_off	Sticky Dirichlet off-diagonal concentration (default: 1).
prior_z_rho_sd	Prior SD for state-specific z_rho values (default: 1.0).
allow_gaps	Logical; if FALSE (default), interior missing values cause an error. If TRUE, they produce a warning and are removed.

Value

A named list suitable as Stan data input.

```
prepare_multilevel_data
```

Prepare data for the multilevel copula VAR model

Description

Prepare data for the multilevel copula VAR model

Usage

```
prepare_multilevel_data(
  data,
  vars,
  id_var = "id",
  time_var = "time",
  center = TRUE,
```

```

  prior_phi_bar_sd = 0.5,
  prior_tau_phi_scale = 0.2,
  prior_sigma_sd = 1,
  prior_rho_sd = 0.5,
  margins = "normal",
  skew_direction = NULL
)

```

Arguments

data	A data frame in long (panel) format.
vars	Character vector of two variable names.
id_var	Name of the unit/person ID column.
time_var	Name of the time column.
center	Logical scalar; person-mean center (default: TRUE).
prior_phi_bar_sd	Prior SD for phi_bar.
prior_tau_phi_scale	Prior scale for tau_phi.
prior_sigma_sd	Prior SD for sigma.
prior_rho_sd	Prior SD for rho.
margins	Character string specifying the marginal distribution. One of "normal" (default) or "exponential".
skew_direction	Length-2 integer vector of +1/-1 for exponential margins.

Value

A named list suitable as Stan data input.

prepare_sem_data	<i>Prepare data for the SEM copula VAR model</i>
------------------	--

Description

Transforms a data frame of indicator variables into a list suitable for the SEM copula Stan model. The measurement model parameters (λ , σ_e) are fixed and passed through to Stan.

Usage

```

prepare_sem_data(
  data,
  indicators,
  J = NULL,
  lambda = NULL,

```

```

sigma_e = NULL,
margins = "normal",
skew_direction = NULL,
time_var = "time",
prior_mu_sd = 0.25,
prior_phi_sd = 0.5,
prior_sigma_sd = 0.5,
prior_rho_sd = 0.75,
method = c("indicator", "naive")
)

```

Arguments

data	A data frame with time series of indicator variables.
indicators	A list of two character vectors, each naming J indicator columns per latent variable.
J	Number of indicators per latent variable.
lambda	Numeric vector of length J with fixed factor loadings.
sigma_e	Fixed measurement error SD (scalar).
margins	Character string specifying the latent innovation margin. One of "normal" (default) or "exponential".
skew_direction	Integer vector of length 2 indicating skew direction for exponential margins. Required when margins = "exponential".
time_var	Name of the time column (default: "time").
prior_mu_sd	Prior SD for intercepts.
prior_phi_sd	Prior SD for VAR coefficients.
prior_sigma_sd	Prior SD for the lognormal prior on the latent innovation scale parameter.
prior_rho_sd	Prior SD for rho_raw.
method	Character string: "indicator" for the fixed measurement model or "naive" for row-mean factor scores.

Value

A named list suitable as Stan data input.

```
print.dcvr_constant_summary
```

Print a dcvr_constant_summary object

Description

Print a dcvr_constant_summary object

Usage

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

Arguments

x A `dcvar_constant_summary` object as returned by `summary.dcvr_constant_fit()`.
... Additional arguments (unused).

Value

Invisibly returns x.

```
print.dcvr_covariate_summary  
                          Print a dcvr_covariate_summary object
```

Description

Print a `dcvr_covariate_summary` object

Usage

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

Arguments

x A `dcvr_covariate_summary` object as returned by `summary()`.
... Additional arguments (unused).

Value

Invisibly returns x.

```
print.dcvr_hmm_summary
```

Print a dcvr_hmm_summary object

Description

Print a `dcvr_hmm_summary` object

Usage

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

Arguments

`x` A `dcvr_hmm_summary` object as returned by `summary.dcvr_hmm_fit()`.
`...` Additional arguments (unused).

