

Package ‘coresynth’

July 20, 2026

Title Fast and Unified Synthetic Control Methods

Version 0.4.0

Description A unified 'Formula' interface to the Synthetic Control Method (SCM) and related panel-data causal inference estimators: Synthetic Difference-in-Differences (SDID), Generalized Synthetic Control (GSC), Matrix Completion (MC), Time-Aware Synthetic Control (TASC), and Synthetic Interventions (SI), together with an experimental-design variant. Computational bottlenecks (quadratic programming, singular value decomposition, and Kalman filtering) are implemented in 'C++' via 'RcppArmadillo'. Methods are described in Abadie, Diamond and Hainmueller (2010) <[doi:10.1198/jasa.2009.ap08746](https://doi.org/10.1198/jasa.2009.ap08746)>, Arkhangelsky, Athey, Hirshberg, Imbens and Wager (2021) <[doi:10.1257/aer.20190159](https://doi.org/10.1257/aer.20190159)>, Xu (2017) <[doi:10.1017/pan.2016.2](https://doi.org/10.1017/pan.2016.2)>, Athey, Bayati, Doudchenko, Imbens and Khosravi (2021) <[doi:10.1080/01621459.2021.1891924](https://doi.org/10.1080/01621459.2021.1891924)>, and Agarwal, Shah and Shen (2025) <[doi:10.1287/opre.2025.1590](https://doi.org/10.1287/opre.2025.1590)>.

License MIT + file LICENSE

URL <https://github.com/yo5uke/coresynth>, <https://yo5uke.com/coresynth/>

BugReports <https://github.com/yo5uke/coresynth/issues>

Encoding UTF-8

Config/roxygen2/markdown TRUE

RoxygenNote 8.0.0

Depends R (>= 4.1.0)

LinkingTo Rcpp, RcppArmadillo

Imports Rcpp, Formula, ggplot2, broom, jsonlite

Suggests testthat (>= 3.0.0), knitr, rmarkdown

VignetteBuilder knitr

Config/testthat/edition 3

NeedsCompilation yes

Author Yosuke Abe [aut, cre]

Maintainer Yosuke Abe <yosuke.abe0507@gmail.com>

Repository CRAN

Date/Publication 2026-07-20 15:00:02 UTC

Contents

augment_scm	3
conformal_inference	3
export_json	5
glance.coresynth_inference	5
gsc_boot	6
gsc_ife_cpp	7
gsc_inference	8
kalman_smoother_cpp	9
loo_donors	10
mspe_ratio_pval	11
placebo_in_time	12
plot.coresynth	13
plot.scm_design	16
plot.scm_placebo	16
plot_data	18
pred	20
scm_design	21
scm_fit	24
scm_inference	27
scm_inner_weights_cpp	28
scm_placebo_cpp	29
scm_placebo_x_cpp	29
scm_weights_cpp	30
sdid_estimate_cpp	32
sdid_inference	33
sdid_placebo_cpp	34
sdid_time_weights_cpp	35
sdid_unit_weights_cpp	35
si_inference	36
si_pcr_cpp	37
soft_impute_cpp	37
tensor_unfold_cpp	38
tidy.coresynth_inference	39
treated_outcomes	39

Index

42

augment_scm

*Augmented Synthetic Control Method (Ridge ASCM)***Description**

Applies a ridge-regression-based bias correction to a fitted SCM object, following Ben-Michael, Feller & Rothstein (2021, JASA). The corrected estimator is:

Usage

```
augment_scm(fit, lambda_ridge = NULL)
```

Arguments

fit	A coresynth object from <code>scm_fit()</code> with method = "scm".
lambda_ridge	Ridge penalty (non-negative). NULL (default) selects the penalty by leave-one-out cross-validation on the control units.

Details

$$\text{tau_aug} = \text{tau_SCM} + (\text{m_tr_post} - \sum_j W_j * \text{m_j_post})$$

where $\text{m_i_post} = Y_{\text{pre_i}}$ β_{hat} is the ridge outcome model prediction for unit i 's mean post-treatment outcome, and β_{hat} is estimated by ridge regression across control units.

Value

A list with:

- att_aug: Augmented ATT estimate
- delta: Bias correction term ($\text{m_tr_post} - \sum_j W_j \text{m_j_post}$)
- att_scm: Original SCM ATT for comparison
- lambda_ridge: Ridge penalty used
- beta_hat: Ridge regression coefficients (length T_pre)

conformal_inference

*Conformal Inference for Synthetic Control Estimators***Description**

Implements the permutation-based conformal inference procedure of Chernozhukov, Wuthrich & Zhu (2021, JASA). The test inverts a sharp null $H_0 : \tau = \tau_0$ by imputing the treated post-treatment counterfactual as $Y_{1t} - \tau_0$, re-estimating the counterfactual proxy on **all** T periods (imposing the null), and computing a moving-block permutation p-value from the estimated residuals. A confidence interval is obtained by test inversion over a grid of candidate τ_0 .

Usage

```
conformal_inference(
  fit,
  tau0 = 0,
  q = 1,
  alternative = c("two.sided", "greater", "less"),
  ci = TRUE,
  level = 0.95,
  grid = NULL,
  n_grid = 200L,
  grid_mult = 4,
  ...
)
```

Arguments

<code>fit</code>	A coresynth object from <code>scm_fit()</code> .
<code>tau0</code>	Null value of the ATT for the reported p-value (default 0).
<code>q</code>	Exponent of the S_q test statistic ($S_q = (T_{\text{post}}^{-1} \sum u_t ^q)^{1/q}$). Default 1, robust to heavy-tailed data (CWZ 2021). Used only for <code>alternative = "two.sided"</code> ; one-sided tests use the signed mean post-treatment residual.
<code>alternative</code>	"two.sided" (default), "greater", or "less".
<code>ci</code>	Logical; construct a confidence interval by test inversion (default TRUE).
<code>level</code>	Confidence level for the interval (default 0.95).
<code>grid</code>	Optional numeric vector of candidate τ_0 values for test inversion. When NULL (default), a grid of <code>n_grid</code> points is centred on the point estimate with half-width <code>grid_mult</code> times the pre-treatment residual standard deviation.
<code>n_grid</code>	Number of grid points when <code>grid = NULL</code> (default 200).
<code>grid_mult</code>	Half-width multiplier when <code>grid = NULL</code> (default 4).
<code>...</code>	Unused.

Details

Supported for **sharp** (single-cohort) fits with method in `c("scm", "sdid", "gsc", "mc", "si")`. Staggered, multi-arm, and tasc fits are not supported (use `sdid_inference()`, `gsc_inference()`, or `si_inference()` instead).

Value

A list of class `c("conformal_inference", "coresynth_inference")` with `estimate`, `se` (NA; conformal has no SE), `p_value` (at `tau0`), `ci_lower`, `ci_upper`, `method` ("conformal"), `n_controls`, `alternative`, `staggered` (FALSE), plus `tau0`, `q`, `grid`, and `p_grid` (p-values along the grid). Compatible with `tidy()` / `glance()`.

References

Chernozhukov, V., Wuthrich, K., & Zhu, Y. (2021). An Exact and Robust Conformal Inference Method for Counterfactual and Synthetic Controls. *Journal of the American Statistical Association*, 116(536), 1849-1864.

export_json

Export coresynth Results to JSON

Description

Generates a comprehensive, standardized JSON record covering all six estimators. Suitable for reproducibility workflows (Xu & Yang 2026) and downstream tooling. Pass the result of `mspe_ratio_pval()` or `gsc_boot()` via the `inference` argument to include inference results.

Usage

```
export_json(x, file = "coresynth_results.json", inference = NULL, digits = 6L)
```

Arguments

<code>x</code>	A coresynth object from <code>scm_fit()</code> .
<code>file</code>	Output file path. Default <code>"coresynth_results.json"</code> . Pass <code>NULL</code> to skip writing and return the R list invisibly.
<code>inference</code>	Optional list from <code>mspe_ratio_pval()</code> or <code>gsc_boot()</code> . When provided, populates the inference section and updates <code>estimate</code> with <code>p_value</code> , <code>se</code> , <code>ci_lower</code> , <code>ci_upper</code> .
<code>digits</code>	Number of significant digits applied to numeric values (default 6L).

Value

Invisibly, the R list that was (or would be) serialized.

glance.coresynth_inference

Glance at an inference result

Description

One-row summary of a `coresynth_inference` (or `sdid_inference`) object.

Usage

```
## S3 method for class 'coresynth_inference'
glance(x, ...)
```

Arguments

x	An inference object.
...	Unused.

Value

A one-row data.frame with columns method, n_controls, staggered, estimate, std.error, p.value, conf.low, conf.high, alternative, n_boot_valid.

gsc_boot

*Parametric Bootstrap Inference for GSC (Xu 2017 S.3)***Description**

Generates the null distribution of the ATT under H0 (no treatment effect) by parametric resampling from the estimated IFE factor model. Under H0, both the control panel and treated unit are generated from the fitted factor model with homoskedastic noise. When the fit includes covariate adjustment (beta), the covariate contribution is included in the simulated DGP and re-estimated in each bootstrap replicate.

