Package ‘DeclareDesign’

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Title Declare and Diagnose Research Designs
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Description Researchers can characterize and learn about the properties of research designs before implementation using ‘DeclareDesign’. Ex ante declaration and diagnosis of designs can help researchers clarify the strengths and limitations of their designs and to improve their properties, and can help readers evaluate a research strategy prior to implementation and without access to results. It can also make it easier for designs to be shared, replicated, and critiqued.

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**cite_design**

*Obtain the preferred citation for a design*

**Description**

Obtain the preferred citation for a design

**Usage**

```r
cite_design(design, ...)
```

**Arguments**

- `design` a design object created using the + operator
- `...` options for printing the citation if it is a BibTeX entry
**compare_diagnoses**

**Compare Diagnoses**

**Description**

Diagnose and compare designs.

**Usage**

```r
compare_diagnoses(design1, design2, sims = 500, bootstrap_sims = 100,
merge_by_estimator = TRUE, alpha = 0.05)
```

**Arguments**

- `design1` A design or a diagnosis.
- `design2` A design or a diagnosis.
- `sims` The number of simulations, defaulting to 1000. `sims` may also be a vector indicating the number of simulations for each step in a design, as described for `simulate_design`. Used for both designs.
- `bootstrap_sims` Number of bootstrap replicates for the diagnosands to obtain the standard errors of the diagnosands, defaulting to 1000. Set to FALSE to turn off bootstrapping. Used for both designs. Must be greater or equal to 100.
- `merge_by_estimator` A logical. Whether to include `estimator_label` in the set of columns used for merging. Defaults to TRUE.
- `alpha` The significance level, 0.05 by default.

**Details**

The function `compare_diagnoses` runs a many-to-many merge matching by `estimand_label` and `term` (if present). If `merge_by_estimator` equals TRUE, `estimator_label` is also included in the merging condition. Any diagnosand that is not included in both designs will be dropped from the merge.

**Value**

A list with a data.frame of compared diagnoses and both diagnoses.

**Examples**

```r
design_a <- declare_population(N = 100, u = rnorm(N)) +
declare_potential_outcomes(
  Y_Z_0 = u,
  Y_Z_1 = u + rnorm(N, mean = 2, sd = 2)) +
declare_assignment(prob = 0.5) +
declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0)) +
declare_reveal()
```
```r

declare_estimator(Y ~ Z, estimand = "ATE")

design_b <- replace_step(design_a, step = "assignment", declare_assignment(prob = 0.3) )

comparison <- compare_diagnoses(design_a, design_b, sims = 40)
```

### compare_functions

**Compare two designs**

#### Description

Compare two designs

#### Usage

```r
compare_designs(design1, design2, format = "ansi8", pager = "off", context = -1L, rmd = FALSE)

compare_design_code(design1, design2, format = "ansi256", mode = "sidebyside", pager = "off", context = -1L, rmd = FALSE)

compare_design_summaries(design1, design2, format = "ansi256", mode = "sidebyside", pager = "off", context = -1L, rmd = FALSE)

compare_design_data(design1, design2, format = "ansi256", mode = "sidebyside", pager = "off", context = -1L, rmd = FALSE)

compare_design_estimates(design1, design2, format = "ansi256", mode = "auto", pager = "off", context = -1L, rmd = FALSE)

compare_design_estimands(design1, design2, format = "ansi256", mode = "sidebyside", pager = "off", context = -1L, rmd = FALSE)
```

#### Arguments

- **design1**: A design object, typically created using the + operator
- **design2**: A design object, typically created using the + operator
- **format**: Format (in console or HTML) options from `diffobj::diffChr`
- **pager**: Pager option from `diffobj::diffChr`
- **context**: Context option from `diffobj::diffChr` which sets the number of lines around differences that are printed. By default, all lines of the two objects are shown. To show only the lines that are different, set `context = 0`; to get one line around differences for context, set to 1.
- **rmd**: Set to `TRUE` use in Rmarkdown HTML output. NB: will not work with `LaTeX`, `Word`, or other .Rmd outputs.
- **mode**: Mode options from `diffobj::diffChr`
Examples

design1 <- declare_population(N = 100, u = rnorm(N)) +
  declare_potential_outcomes(Y ~ Z + u) +
  declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0)) +
  declare_sampling(n = 75) +
  declare_assignment(m = 50) +
  declare_reveal(Y, Z) +
  declare_estimator(Y ~ Z, estimand = "ATE")

design2 <- declare_population(N = 200, u = rnorm(N)) +
  declare_potential_outcomes(Y ~ 0.5*Z + u) +
  declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0)) +
  declare_sampling(n = 100) +
  declare_assignment(m = 25) +
  declare_reveal(Y, Z) +
  declare_estimator(Y ~ Z, model = lm_robust, estimand = "ATE")

compare_designs(design1, design2)
compare_design_code(design1, design2)
compare_design_summaries(design1, design2)
compare_design_data(design1, design2)
compare_design_estimates(design1, design2)
compare_design_estimands(design1, design2)

---

DeclareDesign package

Description
The four main types of functions are to declare a step, to combine steps into designs, and to manipulate designs and designers (functions that return designs).

Design Steps

- declare_population  Population step
- declare_potential_outcomes  Potential outcomes step
- declare_sampling  Sampling step
- declare_assignment  Assignment step
- declare_reveal  Reveal outcomes step
- declare_estimand  Estimand step
- declare_estimator  Estimator step
**Design Objects**

+ Add steps to create a design
  
  *draw_data* Simulate the DGP
  
  *run_design* Simulate the DGP with estimands/estimators

  *diagnose_design* Diagnose a design

  *cite_design* Cite a design

**Design Editing**

  *modify_design* Add, delete or replace a step
  
  *redesign* Modify local variables within a design (advanced)

**Designers**

  *expand_design* Generate designs from a designer

  *designs* See also the DesignLibrary package for designers to use

---

## declare_assignment

*Declare assignment procedure*

### Description

Declare assignment procedure

### Usage

```
declare_assignment(..., handler = assignment_handler, label = NULL)
```

```
assignment_handler(data, ..., assignment_variable = "Z",
                   append_probabilities_matrix = FALSE)
```

### Arguments

- `...` arguments to be captured, and later passed to the handler
- `handler` a tidy-in, tidy-out function
- `label` a string describing the step
- `data` A data.frame.
- `assignment_variable` Name for assignment variable (quoted). Defaults to "Z". Argument to be used with default handler.
- `append_probabilities_matrix` Should the condition probabilities matrix be appended to the data? Defaults to FALSE. Argument to be used with default handler.
declare_assignment

Details

declare_assignment can work with any assignment_function that takes data and returns data. The
default handler is conduct_ra from the randomizr package. This allows quick declaration of many
assignment schemes that involve simple or complete random assignment with blocks and clusters.
The arguments to conduct_ra can include N, block_var, clust_var, m, m_each, prob, prob_each,
block_m, block_m_each, block_prob, block_prob_each, num_arms, and conditions. The argu-
ments you need to specify are different for different designs. For details see the help files for
complete_ra, block_ra, cluster_ra, or block_and_cluster_ra.