Value

Invisibly returns `x`.

```
print.dcvr_multilevel_summary
```

Print a dcvr_multilevel_summary object

Description

Print a `dcvr_multilevel_summary` object

Usage

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

Arguments

`x` A `dcvr_multilevel_summary` object.
`...` Additional arguments (unused).

Value

Invisibly returns `x`.

```
print.dcvr_sem_summary
```

Print a dcvr_sem_summary object

Description

Print a dcvr_sem_summary object

Usage

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

Arguments

x	A dcvr_sem_summary object.
...	Additional arguments (unused).

Value

Invisibly returns x.

```
print.dcvr_summary
```

Print a dcvr_summary object

Description

Print a dcvr_summary object

Usage

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

Arguments

x	A dcvr_summary object as returned by summary.dcvr_fit() .
...	Additional arguments (unused).

Value

Invisibly returns x.

random_effects	<i>Extract random effects from a multilevel fit</i>
----------------	---

Description

Returns posterior summaries for unit-specific VAR coefficients.

Usage

```
random_effects(object, ...)

## Default S3 method:
random_effects(object, ...)

## S3 method for class 'dcvar_multilevel_fit'
random_effects(object, ...)
```

Arguments

object	A dcvar_multilevel_fit object.
...	Additional arguments (unused).

Value

A data frame with columns unit, parameter, mean, sd, q2.5, q97.5.

rho_constant	<i>Generate a constant rho trajectory</i>
--------------	---

Description

Generate a constant rho trajectory

Usage

```
rho_constant(n_time, rho = 0.5)
```

Arguments

n_time	Number of time points.
rho	Constant correlation value (default: 0.5). Must be in [-1, 1].

Value

Numeric vector of length n_time - 1.

Examples

```
rho_constant(100, rho = 0.5)
```

rho_decreasing	<i>Generate a logistically decreasing rho trajectory</i>
----------------	--

Description

Mimics a therapy effect where coupling decreases from high to low.

Usage

```
rho_decreasing(  
  n_time,  
  rho_start = 0.7,  
  rho_end = 0.3,  
  midpoint = NULL,  
  steepness = 0.05  
)
```

Arguments

n_time	Number of time points.
rho_start	Starting rho value (default: 0.7).
rho_end	Ending rho value (default: 0.3).
midpoint	Time point of inflection (default: n_time/2).
steepness	Controls transition sharpness (default: 0.05).

Value

Numeric vector of length n_time - 1.

Examples

```
rho_decreasing(100)
```

rho_double_step	<i>Generate a double-breakpoint (relapse pattern) rho trajectory</i>
-----------------	--

Description

Three-phase trajectory: level A -> level B -> level C.

Usage

```
rho_double_step(
  n_time,
  rho_levels = c(0.7, 0.3, 0.7),
  breakpoints = c(1/3, 2/3),
  transition_width = 0
)
```

Arguments

n_time	Number of time points.
rho_levels	Numeric vector of three rho levels (default: c(0.7, 0.3, 0.7)).
breakpoints	Numeric vector of two breakpoint positions (default: c(1/3, 2/3)). Interpreted as proportions of n_time - 1 if <= 1.
transition_width	Number of time points for smooth transitions (default: 0).

Value

Numeric vector of length n_time - 1.

Examples

```
rho_double_step(100, rho_levels = c(0.7, 0.3, 0.7))
```

rho_increasing	<i>Generate a logistically increasing rho trajectory</i>
----------------	--

Description

Mimics deterioration where coupling increases from low to high.

Usage

```
rho_increasing(
  n_time,
  rho_start = 0.3,
  rho_end = 0.7,
  midpoint = NULL,
  steepness = 0.05
)
```

Arguments

n_time	Number of time points.
rho_start	Starting rho value (default: 0.3).
rho_end	Ending rho value (default: 0.7).
midpoint	Time point of inflection (default: n_time/2).
steepness	Controls transition sharpness (default: 0.05).

Value

Numeric vector of length n_time - 1.