Usage

```
gsc_boot(fit, B = 499L, alpha = 0.05, seed = NULL)
```

Arguments

fit	A coresynth object from <code>scm_fit()</code> with method = "gsc".
B	Bootstrap replications (default 499L).
alpha	Significance level for the confidence interval (default 0.05).
seed	RNG seed for reproducibility (default NULL).

Value

A list with:

- p_value: Two-sided p-value: $\text{mean}(|\text{ATT}^*| \geq |\text{ATT}_{\text{obs}}|)$
- ci_lower: Lower bound of $(1-\alpha)*100\%$ bootstrap CI
- ci_upper: Upper bound of $(1-\alpha)*100\%$ bootstrap CI
- se: Bootstrap standard error
- boot_dist: Numeric vector of length B (bootstrap ATT^* values)
- att_obs: Observed ATT from the original fit

Description

Implements Xu (2017) IFE model with optional covariate adjustment. When X_{co} has $p > 0$ slices, runs an EM loop alternating between: E-step: truncated SVD of $Y_{tilde} = Y_{co} - X_{co} * \beta$. M-step: panel OLS to update β given current factors. When X_{co} has 0 slices (default), falls back to the plain 3-step estimator.

Usage

```
gsc_ife_cpp(Y_co, Y_tr_pre, r, X_co, X_tr_pre, max_iter = 50L, tol = 1e-06)
```

Arguments

<code>Y_co</code>	Control units outcome matrix ($T \times N_{co}$)
<code>Y_tr_pre</code>	Treated units pre-treatment outcomes ($T_{pre} \times N_{tr}$)
<code>r</code>	Number of latent factors (must be $\leq \min(T, N_{co})$)
<code>X_co</code>	Time-varying covariate cube ($T \times N_{co} \times p$). Pass an empty cube (0 slices) for the covariate-free estimator.
<code>X_tr_pre</code>	Time-varying covariate cube for treated units in the pre-treatment window ($T_{pre} \times N_{tr} \times p$). Required for correct Step 2 loading estimation per Xu (2017): λ_{hat} is estimated from $Y_{tr_pre} - X_{tr_pre} * \beta$ (covariate- demeaned). Pass an empty cube (0 slices) to skip demeaning (backward-compatible, but biased when $\beta \neq 0$).
<code>max_iter</code>	Maximum EM iterations (default 50)
<code>tol</code>	Convergence tolerance on relative beta change (default 1e-6)

Value

A list with components:

- `F`: estimated time factors ($T \times r$).
- `L_co`: control-unit factor loadings ($N_{co} \times r$).
- `L_tr`: treated-unit factor loadings ($N_{tr} \times r$).
- `Y_tr_hat`: estimated treated-unit counterfactual outcomes ($T \times N_{tr}$).
- `singular_values`: singular values from the final truncated SVD.
- `beta`: estimated covariate coefficients ($p \times 1$), empty when no covariates are supplied.

gsc_inference

*Non-parametric Inference for GSC (Xu 2017)***Description**

Estimates SE and confidence intervals for the ATT via non-parametric cluster bootstrap or jackknife over control units. Works for both sharp and staggered GSC fits. For staggered fits, bootstrap resamples each cohort's control pool independently, and jackknife uses a per-cohort LOO with delta-method variance aggregation.

Usage

```
gsc_inference(
  fit,
  method = c("bootstrap", "jackknife", "jackknife_global"),
  n_boot = 499L,
  level = 0.95,
  alternative = c("two.sided", "greater", "less"),
  seed = NULL
)
```

Arguments

fit	A coresynth object from <code>scm_fit()</code> with method = "gsc".
method	"bootstrap" (default) or "jackknife".
n_boot	Number of bootstrap replications (default 499L; ignored for jackknife).
level	Confidence level (default 0.95).
alternative	"two.sided" (default), "greater", or "less".
seed	RNG seed for reproducibility (default NULL).

Details

Note: `gsc_boot()` performs a *parametric* bootstrap under H_0 (hypothesis testing). `gsc_inference()` provides *non-parametric* SE and CIs suitable for inference about the ATT magnitude.

Value

A list of class `coresynth_inference`.

kalman_smoother_cpp *Kalman Filter and RTS Smoother (TASC)*

Description

Implements the Kalman filter (forward pass) and Rauch-Tung-Striebel smoother (backward pass) for the state-space model in Rho et al. (2026):

Usage

```
kalman_smoother_cpp(Y, W, A, C, Q, R, z0, P0)
```

Arguments

Y	Observed data matrix (N x T). Use NA for unobserved entries.
W	Observation / loading matrix (N x r)
A	State transition matrix (r x r). Pass diag(r) for random-walk dynamics.
C	State drift vector (r x 1)
Q	State noise covariance (r x r)
R	Observation noise covariance (N x N, diagonal in practice)
z0	Initial state mean (r x 1)
P0	Initial state covariance (r x r)

Details

State: $z(t+1) = A z(t) + C + \eta(t)$, $\eta(t) \sim N(0, Q)$ Observation: $y_t = W z_t + \epsilon_t$, $\epsilon_t \sim N(0, R)$

Observation rows with NA (treated post-intervention) are automatically dropped at each time step so only control-unit rows update the filter.

The P update uses the numerically stable Joseph form: $P(t|t) = (I - K W_{\text{obs}}) P(t|t-1) (I - K W_{\text{obs}})^T + K R_{\text{obs}} K^T$

Value

A list with z_smooth, P_smooth, P_cross, z_pred, z_upd. P_cross is an r x r x (T-1) cube. Slice t (C++ 0-indexed, t=0,...,T-2) stores P(t+1, t | T) (0-indexed), i.e. P(t+2, t+1 | T) in 1-indexed Shumway-Stoffer notation. Formula: $P(t+1|T) * J_t^T$ (eq. 6.68-6.69).

loo_donors

*Leave-One-Out Donor Robustness for SCM***Description**

Iteratively re-estimates the synthetic control excluding one contributing donor at a time, holding the predictor weights V fixed at their baseline values (Abadie, Diamond & Hainmueller 2015, footnote 20). The spread of the leave-one-out ATT estimates shows how much the result hinges on any single donor.

Usage

```
loo_donors(fit, weight_threshold = 1e-06)
```

Arguments

`fit` A sharp coresynth object from `scm_fit()` with method = "scm".

`weight_threshold` Only donors whose baseline weight exceeds this value are dropped (removing a zero-weight donor cannot change the fit). Default 1e-6.

Details

For penalised fits (`lambda_pen` used), the same penalty is re-applied in each leave-one-out QP.

Value

A list with:

- `att_original`: baseline ATT
- `results`: data.frame with one row per excluded donor (`donor`, `weight`, `att_loo`)
- `att_range`: range of the leave-one-out ATTs

See Also

`placebo_in_time()`, `mspe_ratio_pval()`

mspe_ratio_pval *Permutation Inference via MSPE Ratio for SCM*

Description

Computes the Abadie et al. (2010) / Abadie (2021) permutation p-value. For each control unit, a leave-one-out synthetic control is fitted.

Usage

```
mspe_ratio_pval(
  fit,
  mspe_threshold = 0,
  max_iter = 100L,
  tol = 1e-04,
  use_covariates = NULL,
  alternative = c("two.sided", "greater", "less")
)
```

Arguments

fit	A coresynth object from <code>scm_fit()</code> with method = "scm".
mspe_threshold	Minimum pre-treatment MSPE for including a control unit in the two-sided test. Ignored for one-sided tests. Default: 0 (no filtering).
max_iter	Passed to <code>scm_placebo_cpp()</code> (outcomes-only fits) or <code>scm_placebo_x_cpp()</code> (covariate fits). Default 100L.
tol	Passed to <code>scm_placebo_cpp()</code> or <code>scm_placebo_x_cpp()</code> . Default 1e-4.
use_covariates	Controls which predictor specification the placebo refits use. Default NULL (recommended) mirrors the treated fit: if the fit was estimated with a predictors specification, each placebo unit is refit with that same specification (the Abadie et al. 2010 / Synth convention – treated and placebo statistics are computed under one common spec); outcomes-only fits use the fast C++ outcomes-only placebo. Set TRUE/FALSE to force either path; note that FALSE on a covariate fit compares a covariate-based treated statistic against outcomes-only placebo statistics, which breaks the exchangeability logic of the permutation test.
alternative	Direction of the alternative hypothesis: "two.sided" (default) uses the MSPE ratio statistic; "greater" tests whether the treatment increased the outcome; "less" tests whether the treatment decreased the outcome. One-sided tests use the signed ATT as the test statistic.

Details

When `alternative = "two.sided"` (default), the test statistic is the post/pre MSPE ratio, following Abadie et al. (2010). When `alternative = "greater"` or `"less"`, the test statistic is the signed average post-treatment gap (ATT), giving a one-sided permutation test as recommended by Abadie (2021) S.3.5 for improved power when the direction of the treatment effect is known.

The placebo refits mirror the treated fit's outer optimiser and evaluation window: a fit estimated with the multi-start outer search (`v_optim = "multistart"`, or the "auto" default with predictors) or with a `v_window` runs every placebo unit through the same configuration, keeping the permutation statistic exchangeable across units.