By default, declare_assignment declares a simple random assignment with probability 0.5.
Custom assignment handlers should augment the data frame with an appropriate column for the
assignment(s).

Value

A function that takes a data.frame as an argument and returns a data.frame with additional columns
appended including an assignment variable and (optionally) probabilities of assignment.

Examples

# Default handler delegates to conduct_ra

# Declare assignment of m units to treatment
my_assignment <- declare_assignment(m = 50)

# Declare assignment specifying assignment probability for each block
my_assignment <- declare_assignment(block_prob = c(1/3, 2/3), blocks = female)

# Declare assignment of clusters with probability 1/4
my_assignment <- declare_assignment(
  prob = 1/4,
  clusters = classrooms,
  assignment_variable = "X1"
)

# Declare factorial assignment (Approach 1):
# Use complete random assignment to assign T1 and then use T1 as a block to assign T2.
design <- declare_population(N = 4) +
  declare_assignment(assignment_variable = "T1") +
  declare_assignment(blocks = T1, assignment_variable = "T2")
draw_data(design)

# Declare factorial assignment (Approach 2):
# Assign to four conditions and then split into separate factors.
design <- declare_population(N = 4) +
  declare_assignment(conditions = 1:4) +
  declare_step(fabricate, T1 = as.numeric(Z %in% 2:3), T2 = as.numeric(Z %in% 3:4))
draw_data(design)

# Declare assignment using custom handler
custom_assignment <- function(data, assignment_variable = "X") {
  data[, assignment_variable] <- rbinom(n = nrow(data),
    size = 1,
    prob = 0.5)
  data
}

declare_population(N = 6) +
  declare_assignment(handler = custom_assignment, assignment_variable = "X")

declare_design  

**Description**

Declare a design

**Usage**

```r
## S3 method for class 'dd'
lhs + rhs

## S3 method for class 'design'
print(x, verbose = TRUE, ...)

## S3 method for class 'design'
summary(object, verbose = TRUE, ...)
```

**Arguments**

- `lhs`  
  A step in a research design, beginning with a function that draws the population. Steps are evaluated sequentially. With the exception of the first step, all steps must be functions that take a `data.frame` as an argument and return a `data.frame`. Typically, many steps are declared using the `declare_` functions, i.e., `declare_population`, `declare_population`, `declare_sampling`, `declare_potential_outcomes`, `declare_estimand`, `declare_assignment`, and `declare_estimator`.

- `rhs`  
  A second step in a research design

- `x`  
  a design object, typically created using the `+` operator

- `verbose`  
  an indicator for printing a long summary of the design, defaults to `TRUE`

- `...`  
  optional arguments to be sent to summary function

- `object`  
  a design object created using the `+` operator
Details

Users can supply three kinds of functions to create a design:
1. Data generating functions. These include population, assignment, and sampling functions.
2. Estimand functions.
3. Estimator functions.

The location of the estimand and estimator functions in the pipeline of functions determine *when* the values of the estimand and estimator are calculated. This allows users to, for example, differentiate between a population average treatment effect and a sample average treatment effect by placing the estimand function before or after sampling.

Design objects declared with the + operator can be investigated with a series of post-declaration commands, such as `draw_data`, `draw_estimands`, `draw_estimates`, and `diagnose_design`.

The print and summary methods for a design object return some helpful descriptions of the steps in your research design. If randomizr functions are used for any assignment or sampling steps, additional details about those steps are provided.

Value

a list of two functions, the `design_function` and the `data_function`. The `design_function` runs the design once, i.e. draws the data and calculates any estimates and estimands defined in ... , returned separately as two `data.frame`'s. The `data_function` runs the design once also, but only returns the final data.

Examples

```r
my_population <- declare_population(N = 500, noise = rnorm(N))
my_potential_outcomes <- declare_potential_outcomes(Y ~ Z + noise)
my_sampling <- declare_sampling(n = 250)
my_assignment <- declare_assignment(m = 25)
my_estimand <- declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0))
my_estimator <- declare_estimator(Y ~ Z, estimand = my_estimand)
my_mutate <- declare_step(dplyr::mutate, noise_sq = noise^2)
my_reveal <- declare_reveal()

design <- my_population + my_potential_outcomes + my_sampling +
         my_estimand + my_mutate +
         my_assignment + my_reveal + my_estimator

design
df <- draw_data(design)
```
estimates <- draw_estimates(design)
estimands <- draw_estimands(design)

# You can add steps to a design
design <- my_population + my_potential_outcomes
design + my_sampling

# Special Cases
# You may wish to have a design with only one step:
design <- my_population + NULL
design

## Not run:
diagnosis <- diagnose_design(design)
summary(diagnosis)
## End(Not run)

my_population <- declare_population(N = 500, noise = rnorm(N))

my_potential_outcomes <- declare_potential_outcomes(
  Y_Z_0 = noise, Y_Z_1 = noise +
  rnorm(N, mean = 2, sd = 2))

my_sampling <- declare_sampling(n = 250)

my_assignment <- declare_assignment(m = 25)

my_estimand <- declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0))

my_estimator <- declare_estimator(Y ~ Z, estimand = my_estimand)

my_mutate <- declare_step(dplyr::mutate, noise_sq = noise ^ 2)

my_reveal <- declare_reveal()

design <- my_population +
  my_potential_outcomes +
  my_sampling +
  my_estimand +
  my_mutate +
  my_assignment +
  my_reveal +
  my_estimator

summary(design)
**declare_estimand**

**Declare estimand**

**Description**

Declares estimands. Estimands are the subjects of inquiry and can be estimated by an estimator.