Examples

```
rho_increasing(100)
```

rho_random_walk	<i>Generate a random walk rho trajectory on the Fisher-z scale</i>
-----------------	--

Description

Stochastic trajectory matching the DC-VAR data-generating process.

Usage

```
rho_random_walk(n_time, z_init = 0.5, sigma_omega = 0.05, seed = NULL)
```

Arguments

n_time	Number of time points.
z_init	Initial value on Fisher-z scale (default: 0.5, corresponding to rho = 0.46).
sigma_omega	Innovation SD for the random walk (default: 0.05).
seed	Random seed for reproducibility.

Value

Numeric vector of length n_time - 1.

Examples

```
rho_random_walk(100, seed = 42)
```

rho_scenario	<i>Get a named trajectory scenario</i>
--------------	--

Description

Convenience function to retrieve a standard scenario by name.

Usage

```
rho_scenario(scenario, n_time, ...)
```

Arguments

scenario	Character string. One of: <ul style="list-style-type: none"> • Smooth: "constant", "decreasing", "increasing", "random_walk" • Step: "single_middle", "large_change", "small_change", "increase", "double_relapse"
n_time	Number of time points.
...	Additional arguments passed to the generator.

Value

Numeric vector of length $n_time - 1$.

Examples

```
rho_scenario("decreasing", n_time = 100)
rho_scenario("double_relapse", n_time = 150)
```

rho_step	<i>Generate a single-breakpoint (step function) rho trajectory</i>
----------	--

Description

Abrupt change from one rho level to another at a specified time.

Usage

```
rho_step(
  n_time,
  rho_before = 0.7,
  rho_after = 0.3,
  breakpoint = 0.5,
  transition_width = 0
)
```

Arguments

n_time	Number of time points.
rho_before	Rho before breakpoint (default: 0.7).
rho_after	Rho after breakpoint (default: 0.3).
breakpoint	Breakpoint location as a proportion of n_time - 1 (if <= 1) or an absolute time index (default: 0.5).
transition_width	Number of time points for smooth transition. 0 = abrupt (default: 0).

Value

Numeric vector of length n_time - 1.

Examples

```
rho_step(100, rho_before = 0.7, rho_after = 0.3)
```

rho_trajectory	<i>Extract the rho trajectory with credible intervals</i>
----------------	---

Description

Returns a data frame with the posterior mean, SD, and quantiles of the time-varying correlation at each time point.

Usage

```
rho_trajectory(object, ...)

## Default S3 method:
rho_trajectory(object, ...)

## S3 method for class 'dcvar_fit'
rho_trajectory(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)

## S3 method for class 'dcvar_covariate_fit'
```

```

rho_trajectory(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)

## S3 method for class 'dcvar_hmm_fit'
rho_trajectory(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)

## S3 method for class 'dcvar_constant_fit'
rho_trajectory(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)

## S3 method for class 'dcvar_multilevel_fit'
rho_trajectory(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)

## S3 method for class 'dcvar_sem_fit'
rho_trajectory(object, probs = c(0.025, 0.1, 0.5, 0.9, 0.975), ...)

```

Arguments

object	A fitted model object (dcvar_fit, dcvar_covariate_fit, dcvar_hmm_fit, or dcvar_constant_fit).
...	Additional arguments (unused).
probs	Numeric vector of quantile probabilities (default: c(0.025, 0.1, 0.5, 0.9, 0.975)).

Value

A data frame with columns time, mean, sd, and one column per quantile (e.g., q2.5, q10, q50, q90, q97.5). For dcvar_constant_fit objects, the constant rho is expanded to all n_time - 1 time points for consistency with the time-varying models.

See Also

[plot_rho\(\)](#) to visualise the trajectory, [interpret_rho_trajectory\(\)](#) for a text-based summary, [var_params\(\)](#) for VAR parameter extraction.

simulate_breakpoint_data

Simulate data with a breakpoint rho trajectory

Description

Convenience wrapper that combines [rho_step\(\)](#) or [rho_double_step\(\)](#) with [simulate_dcvar\(\)](#) for quick breakpoint simulation studies.