Value

An object of class `scm_placebo` (a list) with:

- `p_value`: Permutation p-value between 0 and 1
- `mspe_ratio_treated`: `MSPE_post / MSPE_pre` for the treated unit (two.sided only)
- `mspe_ratios_all`: Named numeric vector (treated first, then controls); two.sided only
- `placebo_effects`: Named `N_co`-vector of placebo ATT estimates
- `treated_effect`: ATT estimate for the treated unit
- `n_placebo_used`: Number of control units used
- `gaps`: `T x N_co` matrix of placebo gap paths (unit minus its synthetic control over all periods), for the Abadie et al. (2010) Figure 4-7 plot
- `treated_gap`: `T`-vector of the treated unit's gap path
- `mspe_pre_treated`, `mspe_pre_placebo`: Pre-treatment MSPEs used for the relative pruning rule in `plot.scm_placebo()`
- `times`, `T_pre`: Time axis metadata for plotting

See Also

`plot.scm_placebo()` for the placebo gap and MSPE ratio plots.

placebo_in_time	<i>In-Time Placebo (Backdating) Test for SCM</i>
-----------------	--

Description

Re-estimates the synthetic control after artificially backdating the treatment to a pre-treatment period, following Abadie, Diamond & Hainmueller (2015) and Abadie & Vives-i-Bastida (2022, principle 7: "out-of-sample validation is key"). Only pre-treatment data enter the exercise, so the placebo gap after `t0_placebo` is uncontaminated by the actual intervention. A credible design shows no sizable divergence at the backdated treatment time.

Usage

```
placebo_in_time(fit, t0_placebo = NULL)
```

Arguments

<code>fit</code>	A sharp <code>coresynth</code> object from <code>scm_fit()</code> with <code>method = "scm"</code> .
<code>t0_placebo</code>	Backdated treatment period as a 1-based position in <code>fit\$times</code> ; must satisfy $2 \leq t0_placebo < T_pre$. Default <code>floor(T_pre / 2)</code> .

Details

The refit uses the outcomes of periods 1..t0_placebo as predictors (the predictors = NULL default), regardless of how the original fit was specified, because user-supplied pred() windows cannot be lagged automatically (ADH 2015 lag their predictors by hand).

Value

A list with:

- t0_placebo: the backdated treatment period used
- times: time values of the pre-treatment window
- unit_weights: placebo donor weights
- Y_treat, Y_synth, gap: series over the pre-treatment window
- placebo_att: mean placebo gap over (t0_placebo, T_pre]
- fit_rmspe: RMSPE over the placebo fitting window 1..t0_placebo
- eval_rmspe: RMSPE over the placebo post window (t0_placebo, T_pre]

See Also

[rmspe_ratio_pval\(\)](#) for in-space placebos, [loo_donors\(\)](#) for donor-robustness checks.

plot.coresynth	<i>Plot a coresynth model</i>
----------------	-------------------------------

Description

Plot a coresynth model

Usage

```
## S3 method for class 'coresynth'
plot(
  x,
  type = c("trend", "gap", "weights", "pred_weights"),
  colors = NULL,
  labels = NULL,
  vline = list(),
  vline_offset = 0,
  hline = list(),
  fill = NULL,
  top_n = Inf,
  align = FALSE,
  show_donors = 0,
  ...
)
```

Arguments

x	A coresynth object.
type	One of "trend" (observed vs synthetic), "gap" (ATT over time), "weights" (donor unit weight bar chart; SDID fits get a second panel with the time weight profile), or "pred_weights" (the predictor/variable weight matrix V as a bar chart; sharp SCM only).
colors	For type = "trend": a named vector overriding series colors, e.g. <code>c(treated = "black")</code> (valid keys: "treated", "synthetic", plus "donors" when <code>show_donors > 0</code>). For type = "gap": a single color string for the gap line. Ignored for type = "weights" (use fill instead).
labels	For type = "trend": a named vector overriding the legend text of individual series, e.g. <code>c(treated = "California")</code> (valid keys: "treated", "synthetic", plus "donors" when <code>show_donors > 0</code>). Series not mentioned keep their default label; colors and labels address series by the same keys, independent of the displayed legend text. Ignored for other types (no legend).
vline	Aesthetic overrides for the vertical treatment-time line, as a list passed to <code>ggplot2::geom_vline()</code> (e.g. <code>list(color = "red")</code>). NULL or FALSE hides the line entirely. The list may also carry an <code>xintercept</code> element giving one or more absolute positions on the time axis (e.g. <code>list(xintercept = 1988)</code> , or a date string such as "1989-01-01" on a Date axis), replacing the default treatment-time position; for placement relative to the treatment period use <code>vline_offset</code> instead. Applies to "trend" and "gap".
vline_offset	For type = "trend" and "gap": where to draw the vertical treatment line, in periods relative to the first post-treatment period. The default 0 keeps the line at the first post-treatment period; -1 moves it to the last pre-treatment period, and fractional values interpolate between adjacent observed times (-0.5 is midway between the last pre- and first post-treatment period), which works on numeric, Date, and POSIXct axes alike. Cannot be combined with an <code>xintercept</code> element in <code>vline</code> .
hline	Aesthetic overrides for the horizontal zero line in type = "gap", as a list passed to <code>ggplot2::geom_hline()</code> . NULL or FALSE hides the line. Ignored for other types.
fill	For type = "weights" and type = "pred_weights": a single color string overriding the bar fill. Ignored for other types.
top_n	For type = "weights": show only the top_n donors with the largest weights (default Inf keeps every donor with a non-negligible weight). For type = "pred_weights": show only the top_n predictors with the largest V weights (default Inf shows every predictor). Ignored for other types (and for the SDID time weight panel, which is always shown in full).
align	For type = "trend" and "gap": when TRUE, shift the synthetic series by its pre-treatment level gap to the treated series so that both are drawn on the same level. SDID matches trends only up to a free intercept, so its raw trend plot shows the synthetic control at a different level; with <code>align = TRUE</code> the offset is the time-weighted (λ) pre-period gap, which makes the average post-period gap in the plot equal the SDID estimate exactly. Other methods use the plain pre-period

	mean gap (usually a negligible shift, since they already match levels). Default FALSE (raw series).
show_donors	For type = "trend": also draw the outcome paths of the show_donors donor units with the largest weights as thin background lines (Inf shows every donor). Requires a fit that stores donor unit weights and outcomes (sharp SCM/SDID/SI). Default 0 (no donor paths).
...	Ignored.

Value

A ggplot2 plot object.

Examples

```
set.seed(1)
panel <- expand.grid(unit = 1:10, year = 1:20)
panel$treated <- as.integer(panel$unit == 5 & panel$year > 15)
panel$gdp <- panel$unit + 0.5 * panel$year +
  rnorm(nrow(panel)) + 3 * panel$treated
fit <- scm_fit(gdp ~ treated | unit + year, data = panel, method = "scm")

plot(fit, type = "trend")
plot(fit, type = "gap")
plot(fit, type = "weights")
plot(fit, type = "weights", top_n = 5)

# Predictor (V) weights: which predictors the fit leans on
plot(fit, type = "pred_weights")

# Overlay the five largest donors behind the treated/synthetic series
plot(fit, type = "trend", show_donors = 5)

# SDID: align the synthetic series on the lambda-weighted pre-period level
fit_sdid <- scm_fit(gdp ~ treated | unit + year, data = panel, method = "sdid")
plot(fit_sdid, type = "trend", align = TRUE)
plot(fit_sdid, type = "gap", align = TRUE)

# Customize series colors, legend text, and reference lines
plot(fit, type = "trend",
     colors = c(treated = "black"),
     labels = c(treated = "Unit 5"),
     vline = list(color = "red", linetype = "dashed"))

# Move the treatment line one period earlier (last pre-treatment period),
# pin it to an absolute time, or drop it entirely
plot(fit, type = "trend", vline_offset = -1)
plot(fit, type = "trend", vline = list(xintercept = 15.5))
plot(fit, type = "trend", vline = FALSE)
```

plot.scm_design	<i>Plot an scm_design object</i>
-----------------	----------------------------------

Description

Plot an scm_design object

Usage

```
## S3 method for class 'scm_design'
plot(x, type = c("outcome", "gap"), ...)
```

Arguments

x	An scm_design object.
type	"outcome" (default): synthetic treated vs synthetic control outcome series over all periods. "gap": estimated treatment effect in the experimental periods, with split-conformal confidence intervals.
...	Currently ignored.

Value

A ggplot object: for type = "outcome", the synthetic treated and synthetic control outcome series; for type = "gap", the estimated treatment effect over the experimental periods with split-conformal confidence intervals. The object is returned for printing or further customisation.

plot.scm_placebo	<i>Plot SCM In-Space Placebo Results</i>
------------------	--

Description

Visualizes the placebo study returned by `mspe_ratio_pval()`, following Abadie, Diamond & Hainmueller (2010, Section 3.4).