**Usage**

```r
declare_estimand(..., handler = estimand_handler, label = "estimand")
```

```r
declare_estimands(..., handler = estimand_handler, label = "estimand")
```

```r
estimand_handler(data, ..., subset = NULL, term = FALSE, label)
```

**Arguments**

- `...`: arguments to be captured, and later passed to the handler
- `handler`: a tidy-in, tidy-out function
- `label`: a string describing the step
- `data`: a data.frame
- `subset`: a subset expression
- `term`: TRUE/FALSE

**Details**

For the default diagnosands, the return value of the handler should have `estimand_label` and `estimand` columns.

If `term` is TRUE, the names of `...` will be returned in a `term` column, and `estimand_label` will contain the step label. This can be used as an additional dimension for use in diagnosis.

**Value**

a function that accepts a data.frame as an argument and returns a data.frame containing the value of the estimand.

**Examples**

# Set up a design stub for use in examples:

```r
my_population <- declare_population(N = 100, X = rnorm(N))
my_potential_outcomes <- declare_potential_outcomes(
  Y ~ (.25 + X) * Z + rnorm(N))
my_assignment <- declare_assignment(m = 50)
design_stub <- my_population + my_potential_outcomes + my_assignment +
```
declare_reveal()

# Get example data to compute estimands on
dat <- draw_data(design_stub)

# 1. Single estimand
# Declare an average treatment effect (ATE) estimand
my_estimand_ATE <- declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0))
my_estimand_ATE(dat)

# or a conditional estimand
my_estimand_ATT <- declare_estimand(ATT = mean(Y_Z_1 - Y_Z_0),
subset = (Z == 1))
my_estimand_ATT(dat)

# Add estimands to a design along with estimators that reference them
my_estimator <- declare_estimator(Y ~ Z,
estimand = my_estimand_ATE, label = "estimator")
design_one <- design_stub + my_estimand_ATE + my_estimator
draw_estimands(design_one)

# 2. Multiple estimands
# You can also specify multiple estimands for a single estimator
# With multiple estimands, you can use one estimator for both...
my_estimator_two <- declare_estimator(Y ~ Z,
estimand = c(my_estimand_ATE, my_estimand_ATT))
design_two <- design_stub + my_estimand_ATE +
my_estimand_ATT + my_estimator_two
draw_estimands(design_two)

# 3. Paired estimands / estimators from a single model
# For convenience you can also declare multiple estimands
# simultaneously and connect these to the corresponding
# terms for estimates used in the mode.
# Name your estimands the term name they get in your estimator, and set `term = TRUE`
estimands_regression <- declare_estimand(
  `(Intercept)` = mean(Y_{Z=0}),
  `Z` = mean(Y_{Z=1} - Y_{Z=0}),
  term = TRUE,
  label="Regression_Estimands"
)

# For the model based estimator, specify the estimand as usual, but also set `term = TRUE`
estimators_regression <- declare_estimator(
  Y ~ Z,
  estimand = estimands_regression,
  model = lm,
  term = TRUE
)
design_regression <- design_stub + estimands_regression + estimators_regression
run_design(design_regression)

# ----------
# 4. Custom estimand function
# ----------
# You can declare more complex estimands by defining custom estimand functions:
estimand_function <- function(data, label) {
  ret <- with(data, median(Y_{Z=1} - Y_{Z=0}))
  data.frame(estimand_label = label, estimand = ret, stringsAsFactors = FALSE)
}
estimand_custom <- declare_estimand(handler = estimand_function, label = "medianTE")
estimand_custom(dat)

# Use with custom estimators
estimator_function <- function(data){
  data.frame(estimate = with(data, median(Y)))
}
estimator_custom <-
declare_estimator(handler = tidy_estimator(estimator_function),
estimand = estimand_custom)
design_custom <- design_stub + estimand_custom + estimator_custom
run_design(design_custom)

# 5. Batch estimands and estimators
# ----------
# You can declare a group of estimands with distinct labels
# in one go and link them manually to a group of estimators.
# In this case you can add a \code{term} argument to the
# custom estimators to identify them.

f1 <- function(data) {
  data.frame(estimand_label = c("control", "ate"),
             estimand = with(data, c(mean(Y_Z_0), mean(Y_Z_1 - Y_Z_0))),
             stringsAsFactors = FALSE)
}
estimands <- declare_estimand(handler = f1)

f2 <- function(data) data.frame(estimate = with(data,
              c(mean(Y[Z == 0]), mean(Y[Z == 1]) - mean(Y[Z == 0]))),
              term = 1:2)
estimators <- declare_estimator(handler = tidy_estimator(f2),
              estimand = c("control", "ate"), label = "custom")
design <- design_stub + estimands + estimators

## Not run: diagnose_design(design, sims = 20, bootstrap_sims = FALSE,
diagnosands = declare_diagnosands(
  select = c(mean_estimate, mean_estimand)))

## End(Not run)

---

**declare_estimator**  
*Declare estimator*

**Description**

Declares an estimator which generates estimates and associated statistics.

**Usage**

```r
declare_estimator(..., handler = estimator_handler,
                  label = "estimator")
```

```r
declare_estimators(..., handler = estimator_handler,
                    label = "estimator")
```
tidy_estimator(estimator_function)

model_handler(data, ..., model = estimatr::difference_in_means,
              term = FALSE)

estimator_handler(data, ..., model = estimatr::difference_in_means,
              term = FALSE, estimand = NULL, label)

Arguments

... arguments to be captured, and later passed to the handler
handler a tidy-in, tidy-out function
label a string describing the step
estimator_function
  A function that takes a data.frame as an argument and returns a data.frame with
  the estimates, summary statistics (i.e., standard error, p-value, and confidence
  interval) and a label.

data a data.frame
model A model function, e.g. lm or glm. By default, the model is the difference_in_means
        function from the estimatr package.
term Symbols or literal character vector of term that represent quantities of interest,
        i.e. Z. If FALSE, return the first non-intercept term; if TRUE return all term. To
        escape non-standard-evaluation use !!.
estimand a declare_estimand step object, or a character label, or a list of either

Details

tidy_estimator takes an untidy estimation function, and returns a tidy handler which accepts
standard labeling options.

The intent here is to factor out the estimator/estimand labeling so that it can be reused by other
model handlers.