Usage

```
simulate_breakpoint_data(
  n_time,
  type = c("single", "double"),
  rho_before = 0.7,
  rho_after = 0.3,
  rho_levels = c(0.7, 0.3, 0.7),
  breakpoint = 0.5,
  breakpoints = c(1/3, 2/3),
  transition_width = 0,
  mu = c(0, 0),
  Phi = matrix(c(0.3, 0.1, 0.1, 0.3), 2, 2),
  sigma_eps = c(1, 1),
  seed = NULL
)
```

Arguments

n_time	Number of time points.
type	Character; one of "single" (single breakpoint) or "double" (double breakpoint / relapse pattern).
rho_before	Rho before breakpoint (default: 0.7).
rho_after	Rho after breakpoint (default: 0.3).
rho_levels	Numeric vector of three rho levels for double breakpoint (default: c(0.7, 0.3, 0.7)). Only used when type = "double".
breakpoint	Breakpoint location as proportion of n_time - 1 (default: 0.5).
breakpoints	Numeric vector of two breakpoints for double type (default: c(1/3, 2/3)).
transition_width	Number of time points for smooth transition (default: 0 = abrupt).
mu	Intercept vector of length 2 (default: c(0, 0)).
Phi	VAR(1) coefficient matrix, 2x2.
sigma_eps	Innovation SDs, length 2 (default: c(1, 1)).
seed	Random seed.

Value

A named list as returned by [simulate_dcvar\(\)](#).

Examples

```
sim <- simulate_breakpoint_data(n_time = 100, type = "single", seed = 42)
plot(sim$true_params$rho, type = "l")
```

simulate_dcvar	<i>Simulate data from a copula VAR(1) model</i>
----------------	---

Description

Generates bivariate time series data with correlated innovations driven by a specified rho trajectory.

Usage

```
simulate_dcvar(
  n_time,
  rho_trajectory,
  mu = c(0, 0),
  Phi = matrix(c(0.3, 0.1, 0.1, 0.3), 2, 2),
  sigma_eps = c(1, 1),
  margins = "normal",
  skew_direction = NULL,
  skew_params = NULL,
  seed = NULL
)
```

Arguments

<code>n_time</code>	Number of time points.
<code>rho_trajectory</code>	Numeric vector of length <code>n_time - 1</code> specifying the correlation at each time step. Use rho_constant() , rho_decreasing() , etc.
<code>mu</code>	Intercept vector of length 2 (default: <code>c(0, 0)</code>).
<code>Phi</code>	VAR(1) coefficient matrix, 2x2 (default: <code>matrix(c(0.3, 0.1, 0.1, 0.3), 2, 2)</code>).
<code>sigma_eps</code>	Innovation standard deviations, length 2 (default: <code>c(1, 1)</code>). Used for normal margins.
<code>margins</code>	Character: "normal" (default), "exponential", "skew_normal", or "gamma".
<code>skew_direction</code>	Length-2 integer vector of +1/-1. Required for "exponential" and "gamma" margins.
<code>skew_params</code>	Named list of margin-specific parameters. For "skew_normal": alpha (length-2 vector of skew-normal shape params). For "gamma": shape (scalar gamma shape parameter).
<code>seed</code>	Random seed for reproducibility.

Value

A named list with:

- `Y`: `n_time` x 2 observation matrix
- `Y_df`: data frame with columns `time`, `y1`, `y2` (ready for [dcvar\(\)](#))
- `true_params`: list of true parameter values

Examples

```
sim <- simulate_dcvar(n_time = 100, rho_trajectory = rho_decreasing(100))
head(sim$Y_df)
plot(sim$true_params$rho, type = "l")
```

```
simulate_dcvar_multilevel
```

Simulate data from a multilevel copula VAR(1) model

Description

Generates panel data with unit-specific VAR coefficients drawn from a population distribution and a global copula correlation. The simulator matches the fitted multilevel model support by leaving unit-level VAR matrices unconstrained; nonstationary draws are possible.