Usage

```
## S3 method for class 'scm_placebo'
plot(
  x,
  type = c("gaps", "ratios"),
  mspe_prune = Inf,
  colors = NULL,
  labels = NULL,
  vline = list(),
  vline_offset = 0,
```

```

    hline = list(),
    ...
  )

```

Arguments

<code>x</code>	A scm_placebo object from <code>mspe_ratio_pval()</code> .
<code>type</code>	One of "gaps" (ADH 2010, Figures 4-7) or "ratios" (ADH 2010, Figure 8).
<code>mspe_prune</code>	Only for type = "gaps": exclude placebo units whose pre-treatment MSPE exceeds mspe_prune times the treated unit's. Default Inf (no pruning). A rule stated on the RMSPE scale, such as tidysynth's "2 times the treated unit's pre-period RMSPE", corresponds to the squared multiple (mspe_prune = 4).
<code>colors</code>	A named vector overriding series colors, e.g. <code>c(treated = "black")</code> . Valid keys: "treated", "placebo".
<code>labels</code>	A named vector overriding the legend text of individual series, e.g. <code>c(treated = "California")</code> . Valid keys: "treated", "placebo". Series not mentioned keep their default label; colors and labels address series by the same keys, independent of the displayed legend text.
<code>vline</code>	Only for type = "gaps": aesthetic overrides for the vertical treatment-time line, as a list passed to <code>ggplot2::geom_vline()</code> . NULL or FALSE hides the line entirely. The list may also carry an <code>xintercept</code> element giving one or more absolute positions on the time axis, replacing the default treatment-time position.
<code>vline_offset</code>	Only for type = "gaps": where to draw the vertical treatment line, in periods relative to the first post-treatment period. The default 0 keeps the line at the first post-treatment period; -1 moves it to the last pre-treatment period, and fractional values interpolate between adjacent observed times. Cannot be combined with an <code>xintercept</code> element in <code>vline</code> .
<code>hline</code>	Only for type = "gaps": aesthetic overrides for the horizontal zero line, as a list passed to <code>ggplot2::geom_hline()</code> . NULL or FALSE hides the line entirely.
<code>...</code>	Ignored.

Details

type = "gaps" overlays the treated unit's gap path (treated minus synthetic control) on the placebo gap paths obtained by reassigning the intervention to each donor unit (ADH 2010, Figure 4). Placebo units whose synthetic control fits poorly before treatment carry no information about the rarity of a large post-treatment gap, so ADH exclude units whose pre-treatment MSPE exceeds a multiple of the treated unit's: 20, 5, and 2 in their Figures 5-7 (mspe_prune).

type = "ratios" shows the post/pre-treatment MSPE ratio of every unit (ADH 2010, Figure 8), the statistic behind the two-sided permutation p-value; it requires no pruning cutoff by construction.

Value

A ggplot2 plot object.

See Also

[mspe_ratio_pval\(\)](#)

Examples

```
set.seed(1)
panel <- expand.grid(unit = 1:10, year = 1:20)
panel$treated <- as.integer(panel$unit == 5 & panel$year > 15)
panel$gdp <- panel$unit + 0.5 * panel$year +
  rnorm(nrow(panel)) + 3 * panel$treated
fit <- scm_fit(gdp ~ treated | unit + year, data = panel, method = "scm")
placebo <- mspe_ratio_pval(fit)

# Treated gap overlaid on the donor-pool placebo gaps (ADH 2010, Fig. 4)
plot(placebo, type = "gaps")

# Prune poorly fitting placebos and relabel the legend
plot(placebo, type = "gaps", mspe_prune = 5,
      labels = c(treated = "Unit 5"))

# Move the treatment line one period earlier
plot(placebo, type = "gaps", vline_offset = -1)

# Post/pre-treatment MSPE ratios (ADH 2010, Fig. 8)
plot(placebo, type = "ratios")
```

plot_data

Extract the tidy data behind a coresynth plot

Description

Returns the tidy data frame that `plot()` draws for a given type, so the underlying series, weights, or placebo paths can be inspected, joined into a table, or re-plotted directly. `plot()` stays the quick path; `plot_data()` is the handle for anyone who wants to relabel simplified series names, feed the numbers into their own figure, or postprocess them further.

Usage

```
plot_data(x, ...)

## Default S3 method:
plot_data(x, ...)

## S3 method for class 'coresynth'
plot_data(
  x,
  type = c("trend", "gap", "weights", "pred_weights"),
  align = FALSE,
  top_n = Inf,
  show_donors = 0,
```

```

    ...
)

## S3 method for class 'scm_placebo'
plot_data(x, type = c("gaps", "ratios"), mspe_prune = Inf, ...)

```

Arguments

x	A coresynth fit (from <code>scm_fit()</code>) or a <code>scm_placebo</code> object (from <code>mspe_ratio_pval()</code>).
...	Passed to methods (unused by the current methods).
type	For a coresynth fit: one of "trend", "gap", "weights", or "pred_weights", matching <code>plot.coresynth()</code> . For a <code>scm_placebo</code> object: "gaps" or "ratios", matching <code>plot.scm_placebo()</code> .
align	For type = "trend"/"gap": when TRUE, shift the synthetic series by its pre-treatment level gap to the treated series, exactly as in <code>plot.coresynth()</code> . Default FALSE (raw series).
top_n	For type = "weights"/"pred_weights": keep only the top_n largest weights (default Inf, every row).
show_donors	For type = "trend": also return the outcome paths of the show_donors largest-weight donors as series = "Donors" rows, adding a unit column that identifies each donor (NA for the treated and synthetic series). Default 0 (treated and synthetic series only).
mspe_prune	For a <code>scm_placebo</code> object with type = "gaps": drop placebo units whose pre-treatment MSPE exceeds mspe_prune times the treated unit's, as in <code>plot.scm_placebo()</code> . Default Inf (no pruning).

Details

The frame mirrors what the matching `plot(x, type = ...)` call shows, with two deliberate departures that make it a better data source:

- Plain column names (time, value, series, weight, ...) are used instead of the dotted convention of `augment()`, since this is data to manipulate rather than model-augmented observations.
- The cosmetic "drop donors with weight below 1e-4" filter that `plot(type = "weights")` applies is *not* used here: every donor is returned (use `top_n` to subset), so the frame is the complete set of weights.

Only the arguments that change *which rows or values* appear are accepted (`align`, `top_n`, `show_donors`, `mspe_prune`); purely cosmetic arguments of `plot()` (colors, labels, vline, fill, ...) have no data counterpart and are not part of this interface.

Value

A tidy data.frame. Columns by type:

"trend" time, value, series ("Treated" / "Synthetic Control"); with `show_donors > 0`, also "Donors" rows and a unit column.

"gap" time, gap (treated minus synthetic control).

"weights" unit, weight; SDID fits add a panel column ("omega" unit weights, "lambda" time weights), with unit holding the pre-period label for "lambda" rows.

"pred_weights" predictor, weight (sharp SCM only).

"gaps" time, gap, unit (NA for the treated series), series ("Treated" / "Placebo (donor pool)").

"ratios" unit, ratio, series.

See Also

[plot.coresynth\(\)](#), [plot.scm_placebo\(\)](#)

Examples

```
set.seed(1)
panel <- expand.grid(unit = 1:10, year = 1:20)
panel$treated <- as.integer(panel$unit == 5 & panel$year > 15)
panel$gdp <- panel$unit + 0.5 * panel$year +
  rnorm(nrow(panel)) + 3 * panel$treated
fit <- scm_fit(gdp ~ treated | unit + year, data = panel, method = "scm")

head(plot_data(fit, type = "trend"))
plot_data(fit, type = "gap")
plot_data(fit, type = "weights")

# Relabel the simplified series names, then plot it yourself
df <- plot_data(fit, type = "trend")
df$series <- sub("Synthetic Control", "Synthetic Unit 5", df$series)

ggplot2::ggplot(df, ggplot2::aes(time, value, color = series)) +
  ggplot2::geom_line()
```

pred

Predictor Specification for SCM

Description

Creates a single predictor specification for use in [scm_fit\(\)](#) with method = "scm". Pass a [list\(\)](#) of [pred\(\)](#) calls as the predictors argument to define the full covariate matrix.

Usage

```
pred(vars, times, op = "mean")
```

Arguments

vars	Character vector of variable names. All variables share the same times window and op operator. Use separate <code>pred()</code> calls for variables with different time windows.
times	Numeric/integer vector of time values to aggregate over.
op	Aggregation operator applied to each variable over times. One of "mean" (default), "median", or "sum".

Value

A `pred_spec` object (a named list with class "pred_spec").

See Also

`scm_fit()` for the predictors argument that consumes a `list()` of `pred_spec` objects.

Examples

```
# Three variables averaged over the same window
pred(c("lnincome", "retprice", "age15to24"), 1980:1988)

# Single variable at a specific year
pred("cigsale", 1975)

# Single variable averaged over a range
pred("beer", 1984:1988)

# Abadie, Diamond & Hainmueller (2010) California Prop 99 style: combine
# several covariates aggregated over different windows plus three outcome
# lags at specific years. The resulting list is passed to
# scm_fit(..., predictors = predictors).
predictors <- list(
  pred(c("lnincome", "retprice", "age15to24"), 1980:1988),
  pred("beer", 1984:1988),
  pred("cigsale", 1988),
  pred("cigsale", 1980),
  pred("cigsale", 1975)
)
predictors
```

Description

Selects which units to assign to the treatment arm (and which to the control arm) in a planned experiment, following Abadie and Zhao (2026). Both sets of units are chosen by minimising the distance between their weighted-average predictor vectors and the population-average predictor vector $\bar{X}$, so the resulting estimates are less susceptible to post-randomisation bias than pure random assignment.