Value

A function that accepts a data.frame as an argument and returns a data.frame containing the value
of the estimator and associated statistics.

Custom Estimators

estimator_functions implementations should be tidy (accept and return a data.frame)
model implementations should at a minimum provide S3 methods for summary and confint.
Examples

# Declare estimand
my_estimand <- declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0))

# Declare estimator using the default handler using 'difference_in_means'
# estimator from 'estimatr' package. Returns the first non-intercept term
# as estimate
my_estimator_dim <- declare_estimator(Y ~ Z, estimand = "ATE", label = "DIM")

# Use lm function from base R
my_estimator_lm <- declare_estimator(Y ~ Z, estimand = "ATE",
  model = lm, label = "LM")

# Use lm_robust (linear regression with robust standard errors) from
# 'estimatr' package
my_estimator_lm_rob <- declare_estimator(
  Y ~ Z,
  estimand = "ATE",
  model = lm_robust,
  label = "LM_Robust"
)

# Set 'term' if estimate of interest is not the first non-intercept variable
my_estimator_lm_rob_x <- declare_estimator(
  Y ~ X + Z,
  estimand = my_estimand,
  term = "Z",
  model = lm_robust
)

# Use glm from base R
my_estimator_glm <- declare_estimator(
  Y ~ X + Z,
  family = "gaussian",
  estimand = my_estimand,
  term = "Z",
  model = glm
)

# A probit
estimator_probit <- declare_estimator(
  Y ~ Z,
  model = glm,
  family = binomial(link = "probit"),
  term = "Z"
)

# Declare estimator using a custom handler

# Define your own estimator and use the \texttt{tidy_estimator} function for labeling
# Must have `data` argument that is a data.frame
my_estimator_function <- function(data){
  data.frame(estimate = with(data, mean(Y)))
}

my_estimator_custom <- declare_estimator(
  handler = tidy_estimator(my_estimator_function),
  estimand = my_estimand
)

# Customize labeling

my_estimator_function <- function(data){
  data.frame(
    estimator_label = "foo",
    estimand_label = "bar",
    estimate = with(data, mean(Y)),
    n = nrow(data),
    stringsAsFactors = FALSE
  )
}

my_estimator_custom2 <- declare_estimator(handler = my_estimator_function)

# Examples

# First, set up the rest of a design
set.seed(42)

design_def <-
  declare_population(N = 100, X = rnorm(N), W = rexp(N, 1), noise = rnorm(N)) +
  declare_potential_outcomes(Y ~ .25 * Z + noise) +
  declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0)) +
  declare_assignment(m = 50) +
  declare_reveal() +
  my_estimator_dim

draw_estimates(design_def)

# Can also use declared estimator on a data.frame

dat <- draw_data(design_def)
my_estimator_dim(dat)

# ---------
# 2. Using existing estimators
# ---------

design <- replace_step(design_def, my_estimator_dim, my_estimator_lm_rob)
draw_estimates(design)

design <- replace_step(design_def, my_estimator_dim, my_estimator_lm)
draw_estimates(design)
design <- replace_step(design_def, my_estimator_dim, my_estimator_glm)
draw_estimates(design)

# 3. Using custom estimators

design <- replace_step(design_def, my_estimator_dim, my_estimator_custom)
draw_estimates(design)

# The names in your custom estimator return should match with
# your diagnosands when diagnosing a design
my_median <- function(data) data.frame(med = median(data$Y))

my_estimator_median <- declare_estimator(
  handler = tidy_estimator(my_median),
  estimand = my_estimand
)
design <- replace_step(design_def, my_estimator_dim, my_estimator_median)
draw_estimates(design)

my_diagnosand <- declare_diagnosands(med_to_estimand = mean(med - estimand),
  keep_defaults = FALSE)

## Not run:
diagnose_design(design, diagnosands = my_diagnosand, sims = 5,
  bootstrap_sims = FALSE)
## End(Not run)

# 4. Multiple estimators per estimand

design_two <- insert_step(design_def, my_estimator_lm,
  after = my_estimator_dim)
draw_estimates(design_two)

## Not run:
diagnose_design(design_two, sims = 5, bootstrap_sims = FALSE)
## End(Not run)

---

**Declare the size and features of the population**

---

**declare_population**

**Description**

Declare the size and features of the population

**Usage**

`declare_population(..., handler = fabricate, label = NULL)`

**Arguments**

- `...` arguments to be captured, and later passed to the handler
- `handler` a tidy-in, tidy-out function
- `label` a string describing the step

**Value**

A function that returns a data.frame.

**Examples**

```r
# Default handler is fabricatr::fabricate

# Declare a single-level population with no covariates
my_population <- declare_population(N = 100)

# Declare a population from existing data
my_population <- declare_population(sleep)

# Declare a single-level population with a covariate
my_population <- declare_population(
  N = 6,
  gender = draw_binary(N, prob = 0.5),
  height_ft = rnorm(N, mean = 5 + 4/12 + 4/12 * gender, sd = 3/12)
)
my_population()

# Declare a two-level hierarchical population
# containing cities within regions and a
# pollution variable defined at the city level

my_population <- declare_population(
  regions = add_level(N = 5),
  cities = add_level(N = 10, pollution = rnorm(N, mean = 5))
)
my_population()

# Declare a population using a custom function

my_population_function <- function(N) {
  data.frame(u = rnorm(N))
}
```
my_population_custom <- declare_population(N = 10, handler = my_population_function)
my_population_custom()

---

**declare_potential_outcomes**

Declare potential outcomes

**Description**

Declare potential outcomes

**Usage**

```
declare_potential_outcomes(..., handler = potential_outcomes_handler,
  label = NULL)
```

```
potential_outcomes.formula(formula, conditions = c(0, 1),
  assignment_variables = "Z", data, level = NULL,
  label = outcome_variable)
```

```
potential_outcomes.NULL(formula = stop("Not provided"), ..., data,
  level = NULL)
```

**Arguments**

- `...`: arguments to be captured, and later passed to the handler
- `handler`: a tidy-in, tidy-out function
- `label`: a string describing the step
- `formula`: a formula to calculate potential outcomes as functions of assignment variables.
- `conditions`: see `expand_conditions`. Provide values (e.g. `conditions = 1:4`) for a single assignment variable. If multiple assignment variables, provide named list (e.g. `conditions = list(Z1 = 0:1, Z2 = 0:1)`). Defaults to `0:1` if no conditions provided.
- `assignment_variables`: The name of the assignment variable. Generally not required as names are taken from `conditions`.
- `data`: a data.frame
- `level`: a character specifying a level of hierarchy for fabricate to calculate at
**Details**

A `declare_potential_outcomes` declaration returns a function. The function takes and returns a data frame with potential outcomes columns appended. These columns describe the outcomes that each unit would express if that unit were in the corresponding treatment condition.