Usage

```
simulate_dcvar_multilevel(
  N = 40,
  n_time = 100,
  phi_bar = c(0.3, 0.1, 0.1, 0.3),
  tau_phi = c(0.1, 0.05, 0.05, 0.1),
  sigma = c(1, 1),
  rho = 0.3,
  burnin = 30,
  center = TRUE,
  seed = NULL
)
```

Arguments

N	Number of units.
n_time	Number of time points per unit.
phi_bar	Population mean for VAR coefficients (length-4 vector: phi11, phi12, phi21, phi22).
tau_phi	Population SD for each VAR coefficient (length-4 vector).
sigma	Innovation SDs (length-2 vector).
rho	Global copula correlation.
burnin	Number of burn-in observations to discard (default: 30).
center	Logical; person-mean center the data (default: TRUE).
seed	Random seed for reproducibility.

Value

A named list with:

- data: panel data frame with columns id, time, y1, y2
- true_params: list of true parameter values
- person_means: N x 2 matrix of person means (before centering)

simulate_dcvar_sem *Simulate data from a SEM copula VAR(1) model*

Description

Generates indicator-level time series data from a latent VAR(1) process with Gaussian copula dependence and a fixed measurement model.

Usage

```
simulate_dcvar_sem(
  n_time = 200,
  J = 3,
  lambda = rep(sqrt(0.8), 3),
  sigma_e = sqrt(0.2),
  Phi = matrix(c(0.5, 0.15, 0.15, 0.3), 2, 2),
  mu = c(0, 0),
  margins = "normal",
  sigma = c(1, 1),
  sigma_exp = c(1, 1),
  skew_direction = NULL,
  rho = 0.3,
  burnin = 0,
  seed = NULL
)
```

Arguments

n_time	Number of time points.
J	Number of indicators per latent variable.
lambda	Numeric vector of length J with factor loadings.
sigma_e	Measurement error SD (scalar).
Phi	2x2 VAR coefficient matrix.
mu	Length-2 intercept vector.
margins	Character string specifying the latent innovation margin. One of "normal" (default) or "exponential".
sigma	Length-2 latent innovation SD vector for normal margins.

sigma_exp	Length-2 shifted-exponential scale vector for exponential margins.
skew_direction	Integer vector of length 2 indicating skew direction for exponential margins. Required when margins = "exponential".
rho	Copula correlation.
burnin	Retained for backward compatibility but ignored. Default 0 keeps the default simulation path aligned with the fitted SEM model, which conditions on $x_0 = 0$ and treats the first returned state as observed rather than drawn after a burn-in period.
seed	Random seed for reproducibility.

Value

A named list with:

- data: data frame with columns time, y1_1, ..., y1_J, y2_1, ..., y2_J
- true_params: list of true parameter values
- latent_states: n_time x 2 matrix of true latent states
- innovations: n_time x 2 matrix of true innovations

var_params	<i>Extract VAR(1) parameter summaries</i>
------------	---

Description

Returns posterior summaries for the VAR parameters: intercepts (μ), coefficients (Φ), innovation SDs (σ_{eps}), and σ_{omega} (DC-VAR only).

Usage

```
var_params(object, ...)

## Default S3 method:
var_params(object, ...)

## S3 method for class 'dcvar_model_fit'
var_params(object, ...)

## S3 method for class 'dcvar_multilevel_fit'
var_params(object, ...)

## S3 method for class 'dcvar_sem_fit'
var_params(object, ...)
```

Arguments

object	A fitted model object.
...	Additional arguments (unused).

Details

For multilevel models, returns population-level parameters `phi_bar` (mean VAR coefficients), `tau_phi` (between-unit SDs), `sigma` (innovation SDs), and `rho` (copula correlation). These correspond to `Phi`, `sigma_eps`, and `rho` in single-level models.

Value

A named list of data frames with columns `variable`, `mean`, `sd`, `q2.5`, `q97.5`.

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