Usage

```
scm_design(
  data,
  outcome,
  unit,
  time,
  T0,
  T_fit = NULL,
  m_min = 1L,
  m_max = 1L,
  f = NULL,
  predictors = NULL,
  design = c("base", "weakly_targeted", "unit_level"),
  beta = 1,
  xi = 1,
  alpha = 0.05,
  normalize = TRUE,
  max_subsets = 100000L
)
```

Arguments

<code>data</code>	Long-format data frame (one row per unit–time).
<code>outcome</code>	Name of the outcome column.
<code>unit</code>	Name of the unit identifier column.
<code>time</code>	Name of the time identifier column.
<code>T0</code>	Last pre-experimental period (a value present in the time column). Periods after <code>T0</code> are the experimental periods.
<code>T_fit</code>	Number of fitting periods, counted from the start of the pre-experimental phase. Defaults to <code>NULL</code> , which uses all pre-experimental periods for fitting (no blank periods; inference disabled). When <code>T_fit</code> is smaller than the total number of pre-experimental periods, the remaining periods become blank periods used for inference.
<code>m_min</code>	Minimum number of units assigned to treatment (default 1).
<code>m_max</code>	Maximum number of units assigned to treatment (default 1).
<code>f</code>	Named numeric vector of population weights f_j . Defaults to uniform weights $1/J$. Will be normalised to sum to 1.
<code>predictors</code>	A <code>list()</code> of <code>pred()</code> specifications that define the predictor matrix X_j . Defaults to <code>NULL</code> , which uses all fitting-period outcome values as predictors.
<code>design</code>	Design formulation: "base" (default), "weakly_targeted", or "unit_level".
<code>beta</code>	Trade-off parameter $\beta > 0$ for the Weakly targeted design (default 1).
<code>xi</code>	Trade-off parameter $\xi > 0$ for the Unit-level design (default 1).
<code>alpha</code>	Significance level for confidence intervals (default 0.05).

normalize	If TRUE (default), each row of the predictor matrix is divided by its cross-unit standard deviation before optimisation, so predictors measured on different scales contribute equally.
max_subsets	Maximum number of treatment-set candidates to evaluate before switching to random sampling (default 100 000).

Details

Three design formulations are available:

- "base" (eq. 7): both the synthetic treated and the synthetic control independently target the population average $\bar{X}$.
- "weakly_targeted" (eq. 9): the treated and control weights jointly minimise the distance of the synthetic treated to $\bar{X}$ plus beta times the distance between the synthetic control and the synthetic treated.
- "unit_level" (eq. 10): each treated unit gets its own synthetic control; the treated weights trade off matching $\bar{X}$ against xi times each treated unit's own synthetic-control fit, and the aggregate control weight is the w-weighted combination of the per-unit controls (eq. 11).

Inference uses "blank periods" — pre-experimental periods whose outcomes were *not* used to estimate the weights. Set T_{fit} strictly smaller than the number of pre-experimental periods to enable the permutation test and split-conformal confidence intervals from Section 3 of Abadie and Zhao (2026).

Value

An object of class "scm_design" with components:

- treated_units: unit identifiers selected for treatment
- control_units: unit identifiers in the control pool
- w: J-length weight vector for the synthetic treated unit (sums to 1)
- v: J-length weight vector for the synthetic control unit (sums to 1)
- tau_hat: estimated treatment effects for each experimental period
- p_value: permutation p-value (NA when blank periods are unavailable)
- ci_lower, ci_upper: per-period split-conformal confidence interval
- Y_synth_tr, Y_synth_co: synthetic treated/control series (all periods)
- estimate: ATT (mean of tau_hat)

References

Abadie, A. and Zhao, J. (2026). "Synthetic Controls for Experimental Design." MIT Working Paper.

scm_fit

*Fit a Synthetic Control Method Model***Description**

Unified formula interface for Synthetic Control and related causal inference methods. The formula syntax is:

Usage

```
scm_fit(
  formula,
  data,
  method = c("scm", "sdid", "gsc", "mc", "tasc", "si"),
  predictors = NULL,
  covariates = NULL,
  v_selection = c("insample", "oos"),
  donor_mspe_threshold = Inf,
  lambda_pen = NULL,
  v_optim = c("auto", "coord_descent", "bfgs", "multistart"),
  v_window = NULL,
  nu = NULL,
  fixedeff = FALSE,
  ...
)
```

Arguments

formula	A Formula object, e.g. $y \sim D \mid \text{unit} + \text{time}$.
data	A data.frame in long format (one row per unit-time).
method	One of "scm", "sdid", "gsc", "mc", "tasc", "si".
predictors	A list() of <code>pred()</code> specifications that define the predictor matrix for SCM (see Abadie et al. 2010, S.2.3). Each <code>pred()</code> entry aggregates one or more variables over a time window. Pass NULL (default) to use all pre-treatment outcome periods as predictors. Applies to method = "scm" only. Predictor rows are scaled by their standard deviation across all units before optimisation, matching the Synth reference implementation (ADH 2011, JSS); pass <code>scale_predictors = FALSE</code> to disable.
covariates	An optional named list of additional time-varying covariates to partial out before estimation. Each element is a character string naming a column in data. Supported for method = "sdid", "scm", and "gsc".
v_selection	V matrix selection method for method = "scm". "insample" (default) follows Abadie et al. (2010): V is chosen by minimising in-sample pre-treatment MSPE. "oos" follows Abadie (2021) S.3.2 / ADH (2015): the pre-treatment window is split into a training half and a validation half. In the default outcomes-as-predictors case, candidate $W(V)$ are fitted on training-half outcomes only, V^*

minimises the validation-half MSPE, and the final W^* is refit with V^* on the outcomes of the last $\text{floor}(T_{\text{pre}}/2)$ pre-treatment periods (so $v_weights$ has $\text{floor}(T_{\text{pre}}/2)$ entries). With user-supplied predictors, the predictor matrix is fixed and only the MSPE evaluation window is restricted to the validation half; lag your `pred()` windows to the training period for a fully out-of-sample exercise.

`donor_mspe_threshold`

Donor pool filtering threshold (Abadie 2021 S.4). For method = "scm" only. Each donor's individual pre-treatment MSPE (using that donor alone as the counterfactual) is divided by the minimum such MSPE across all donors. Donors whose ratio exceeds this threshold are excluded from estimation. Inf (default) disables filtering.

`lambda_pen`

Penalised SCM parameter (Abadie & L'Hour 2021, JASA). For method = "scm" only. NULL (default) runs standard unpenalised SCM. "auto" selects the penalty via out-of-sample pre-treatment MSPE on the same validation window as `v_selection` = "oos". A non-negative number uses that value directly.

`v_optim`

Outer V-optimisation method for method = "scm". The outer problem (choose V so that the implied donor weights $W(V)$ minimise pre-treatment outcome MSPE) is non-convex, and a single local search can settle in a poor basin when predictors are supplied. "auto" (default) therefore selects "multistart" for predictor-based fits and "coord_descent" for outcomes-only fits (where the single start is empirically reliable). "multistart" runs a deterministic multi-start search: a fixed start set (uniform V , one-hot V per predictor, and 100 fixed-seed random draws) is screened at one inner QP each, the leaders are polished by coordinate descent, and the winner is refined by a Nelder-Mead pass. Its solution is never worse (in pre-treatment loss) than "coord_descent", at roughly the cost of a handful of single-start fits, and is fully reproducible (no RNG state is consumed). "coord_descent" is the classic single-start coordinate descent with an 11-point grid, and is also the outcomes-only and staggered engine and the multi-start never-worse reference. "bfgs" (a single-start L-BFGS-B) is **deprecated** and will be removed in a future release: it has no advantage over "multistart" (which dominates it on predictor fits) or "coord_descent". `mspe_ratio_pval()` mirrors a multi-start fit in its placebo refits so the permutation test stays symmetric.

`v_window`

Optional vector of pre-treatment time values (matching the time index in data) over which the outer V optimisation evaluates the pre-treatment fit, for method = "scm" (sharp fits only). NULL (default) evaluates on all pre-treatment periods. The window restricts only the outer evaluation loss: predictor matrices (or the full pre-treatment outcome rows in the outcomes-only case) still enter the inner QP unchanged, and the reported loss and `mspe_ratio_pval()` MSPE components always cover the full pre-treatment window. Cannot be combined with `v_selection` = "oos", which manages its own train/validation split.

`nu`

Partial pooling parameter for **staggered** SCM fits (Ben-Michael, Feller & Rothstein 2022, JRSS-B). NULL (default) keeps the per-cohort V-optimised SCM path. A number in $[0, 1]$ switches to partially pooled SCM: all cohort weight vectors are chosen jointly to minimise $\text{nu} * (\text{normalised pooled pre-treatment imbalance})^2 + (1 - \text{nu}) * \text{MSPE}$ so the aggregate ATT is anchored by the pooled fit. `nu = 0` is separate per-cohort SCM with uniform lag weights, `nu = 1` fully pooled, and `nu = "auto"`

uses the paper's heuristic (the ratio of the pooled to the average per-cohort imbalance of the separate solution). The pooled path is outcomes-only and cannot be combined with `donor_mspe_threshold`, `lambda_pen`, or `v_selection = "oos"`. Balance diagnostics are stored in `fit$pooling`. For `method = "scm"` on staggered panels only.