Declaring a potential outcomes function requires postulating a particular causal process. One can then assess how designs fare under the postulated process. Multiple processes can be considered in a single design or across design. For instance one could declare two processes that rival theories would predict.

Potential outcomes can be declared as separate variables or by using a formula. See examples below.

**Value**

a function that returns a data.frame

**Examples**

```r
# Declare potential outcomes using default handler

# There are two ways of declaring potential outcomes:
# As separate variables

my_potential_outcomes <- declare_potential_outcomes(
  Y_0 = .05,
  Y_1 = .30 + .01 * age
)

# Using a formula

my_potential_outcomes <- declare_potential_outcomes(
  formula = Y ~ .05 + .25 * Z + .01 * age * Z
)

# 'conditions' defines the "range" of the potential outcomes function

my_potential_outcomes <- declare_potential_outcomes(
  formula = Y ~ .05 + .25 * Z + .01 * age * Z,
  conditions = 1:4
)

# Multiple assignment variables can be specified in 'conditions'. For example,
# in a 2x2 factorial potential outcome:

my_potential_outcomes <- declare_potential_outcomes(
  formula = Y ~ .05 + .25 * Z1 + .01 * age * Z2,
  conditions = list(Z1 = 0:1, Z2 = 0:1)
)

# You can also declare potential outcomes using a custom handler

my_po_function <- function(data) {
  data$Y_treated <- rexp(nrow(data), .2)
}
```
declarereveal

data$Y\textunderscore\text{untreated} \leftarrow \text{rexp}(\text{nrow}(\text{data}), .4)
data
}
custom\textunderscore\text{potential} \leftarrow \text{declare\_potential\_outcomes}(\text{handler} = \text{my\_po\_function})

---

**declare_reveal**

*Declare a reveal outcomes step*

**Description**

Potential outcomes declarations indicate what outcomes would obtain for different possible values of assignment variables. To reveal actual outcomes we combine assignments with potential outcomes. **declare_reveal** provides information on how this revelation should be implemented, identifying the relevant assignment variables (for example created by **declare_assignment**) and outcome variables. Revelation steps are usefully included after declaration of all assignments of conditions required to determine the realized outcome. If a revelation is not declared DeclareDesign will try to guess appropriate revelations though explicit revelation is recommended.

**Usage**

```r
declare_reveal(..., handler = reveal_outcomes_handler, label = NULL)
reveal_outcomes_handler(data = NULL, outcome_variables = Y,
assignment_variables = Z, attrition_variables = NULL, ...)
```

**Arguments**

- `...`: arguments to be captured, and later passed to the handler
- `handler`: a tidy-in, tidy-out function
- `label`: a string describing the step
- `data`: A data.frame containing columns for assignment and potential outcomes.
- `outcome_variables`: The outcome prefix(es) of the potential outcomes.
- `assignment_variables`: Unquoted name(s) of the assignment variable(s).
- `attrition_variables`: Unquoted name of the attrition variable.

**Details**

declare_reveal declares how outcomes should be realized. A "revelation" uses the random assignment to pluck out the correct potential outcomes (Gerber and Green 2012, Chapter 2). If you create a simple design (with assignment variable `Z` and outcome variable `Y`) with the `+` operator but omit a reveal declaration, DeclareDesign will attempt to insert a revelation step automatically. If you
have multiple outcomes to reveal or different names for the outcome or assignment variables, use `declare_reveal` to customize which outcomes are revealed. Revelation requires that every named outcome variable is a function of every named assignment variable within a step. Thus if multiple outcome variables depend on different assignment variables, multiple revelations are needed.

**Examples**

```r
my_population <- declare_population(N = 100, noise = rnorm(N))
my_potential_outcomes <- declare_potential_outcomes(
  Y_Z_0 = noise, Y_Z_1 = noise +
  rnorm(N, mean = 2, sd = 2))
my_assignment <- declare_assignment(m = 50)
my_reveal <- declare_reveal()
design <- my_population +
  my_potential_outcomes +
  my_assignment +
  my_reveal
design

# Here the + operator results in the same design being
# created, because it automatically adds a declare_reveal step.
design <- my_population + my_potential_outcomes + my_assignment

# Declaring multiple assignment variables or multiple outcome variables
population <- declare_population(N = 10)
potentials_1 <- declare_potential_outcomes(Y1 ~ Z)
potentials_2 <- declare_potential_outcomes(Y2 ~ 1 + 2*Z)
potentials_3 <- declare_potential_outcomes(Y3 ~ 1 - X*Z, conditions = list(X = 0:1, Z = 0:1))
assignment_Z <- declare_assignment(assignment_variable = "Z")
assignment_X <- declare_assignment(assignment_variable = "X")
reveal_1 <- declare_reveal(outcome_variables = c("Y1", "Y2"), assignment_variables = "Z")
reveal_2 <- declare_reveal(outcome_variables = c("Y3", assignment_variables = c("X", "Z"))

# Note here that the reveal cannot be done in one step, e.g. by using
# declare_reveal(outcome_variables = c("Y1", "Y2", "Y3"),
# assignment_variables = c("X", "Z"))
# The reason is that in each revelation all outcome variables should be a
# function of all assignment variables.
# declare_reveal can also be used to declare outcomes that include attrition
population <- declare_population(N = 100, age = sample(18:95, N, replace = TRUE))
potential_outcomes_Y <- declare_potential_outcomes(Y ~ .25 * Z + .01 * age * Z)
```
assignment <- declare_assignment(m = 25)

potential_outcomes_attrition <-
    declare_potential_outcomes(R ~ rbinom(n = N, size = 1, prob = pnorm(Y_Z_0)))

reveal_attrition <- declare_reveal(outcome_variables = "R")
reveal_outcomes <- declare_reveal(outcome_variables = "Y", attrition_variables = "R")

my_design <- population + potential_outcomes_Y + potential_outcomes_attrition +
    my_assignment + reveal_attrition + reveal_outcomes

**declare_sampling**  
*Declare sampling procedure*

**Description**  
Declare sampling procedure

**Usage**  
declare_sampling(..., handler = sampling_handler, label = NULL)

sampling_handler(data, ..., sampling_variable = "S")

**Arguments**

...  
arguments to be captured, and later passed to the handler

handler  
a tidy-in, tidy-out function

label  
a string describing the step

data  
A data.frame.

sampling_variable  
The prefix for the sampling inclusion probability variable.