`fixedeff` If TRUE, staggered SCM demeans every unit by its own pre-treatment mean within each cohort before fitting (intercept shift; Ben-Michael, Feller & Rothstein 2022, Section 5.1), which turns the estimator into a weighted difference-in-differences and typically improves fit when outcome levels differ across units. The reported `Y_synth` is shifted back to the raw outcome scale. Works with both the default and the partially pooled path. For `method = "scm"` on staggered panels only. Default FALSE.

... Additional arguments forwarded to the specific method (e.g. `r`, `lambda`, `zeta2`).

Details

```
outcome ~ treatment | unit_id + time_id
```

Value

An object of classes `c("coresynth_<method>", "coresynth")`. Fits with staggered adoption additionally inherit from `"coresynth_staggered"`, and multi-arm SI fits from `"coresynth_multiarm"`; S3 methods such as `tidy()` and `augment()` dispatch on these subclasses. All methods return at minimum:

- `method`: estimator name
- `estimate`: average treatment effect (ATT)
- `times`: time index vector
- `T_pre`: number of pre-treatment periods
- `Y_treat`: treated unit outcome series
- `gap`: treatment effect series (`Y_treat` - counterfactual)

Examples

```
# Synthetic balanced panel: 10 units over 20 periods, unit 1 treated
# after period 15.
set.seed(1)
panel <- expand.grid(unit = 1:10, year = 1:20)
panel$treated <- as.integer(panel$unit == 1 & panel$year > 15)
panel$gdp <- panel$unit + 0.5 * panel$year +
  rnorm(nrow(panel)) + 3 * panel$treated

fit <- scm_fit(gdp ~ treated | unit + year, data = panel, method = "sdid")
summary(fit)

# Visualise the estimated gap (requires ggplot2)
plot(fit, type = "gap")
```

scm_inference

*Wild Bootstrap Inference for Staggered SCM***Description**

Confidence intervals and p-values for the aggregate ATT of a staggered SCM fit via the weighted multiplier (wild) bootstrap of Ben-Michael, Feller & Rothstein (2022, Section 5.3), adapting Otsu & Rai (2017). The aggregate ATT is written as a weighted average of per-treated-unit effect contributions; each bootstrap draw perturbs those contributions with independent golden-ratio two-point multipliers (mean 0, variance 1) while donor weights and outcomes are kept fixed.

Usage

```
scm_inference(
  fit,
  method = "wild_bootstrap",
  n_boot = 1000L,
  level = 0.95,
  alternative = c("two.sided", "greater", "less"),
  seed = NULL
)
```

Arguments

<code>fit</code>	A staggered SCM fit from <code>scm_fit()</code> (method = "scm" on a panel with multiple adoption times). Sharp fits are rejected: use <code>mspe_ratio_pval()</code> or <code>conformal_inference()</code> instead.
<code>method</code>	Only "wild_bootstrap" is available.
<code>n_boot</code>	Number of bootstrap draws. Default 1000.
<code>level</code>	Confidence level. Default 0.95.
<code>alternative</code>	Direction of the alternative hypothesis for the p-value: "two.sided" (default), "greater", or "less".
<code>seed</code>	Optional RNG seed.

Details

Works with both staggered SCM paths (`nu = NULL` legacy and the partially pooled path) and honours the cohort aggregation weights `N_treated x T_post`. For intercept-shifted fits (`fixedeff = TRUE`) the per-unit contributions are computed in difference-in-differences form, i.e. each treated unit is demeaned by its own pre-treatment mean.

With very few treated units the multiplier distribution has few atoms, so the bootstrap is unreliable; a warning is issued below 5 treated units.

Value

A `coresynth_inference` object with the standard fields (`estimate`, `se`, `p_value`, `ci_lower`, `ci_upper`, `method`, `staggered`, `n_controls`, `alternative`, `boot_est`s), compatible with `tidy.coresynth_inference()` and `glance.coresynth_inference()`. `n_treated` additionally records the number of treated units resampled by the multipliers.

References

Ben-Michael, E., Feller, A., & Rothstein, J. (2022). Synthetic controls with staggered adoption. *JRSS-B*, 84(2), 351-381.

Examples

```
set.seed(1)
dat <- expand.grid(time = 1:20, id = paste0("u", 1:12))
dat$y <- rnorm(nrow(dat)) + as.numeric(factor(dat$id))
dat$d <- as.integer(
  (dat$id == "u1" & dat$time > 10) | (dat$id == "u2" & dat$time > 14)
)
fit <- scm_fit(y ~ d | id + time, data = dat, method = "scm")
scm_inference(fit, n_boot = 200, seed = 1)
```

scm_inner_weights_cpp *SCM Inner Weights (QP Given V)*

Description

Solves the inner-loop QP for SCM: given a fixed diagonal metric matrix V , finds donor weights W on the simplex minimising the V -weighted covariate loss.

Usage

```
scm_inner_weights_cpp(X0, X1, V_diag)
```

Arguments

<code>X0</code>	Covariate matrix for control units ($k \times N_{\text{co}}$)
<code>X1</code>	Covariate vector for the treated unit ($k \times 1$)
<code>V_diag</code>	Diagonal of the metric matrix V ($k \times 1$, non-negative, need not sum to 1)

Value

Donor weight vector W ($N_{\text{co}} \times 1$) on the unit simplex

scm_placebo_cpp

*Fast Leave-One-Out Placebo Test for SCM (Abadie et al. 2010)***Description**

For each control unit, treats it as pseudo-treated and fits SCM weights from the remaining $N_{co}-1$ donors. Returns MSPE components for constructing MSPE-ratio permutation p-values in R.

Usage

```
scm_placebo_cpp(Y_pre, Y_post, max_iter = 100L, tol = 1e-04, z_rows = NULL)
```

Arguments

<code>Y_pre</code>	Control pre-treatment outcomes ($T_{pre} \times N_{co}$)
<code>Y_post</code>	Control post-treatment outcomes ($T_{post} \times N_{co}$)
<code>max_iter</code>	Outer coordinate-descent iterations (default 100)
<code>tol</code>	Convergence tolerance for V updates (default $1e-4$)
<code>z_rows</code>	Optional 1-based pre-period row indices of the outer evaluation window (the <code>v_window</code> of the treated fit), so each placebo refit optimises V on the same window. NULL (default) uses all rows. MSPE components are always computed on the full pre/post windows.

Value

A list with:

- `mspe_pre`: N_{co} -vector of pre-treatment MSPE per placebo unit
- `mspe_post`: N_{co} -vector of post-treatment MSPE per placebo unit
- `effects`: N_{co} -vector of mean post-period gap per placebo unit
- `gaps`: $(T_{pre} + T_{post}) \times N_{co}$ matrix of placebo gap paths

scm_placebo_x_cpp

*Fast Leave-One-Out Placebo Test for SCM with a Predictor Specification***Description**

Covariate-spec counterpart of `scm_placebo_cpp()`: for each control unit, treats it as pseudo-treated with its own predictor column $X0[, i]$ and fits the nested V/W optimisation against the remaining donors' predictors $X0[, -i]$, evaluating the prediction loss on pre-treatment outcomes. Each leave-one-out problem is identical to a `scm_weights_cpp()` call on the same submatrices; iterations are independent and run in parallel under OpenMP.

Usage

```
scm_placebo_x_cpp(
  X0,
  Y_pre,
  Y_post,
  max_iter = 100L,
  tol = 1e-04,
  z_rows = NULL,
  multistart = FALSE
)
```

Arguments

<code>X0</code>	Predictor matrix for control units ($k \times N_{co}$), on the same scale as the treated fit (SD-scaled when <code>scale_predictors = TRUE</code>)
<code>Y_pre</code>	Control pre-treatment outcomes ($T_{pre} \times N_{co}$)
<code>Y_post</code>	Control post-treatment outcomes ($T_{post} \times N_{co}$)
<code>max_iter</code>	Outer coordinate-descent iterations (default 100)
<code>tol</code>	Convergence tolerance for V updates (default $1e-4$)
<code>z_rows</code>	Optional 1-based pre-period row indices of the outer evaluation window (the <code>v_window</code> of the treated fit), so each placebo refit optimises V on the same window. NULL (default) uses all rows. MSPE components are always computed on the full pre/post windows.
<code>multistart</code>	If TRUE, each placebo refit uses the same deterministic multi-start outer search as the treated fit, keeping the permutation test symmetric.

Value

A list with:

- `mspe_pre`: N_{co} -vector of pre-treatment MSPE per placebo unit
- `mspe_post`: N_{co} -vector of post-treatment MSPE per placebo unit
- `effects`: N_{co} -vector of mean post-period gap per placebo unit
- `gaps`: $(T_{pre} + T_{post}) \times N_{co}$ matrix of placebo gap paths A placebo unit whose solver fails yields NaN entries.

scm_weights_cpp

SCM Outer Weights (Joint Optimization of W and V)

Description

Jointly optimises donor weights W (on the simplex) and the diagonal metric matrix V via coordinate descent on the pre-treatment prediction MSPE, following Abadie, Diamond & Hainmueller (2010).