**Details**

declare_sampling can work with any sampling_function that takes data and returns data. The default handler is draw_rs from the randomizr package. This allows quick declaration of many sampling schemes that involve strata and clusters.

The arguments to draw_rs can include N, strata, clusters, n, prob, strata_n, and strata_prob. The arguments you need to specify are different for different designs.

Note that declare_sampling works similarly to declare_assignment a key difference being that declare_sampling functions subset data to sampled units rather than simply appending an indicator for membership of a sample (assignment). If you need to sample but keep the dataset use declare_assignment and define further steps (such as estimation) with respect to subsets defined by the assignment.

For details see the help files for complete_rs, strata_rs, cluster_rs, or strata_and_cluster_rs
Value

A function that takes a data.frame as an argument and returns a data.frame subsetted to sampled observations and (optionally) augmented with inclusion probabilities and other quantities.

Examples

# Default handler is `draw_rs` from `randomizr` package

# Simple random sampling
my_sampling <- declare_sampling(n = 50)

# Stratified random sampling
my_stratified_sampling <- declare_sampling(strata = female)

# Custom random sampling functions

my_sampling_function <- function(data, n=nrow(data)) {
  data[sample(n,n,replace=TRUE), , drop=FALSE]
}

my_sampling_custom <- declare_sampling(handler = my_sampling_function)

my_sampling_custom(sleep)

---

**declare_step**  
Declare a custom step

Description

With declare_step, you can include any function that takes data as one of its arguments and returns data in a design declaration. The first argument is always a "handler", which is the name of the data-in, data-out function. For handy data manipulations use declare_step(fabricate,...).

Usage

```r
declare_step(..., handler = function(data, ...f, ...) ...f(data, ...),
  label = NULL)
```

Arguments

- `...` arguments to be captured, and later passed to the handler
- `handler` a tidy-in, tidy-out function
- `label` a string describing the step

Value

A function that returns a data.frame.
Examples

```r
population <- declare_population(N = 5, noise = rnorm(N))
manipulate <- declare_step(fabricate, noise_squared = noise^2, zero = 0)

design <- population + manipulate
draw_data(design)
```

deprecated

### Deprecated functions

The function `get_estimands` has been replaced with `draw_estimands`.

Usage

```r
get_estimands(...)
```

Arguments

... options sent to the old version of `get_estimands`.

diagnosand_handler

### Declare diagnosands

**Description**

Declare diagnosands

**Usage**

```r
diagnosand_handler(data, ..., select, subtract, keep_defaults = TRUE, subset = NULL, alpha = 0.05, label)
```

```r
declare_diagnosands(..., handler = diagnosand_handler, label = NULL)
```
**diagnosand_handler**

**Arguments**

- `data` A data.frame.
- `...` A set of new diagnosands.
- `select` A set of the default diagnosands to report e.g., `select = c(bias, rmse)`.
- `subtract` A set of the default diagnosands to exclude e.g., `subtract = c(bias, rmse)`. Do not provide values for both `select` and `subtract`.
- `keep_defaults` A flag for whether to report the default diagnosands. Defaults to `TRUE`.
- `subset` A subset of the simulations data frame within which to calculate diagnosands e.g. `subset = p.value < .05`.
- `alpha` Alpha significance level. Defaults to `.05`.
- `label` Label for the set of diagnosands.
- `handler` a tidy-in, tidy-out function

**Details**

If `term` is `TRUE`, the names of ... will be returned in a `term` column, and `estimand_label` will contain the step label. This can be used as an additional dimension for use in diagnosis.

Diagnosands summarize the simulations generated by `diagnose_design` or `simulate_design`. Typically, the columns of the resulting simulations data.frame include the following variables: estimate, std.error, p.value, conf.low, conf.high, and estimand. Many diagnosands will be a function of these variables.

By default (`keep_defaults = TRUE`), a set of common diagnosands are reported:

- `bias = mean(estimate - estimand)`
- `rmse = sqrt(mean((estimate - estimand)^2))`
- `power = mean(p.value < .05)`
- `coverage = mean(estimand <= conf.high & estimand >= conf.low)`
- `mean_estimate = mean(estimate)`
- `sd_estimate = sd(estimate)`
- `type_s_rate = mean((sign(estimate) != sign(estimand))[p.value < alpha])`
- `mean_estimand = mean(estimand)`

**Value**

A function that returns a data.frame

**Examples**

```r
my_population <- declare_population(N = 500, noise = rnorm(N))

my_potential_outcomes <- declare_potential_outcomes(
  Y_Z_0 = noise, Y_Z_1 = noise + rnorm(N, mean = 2, sd = 2))

my_assignment <- declare_assignment()
```
my_estimand <- declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0))
my_estimator <- declare_estimator(Y ~ Z, estimand = my_estimand)
my_reveal <- declare_reveal()

design <- my_population + my_potential_outcomes + my_estimand + my_assignment + my_reveal + my_estimator

## Not run:
# using built-in defaults:
diagnosis <- diagnose_design(design)
diagnosis

## End(Not run)

# You can select a set of those diagnosands via the \code{select} argument e.g.,
my_diagnosands <- declare_diagnosands(select = c(bias, rmse))

## Not run:
diagnosis <- diagnose_design(design, diagnosands = my_diagnosands)
diagnosis

## End(Not run)
## Not run:
## Not run:
design <- set_diagnosands(design, diagnosands = my_diagnosands)
diagnosis <- diagnose_design(design)
diagnosis

## End(Not run)

# Alternatively, you can report all of the default diagnosands and subtract a subset of them e.g.,
my_diagnosands <- declare_diagnosands(subtract = type_s_rate)

## Not run:
diagnosis <- diagnose_design(design, diagnosands = my_diagnosands)
diagnosis

## End(Not run)
## Not run:
## Not run:
design <- set_diagnosands(design, diagnosands = my_diagnosands)
diagnosis <- diagnose_design(design)
diagnosis