Usage

```
scm_weights_cpp(
  X0,
  X1,
  Z0,
  Z1,
  max_iter = 100L,
  tol = 1e-04,
  t_train = -1L,
  z_rows = NULL,
  multistart = FALSE
)
```

Arguments

<code>X0</code>	Covariate matrix for control units ($k \times N_{co}$, typically pre-treatment outcomes)
<code>X1</code>	Covariate vector for the treated unit ($k \times 1$)
<code>Z0</code>	Outcome matrix for control units in the pre-treatment window ($T_{pre} \times N_{co}$)
<code>Z1</code>	Outcome vector for the treated unit in the pre-treatment window ($T_{pre} \times 1$)
<code>max_iter</code>	Maximum coordinate-descent iterations (default 100)
<code>tol</code>	Convergence tolerance on MSPE improvement (default $1e-4$)
<code>t_train</code>	Validation-window split for V selection. -1 (default): V selected on the full Z window (in-sample). Positive: rows $t_train..(T_{pre}-1)$ of Z form the validation window used to select V (W is fitted on the full X throughout); after selecting V^* , W is refit and the reported loss uses the full Z window.
<code>z_rows</code>	Optional 1-based row indices of Z defining the evaluation window for the outer V optimisation (the <code>v_window</code> argument of <code>scm_fit()</code>). NULL (default) evaluates on the full Z window. Takes precedence over <code>t_train</code> ; the reported loss always uses the full Z window.
<code>multistart</code>	If TRUE, the outer V optimisation runs a deterministic multi-start search (screened start set, coordinate-descent polish, Nelder-Mead refinement) instead of a single coordinate-descent pass from the uniform V. The result is never worse (in outer loss) than the single-start path.

Details

When `t_train > 0`, V is selected by minimising MSPE on a validation window (rows $t_train..T_{pre}-1$ of Z) while W is fitted on the full predictor matrix X. This is appropriate when X is a fixed predictor matrix that contains no validation-period outcome information (the user-supplied predictors case). For the outcomes-only case the proper Abadie (2021) S.3.2 train/validation split is implemented in R (`.scm_oos_outcomes()`): candidate $W(V)$ are fitted on training-half outcomes only, by passing the training rows as X and the validation rows as Z to this function with `t_train = -1`.

Value

A list with:

- W : Donor weight vector ($N_{co} \times 1$) on the unit simplex
- V : Optimal metric diagonal ($k \times 1$, normalised to sum to 1)
- $loss$: Final pre-treatment prediction loss (full pre-treatment window)

sdid_estimate_cpp	<i>Calculate SDID Estimate (τ_{sdid})</i>
-------------------	---

Description

Given unit weights ω and time weights λ , computes the SDID estimator as a weighted two-way difference:

Usage

```
sdid_estimate_cpp(Y_pre_co, Y_post_co, Y_pre_tr, Y_post_tr, omega, lambda)
```

Arguments

Y_{pre_co}	Control pre-treatment outcomes ($T_{pre} \times N_{co}$)
Y_{post_co}	Control post-treatment outcomes ($T_{post} \times N_{co}$)
Y_{pre_tr}	Treated pre-treatment outcomes ($T_{pre} \times 1$)
Y_{post_tr}	Treated post-treatment outcomes ($T_{post} \times 1$)
ω	Unit weights ($N_{co} \times 1$)
λ	Time weights ($T_{pre} \times 1$)

Details

$$\tau_{sdid} = (Y_{tr_post_mean} - Y_{tr_pre_wt}) - (Y_{co_post_wt} - Y_{co_pre_wt})$$

Value

A single numeric value: the SDID treatment-effect estimate τ_{sdid} .

sdid_inference

*Inference for Synthetic Difference-in-Differences***Description**

Computes standard errors and p-values for a SDID estimate using one of four methods, following Clarke et al. (2023): permutation placebo test (Algorithm 4), cluster bootstrap (Algorithm 2), leave-one-out jackknife (Algorithm 3), or (staggered fits only) a global jackknife across the unique control units of all cohorts.

Usage

```
sdid_inference(
  fit,
  method = c("placebo", "bootstrap", "jackknife", "jackknife_global"),
  n_boot = 200L,
  level = 0.95,
  alternative = c("two.sided", "greater", "less"),
  seed = NULL
)
```

Arguments

<code>fit</code>	A coresynth object with <code>method = "sdid"</code> (sharp or staggered).
<code>method</code>	Inference method: "placebo" (permutation), "bootstrap", "jackknife", or "jackknife_global" (staggered only).
<code>n_boot</code>	Number of bootstrap replications (only for <code>method = "bootstrap"</code>).
<code>level</code>	Confidence level for the interval (all methods).
<code>alternative</code>	Direction of the alternative hypothesis: "two.sided", "greater", or "less".
<code>seed</code>	Integer seed for reproducibility (only for <code>method = "bootstrap"</code>).

Details

For `method = "placebo"`, the p-value is the permutation p-value, while the standard error is the dispersion of the placebo distribution (Clarke et al. 2023, Algorithm 4) and the confidence interval is the normal approximation around the estimate with that SE. The placebo SE assumes the treated unit's noise is comparable to the control units'; interpret it with caution when the donor pool is small.

Value

A list with:

- `estimate`: The SDID point estimate.
- `se`: Standard error (placebo: placebo-distribution SD, Algorithm 4).
- `p_value`: Permutation or normal-approximation p-value.

- `ci_lower`, `ci_upper`: Confidence interval bounds.
- `method`: The inference method used.
- `n_controls`: Number of control units.
- `alternative`: The alternative hypothesis direction.
- `placebo_effects`: Named vector of LOO placebo effects (placebo only).
- `boot_est`s: Bootstrap estimate distribution (bootstrap only).

sdid_placebo_cpp

Fast Placebo Test for SDID

Description

For each control unit, treats it as the "pseudo-treated" unit and estimates the leave-one-out SDID effect. The distribution of these placebo effects provides a permutation-based null distribution for inference.

Usage

```
sdid_placebo_cpp(Y_pre, Y_post, time_weights, zeta2)
```

Arguments

<code>Y_pre</code>	Control units pre-treatment outcomes ($T_{pre} \times N_{co}$)
<code>Y_post</code>	Control units post-treatment outcomes ($T_{post} \times N_{co}$)
<code>time_weights</code>	Lambda weights for pre-treatment periods ($T_{pre} \times 1$)
<code>zeta2</code>	Ridge penalty (same as used in the main estimate)

Value

A numeric vector of length N_{co} . Each element is the leave-one-out placebo SDID effect obtained by treating that control unit as the pseudo-treated unit; the vector serves as a permutation-based null distribution for inference.

sdid_time_weights_cpp *Calculate SDID Time Weights (lambda)*

Description

Solves the time-weight QP (with implicit intercept $\lambda_{0,0}$ concentrated out):

Usage

```
sdid_time_weights_cpp(Y_pre_co, Y_post_target, zeta_t)
```

Arguments

<code>Y_pre_co</code>	Pre-treatment outcomes for control units, row-demeaned ($T_{pre} \times N_{co}$)
<code>Y_post_target</code>	Post-treatment mean per control unit, demeaned ($N_{co} \times 1$)
<code>zeta_t</code>	Ridge penalty for time weights (paper: $1e-6 * \sigma_{hat}$)

Details

min over λ in Δ_{pre} : $\|Y_{post_target} - Y_{pre_co}^T \lambda\|^2 + zeta_t^2 * N_{co} * \|\lambda\|^2$

The caller is responsible for pre-demeaning `Y_pre_co` (row-wise) and `Y_post_target` (subtract the cross-unit mean) to concentrate out $\lambda_{0,0}$, as described in Arkhangelsky et al. (2021) Algorithm 1, Eq. (2.3).

Value

A numeric vector of length T_{pre} holding the SDID time weights λ (non-negative and summing to one).

sdid_unit_weights_cpp *Calculate SDID Unit Weights (omega)*

Description

Solves the regularized QP: min over ω in Δ : $\sum_t (\sum_i \omega_i Y_{it} - Y_{tr_t})^2 + zeta^2 * T_{pre} * \|\omega\|^2$

Usage

```
sdid_unit_weights_cpp(Y_pre, Y_tr_pre, zeta2)
```

Arguments

Y_pre	Pre-treatment outcome matrix for control units (T_pre x N_co)
Y_tr_pre	Pre-treatment outcome vector for treated unit (T_pre x 1), averaged if multiple
zeta2	Ridge penalty parameter (zeta^2). The code internally multiplies by T_pre per the paper.

Details

This corresponds to equation (5) in Arkhangelsky et al. (2021).

Value

A numeric vector of length N_co holding the SDID unit weights omega (non-negative and summing to one).

si_inference	<i>Non-parametric Inference for SI (Agarwal et al. 2025)</i>
--------------	--

Description

Estimates SE and confidence intervals for the ATT via non-parametric cluster bootstrap or jackknife over control units. Works for both sharp and staggered SI fits. For staggered fits, bootstrap resamples each cohort’s control pool independently, and jackknife uses a per-cohort LOO with delta-method variance aggregation.