## End(Not run)

# You can add your own diagnosands in addition to or instead of the defaults e.g.,
my_diagnosands <-
declare_diagnosands(median_bias = median(estimate - estimand))

## Not run:
## diagnose_design

Generates diagnosands from a design or simulations of a design.

```r

diagnosis <- diagnose_design(design, diagnosands = my_diagnosands)
diagnosis

## End(Not run)
## Not run:
design <- set_diagnosands(design, diagnosands = my_diagnosands)
diagnosis <- diagnose_design(design)
diagnosis

## End(Not run)

# or to report only \code{median_bias}

my_diagnosands <-
  declare_diagnosands(median_bias = median(estimate - estimand),
                      keep_defaults = FALSE)

## Not run:
diagnosis <- diagnose_design(design, diagnosands = my_diagnosands)
diagnosis

## End(Not run)
## Not run:
design <- set_diagnosands(design, diagnosands = my_diagnosands)
diagnosis <- diagnose_design(design)
diagnosis

## End(Not run)

# Below is the code that makes the default diagnosands.
# You can use these as a model when writing your own diagnosands.

default_diagnosands <- declare_diagnosands(
bias = mean(estimate - estimand),
rmse = sqrt(mean((estimate - estimand) ^ 2)),
power = mean(p.value < alpha),
coverage = mean(estimand <= conf.high & estimand >= conf.low),
mean_estimate = mean(estimate),
sd_estimate = sd(estimate),
mean_se = mean(std.error),
type_s_rate = mean((sign(estimate) != sign(estimand))[p.value < alpha]),
mean_estimand = mean(estimand)
)

---

diagnose_design  Diagnose the design

Description

Generates diagnosands from a design or simulations of a design.
Usage

```r
diagnose_design(..., diagnosands = NULL, sims = 500,
   bootstrap_sims = 100, add_grouping_variables = NULL)

diagnose_designs(..., diagnosands = NULL, sims = 500,
   bootstrap_sims = 100, add_grouping_variables = NULL)
```

Arguments

- `...`: A design or set of designs typically created using the `+` operator, or a `data.frame` of simulations, typically created by `simulate_design`.
- `diagnosands`: A set of diagnosands created by `declare_diagnosands`. By default, these include bias, root mean-squared error, power, frequentist coverage, the mean and standard deviation of the estimate(s), the "type S" error rate (Gelman and Carlin 2014), and the mean of the estimand(s).
- `sims`: The number of simulations, defaulting to 500. `sims` may also be a vector indicating the number of simulations for each step in a design, as described for `simulate_design`.
- `bootstrap_sims`: Number of bootstrap replicates for the diagnosands to obtain the standard errors of the diagnosands, defaulting to 100. Set to `FALSE` to turn off bootstrapping.
- `add_grouping_variables`: Variables used to generate groups of simulations for diagnosis. Added to list default list: c("design_label", "estimand_label", "estimator_label", "term")

Details

If the diagnosand function contains a `group_by` attribute, it will be used to split-apply-combine diagnosands rather than the intersecting column names.

If `sims` is named, or longer than one element, a fan-out strategy is created and used instead.

If the packages `future` and `future.apply` are installed, you can set `plan` to run multiple simulations in parallel.

Value

A list with a data frame of simulations, a data frame of diagnosands, a vector of diagnosand names, and if calculated, a data frame of bootstrap replicates.

Examples

```r
my_population <- declare_population(N = 500, noise = rnorm(N))

my_potential_outcomes <- declare_potential_outcomes(
   Y_Z_0 = noise, Y_Z_1 = noise +
   rnorm(N, mean = 2, sd = 2))

my_assignment <- declare_assignment()

my_estimand <- declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0))
```
my_reveal <- declare_reveal()

my_estimator <- declare_estimator(Y ~ Z, estimand = my_estimand)

design <- my_population +
    my_potential_outcomes +
    my_estimand +
    my_assignment +
    my_reveal +
    my_estimator

## Not run:
# using built-in defaults:
diagnosis <- diagnose_design(design)
diagnosis

## End(Not run)

# using a user-defined diagnosand
my_diagnosand <- declare_diagnosands(absolute_error = mean(abs(estimate - estimand)))

## Not run:
diagnosis <- diagnose_design(design, diagnosands = my_diagnosand)
diagnosis

generate_diagnosands(diagnosis)

generate_simulations(diagnosis)

## End(Not run)

# Using an existing data frame of simulations
## Not run:
simulations <- simulate_design(designs, sims = 2)
diagnosis <- diagnose_design(simulations_df = simulations_df)

## End(Not run)

---

diagnosis_helpers  Explore your design diagnosis

**Description**

Explore your design diagnosis

**Usage**

get_diagnosands(diagnosis)
get_simulations(diagnosis)

Arguments

diagnosis A design diagnosis created by diagnose_design.

Examples

my_population <- declare_population(N = 500, noise = rnorm(N))

my_potential_outcomes <- declare_potential_outcomes(
  Y_Z_0 = noise, Y_Z_1 = noise +
  rnorm(N, mean = 2, sd = 2))

my_assignment <- declare_assignment()

my_estimand <- declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0))

my_estimator <- declare_estimator(Y ~ Z, estimand = my_estimand)

my_reveal <- declare_reveal()

design <- my_population +
  my_potential_outcomes +
  my_estimand +
  my_assignment +
  my_reveal +
  my_estimator

## Not run:
# using built-in defaults:
diagnosis <- diagnose_design(design)
diagnosis

## End(Not run)

# using a user-defined diagnosand
my_diagnosand <- declare_diagnosands(absolute_error = mean(abs(estimate - estimand)))

## Not run:
diagnosis <- diagnose_design(design, diagnosands = my_diagnosand)
diagnosis

get_diagnosands(diagnosis)

get_simulations(diagnosis)

reshape_diagnosis(diagnosis)

## End(Not run)
**draw_functions**

*Draw data, estimates, and estimands from a design*

**Description**

Draw data, estimates, and estimands from a design.

**Usage**