Usage

```
si_inference(  
  fit,  
  method = c("bootstrap", "jackknife", "jackknife_global"),  
  n_boot = 499L,  
  level = 0.95,  
  alternative = c("two.sided", "greater", "less"),  
  seed = NULL  
)
```

Arguments

fit	A coresynth object from <code>scm_fit()</code> with method = "si".
method	"bootstrap" (default) or "jackknife".
n_boot	Number of bootstrap replications (default 499L; ignored for jackknife).
level	Confidence level (default 0.95).
alternative	"two.sided" (default), "greater", or "less".
seed	RNG seed for reproducibility (default NULL).

Value

A list of class coresynth_inference.

si_pcr_cpp	<i>SI-PCR: Synthetic Interventions via Principal Component Regression</i>
------------	---

Description

Implements the SI-PCR estimator of Agarwal et al. (2025). Uses the top-k SVD of pre-treatment control outcomes to find donor weights that predict each treated unit’s pre-treatment trajectory, then applies those weights to post-treatment control outcomes.

Usage

```
si_pcr_cpp(Y_pre_co, Y_post_co, Y_pre_tr, k)
```

Arguments

- | | |
|-----------|---|
| Y_pre_co | Pre-treatment control outcomes (T_pre x N_co) |
| Y_post_co | Post-treatment control outcomes (T_post x N_co) |
| Y_pre_tr | Pre-treatment treated outcomes (T_pre x N_tr) |
| k | Number of SVD components to retain |

Value

- A list with:
- W: Donor weight matrix (N_co x N_tr)
 - Y_hat: Counterfactual post-treatment outcomes (T_post x N_tr)

soft_impute_cpp	<i>Fast Matrix Completion using Soft-Impute Algorithm</i>
-----------------	---

Description

Solves: $\min_L (1/2) \|O - (Y - L)\|_F^2 + \lambda \|L\|_*$ via iterative SVD soft-thresholding (Mazumder, Hastie, Tibshirani 2010). Note: λ is NOT normalized by $|O|$. Default $\lambda = 0.01 * \sigma_{\max}(Y)$.

Usage

```
soft_impute_cpp(Y, 0, lambda, max_iter = 1000L, tol = 1e-05)
```

Arguments

Y	Observed outcome matrix (N x T). Unobserved entries should be 0.
O	Binary mask matrix (N x T): 1 = observed, 0 = missing (treated post).
lambda	Nuclear norm penalty (soft-threshold on singular values).
max_iter	Maximum iterations.
tol	Convergence tolerance (relative Frobenius norm change).

Value

A numeric matrix of the same dimension as Y (N x T): the completed low-rank matrix L that minimises the soft-thresholded nuclear-norm objective.

tensor_unfold_cpp	<i>Tensor Unfolding (Matricization) for Synthetic Interventions</i>
-------------------	---

Description

Tensor Unfolding (Matricization) for Synthetic Interventions

Usage

tensor_unfold_cpp(T_cube, mode)

Arguments

T_cube	A 3D array (cube) of dimensions (n1, n2, n3)
mode	The mode to unfold along (1, 2, or 3)

Value

A numeric matrix: the mode-mode unfolding (matricization) of T_cube, with dimensions n1 x (n2 * n3), n2 x (n1 * n3), or n3 x (n1 * n2) for mode 1, 2, or 3 respectively.

```
tidy.coresynth_inference
```

Tidy an inference result

Description

Coerces a `coresynth_inference` or `sdid_inference` object to a one-row tidy data.frame with broom-style column names so it can be combined with regression output for paper tables.

Usage

```
## S3 method for class 'coresynth_inference'
tidy(x, conf.int = TRUE, ...)
```

Arguments

<code>x</code>	A <code>coresynth_inference</code> (or <code>sdid_inference</code>) object returned by <code>sdid_inference()</code> , <code>gsc_inference()</code> , or <code>si_inference()</code> .
<code>conf.int</code>	Logical. Include <code>conf.low</code> / <code>conf.high</code> columns when CI is available (default TRUE). Methods without a CI report NA.
<code>...</code>	Unused.

Value

A one-row data.frame with columns `term`, `estimate`, `std.error`, `statistic`, `p.value`, `conf.low`, `conf.high`, `method`, `alternative`, `n_controls`, `staggered`.

```
treated_outcomes
```

Extract Outcome Series from a coresynth Fit

Description

Accessor generics that return the outcome series stored in a fitted `coresynth` object under a uniform interface, regardless of the estimation method:

Usage

```
treated_outcomes(x, ...)

## S3 method for class 'coresynth'
treated_outcomes(x, na.rm = FALSE, ...)

synthetic_outcomes(x, ...)

## S3 method for class 'coresynth'
```

```

synthetic_outcomes(x, na.rm = FALSE, ...)

## S3 method for class 'coresynth_tasc'
synthetic_outcomes(x, na.rm = FALSE, ...)

donor_outcomes(x, ...)

## S3 method for class 'coresynth_scm'
donor_outcomes(x, ...)

## S3 method for class 'coresynth_sdid'
donor_outcomes(x, ...)

## S3 method for class 'coresynth_si'
donor_outcomes(x, ...)

## S3 method for class 'coresynth_gsc'
donor_outcomes(x, ...)

## S3 method for class 'coresynth_mc'
donor_outcomes(x, ...)

## S3 method for class 'coresynth_tasc'
donor_outcomes(x, ...)

## S3 method for class 'coresynth'
donor_outcomes(x, ...)

```

Arguments

<code>x</code>	A <code>coresynth</code> object from <code>scm_fit()</code> .
<code>...</code>	Passed to methods.
<code>na.rm</code>	Logical; passed to the per-period averaging over multiple treated units (default FALSE).

Details

- `treated_outcomes()`: the treated unit's observed outcome series (length T). When several units are treated, their per-period mean.
- `synthetic_outcomes()`: the estimated counterfactual series (length T), i.e. the synthetic control or model-fitted outcome.
- `donor_outcomes()`: the $T \times N_{co}$ matrix of observed donor (control unit) outcomes over all periods.

Each accessor returns NULL when the requested series is not stored in the fit. In particular, staggered-adoption fits keep their data per cohort (in `fit$cohort_fits`), so the sharp-fit accessors return NULL for them.

Value

For `treated_outcomes()` and `synthetic_outcomes()`, a numeric vector of length T , or NULL.
For `donor_outcomes()`, a $T \times N_{co}$ numeric matrix (donors in columns, named when unit names are available), or NULL.

Examples

```
set.seed(1)
panel <- expand.grid(unit = 1:10, year = 1:20)
panel$treated <- as.integer(panel$unit == 1 & panel$year > 15)
panel$gdp <- panel$unit + 0.5 * panel$year +
  rnorm(nrow(panel)) + 3 * panel$treated
fit <- scm_fit(gdp ~ treated | unit + year, data = panel, method = "scm")

y1 <- treated_outcomes(fit) # observed treated series
y1_0 <- synthetic_outcomes(fit) # synthetic counterfactual
Yco <- donor_outcomes(fit) # donor outcome matrix
all.equal(y1 - y1_0, unname(fit$gap))
```

Index

augment(), 19, 26
augment_scm, 3

conformal_inference, 3
conformal_inference(), 27

donor_outcomes (treated_outcomes), 39

export_json, 5

ggplot2::geom_hline(), 14, 17
ggplot2::geom_vline(), 14, 17
glance(), 4
glance.coresynth_inference, 5
glance.coresynth_inference(), 28
gsc_boot, 6
gsc_boot(), 5
gsc_ife_cpp, 7
gsc_inference, 8
gsc_inference(), 39

kalman_smoother_cpp, 9

loo_donors, 10
loo_donors(), 13

mspe_ratio_pval, 11
mspe_ratio_pval(), 5, 10, 13, 16, 17, 19, 25, 27

placebo_in_time, 12
placebo_in_time(), 10
plot(), 18, 19
plot.coresynth, 13
plot.coresynth(), 19, 20
plot.scm_design, 16
plot.scm_placebo, 16
plot.scm_placebo(), 12, 19, 20
plot_data, 18
pred, 20
pred(), 22, 24, 25

scm_design, 21
scm_fit, 24
scm_fit(), 3–6, 8, 10–12, 19–21, 27, 31, 36, 40
scm_inference, 27
scm_inner_weights_cpp, 28
scm_placebo_cpp, 29
scm_placebo_cpp(), 11, 29
scm_placebo_x_cpp, 29
scm_placebo_x_cpp(), 11
scm_weights_cpp, 30
scm_weights_cpp(), 29
sdid_estimate_cpp, 32
sdid_inference, 33
sdid_inference(), 39
sdid_placebo_cpp, 34
sdid_time_weights_cpp, 35
sdid_unit_weights_cpp, 35
si_inference, 36
si_inference(), 39
si_pcr_cpp, 37
soft_impute_cpp, 37
synthetic_outcomes (treated_outcomes), 39

tensor_unfold_cpp, 38
tidy(), 4, 26
tidy.coresynth_inference, 39
tidy.coresynth_inference(), 28
treated_outcomes, 39