```r
draw_data(design, data = NULL, start = 1, end = length(design))
draw_estimands(...) 
draw_estimates(...) 
```

**Arguments**

- `design`: A design object, typically created using the + operator.
- `data`: A data.frame object with sufficient information to get the data, estimates, estimands, an assignment vector, or a sample.
- `start`: (Defaults to 1) a scalar indicating which step in the design to begin with. By default all data steps are drawn, from step 1 to the last step of the design.
- `end`: (Defaults to `length(design)`) a scalar indicating which step in the design to finish drawing data by.
- `...`: A design or set of designs typically created using the + operator.

**Examples**

```r
design <- declare_population(N = 100, u = rnorm(N)) + 
    declare_potential_outcomes(Y ~ Z + u) + 
    declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0)) + 
    declare_sampling(n = 75) + 
    declare_assignment(m = 50) + 
    declarereveal(Y, Z) + 
    declare_estimator(Y ~ Z, estimand = "ATE")

dat <- draw_data(design)

dat_no_sampling <- draw_data(design, end = 3)

draw_estimands(design)

draw_estimates(design)
```
### expand_design

Declare a design via a designer

---

**Description**

`expand_design` easily generates a set of designs from a designer function.

**Usage**

```r
default_design(designer, ..., expand = TRUE, prefix = "design")
```

**Arguments**

- `designer`: a function which yields a design
- `...`: Options sent to the designer
- `expand`: boolean - if true, form the cross product of the `...`, otherwise recycle them
- `prefix`: prefix for the names of the designs, i.e. if you create two designs they would be named `prefix_1`, `prefix_2`

**Value**

If set of designs is size one, the design, otherwise a `by`-list of designs. Designs are given a parameters attribute with the values of parameters assigned by `expand_design`.

**Examples**

```r
## Not run:
# in conjunction with DesignLibrary
library(DesignLibrary)
designs <- expand_design(multi_arm_designer, outcome_means = list(c(3,2,4), c(1,4,1)))
# with a custom designer function
designer <- function(N) {
  pop <- declare_population(N = N, noise = rnorm(N))
  pos <- declare_potential_outcomes(Y ~ 0.20 * Z + noise)
  assign <- declare_assignment(m = N / 2)
  mand <- declare_estimand(ATE = mean(Y | Z_1 - Y | Z_0))
  mator <- declare_estimator(Y ~ Z, estimand = mand)
  pop + pos + assign + mand + mator
}
# it returns list of eight designs
designs <- expand_design(designer, N = seq(30, 100, 10))
```
# diagnose a list of designs created by expand_design or redesign
diagnosis <- diagnose_design(designs, sims = 50)

# returns a single design
large_design <- expand_design(designer, N = 200)
diagnose_large_design <- diagnose_design(large_design, sims = 50)

## End(Not run)

get_functions

Get estimates, estimands, assignment vectors, or samples from a design given data

Description
Get estimates, estimands, assignment vectors, or samples from a design given data

Usage
get_estimates(design, data = NULL, start = 1, end = length(design))
draw_assignment(design, data = NULL, start = 1, end = length(design))
draw_sample(design, data = NULL, start = 1, end = length(design))

Arguments
design A design object, typically created using the + operator
data A data.frame object with sufficient information to get the data, estimates, estimands, an assignment vector, or a sample.
start (Defaults to 1) a scalar indicating which step in the design to begin with. By default all data steps are drawn, from step 1 to the last step of the design.
end (Defaults to length(design)) a scalar indicating which step in the design to finish with.

Examples

design <- declare_population(N = 100, u = rnorm(N)) +
declare_outcomes(Y ~ Z + u) +
declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0)) +
declare_sampling(n = 75) +
declare_assignment(m = 50) +
declare_reveal(Y, Z) +
declare_estimator(Y ~ Z, estimand = "ATE")
dat <- draw_data(design)
draw_data(design, data = dat, start = 2)
get_estimates(design, data = dat)
draw_assignment(design, data = dat)
draw_sample(design, data = dat)

modify_design

Modify a design after the fact

Description
Insert, delete and replace steps in an (already declared) design object.

Usage
insert_step(design, new_step, before, after)
delete_step(design, step)
replace_step(design, step, new_step)

Arguments
design A design object, usually created using the + operator, expand_design, or the design library.
new_step The new step; Either a function or a partial call.
before The step before which to add steps.
after The step after which to add steps.
step The quoted label of the step to be deleted or replaced.

Details
See modify_design for details.

Value
A new design object.
Examples

```r
my_population <- declare_population(N = 100, noise = rnorm(N), label = "my_pop")

my_potential_outcomes <-
    declare_potential_outcomes(Y_Z_0 = noise,
                               Y_Z_1 = noise + rnorm(N, mean = 2, sd = 2))

my_assignment <- declare_assignment(m = 50)
my_assignment_2 <- declare_assignment(m = 25)

design <- my_population + my_potential_outcomes + my_assignment

design

insert_step(design, declare_step(dplyr::mutate, income = noise^2), after = my_assignment)
insert_step(design, declare_step(dplyr::mutate, income = noise^2), before = my_assignment)

# If you are using a design created by a designer, for example from
# the DesignLibrary package, you will not have access to the step
# objects. Instead, you can always use the label of the step.

# get the labels for the steps
names(design)

insert_step(design, declare_sampling(n = 50), after = "my_pop")

delete_step(design, my_assignment)
replace_step(design, my_assignment, declare_step(dplyr::mutate, words = "income"))
```

Description

Explore your design
Print code to recreate a design

Usage

```
print_code(design)
```

Arguments

```
design A design object, typically created using the + operator
```
Examples

```r
design <-
  declare_population(N = 500, noise = rnorm(N)) +
  declare_potential_outcomes(Y ~ noise + Z * rnorm(N, 2, 2)) +
  declare_sampling(n = 250) +
  declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0)) +
  declare_step(dplyr::mutate, noise_sq = noise^2) +
  declare_assignment(m = 25) +
  declare_reveal() +
  declare_estimator(Y ~ Z, estimand = "my_estimand")

design
df <- draw_data(design)
estimates <- draw_estimates(design)
estimands <- draw_estimands(design)

print_code(design)

my_population <- declare_population(N = 100)
my_assignment <- declare_assignment(m = 50)
my_design <- my_population + my_assignment

print_code(my_design)
```

redesign

### Redesign

Quickly generates a design from an existing one by resetting symbols used in design handler parameters in a step’s environment (Advanced).

#### Usage

```r
redesign(design, ..., expand = TRUE)
```

#### Arguments

- **design**: An object of class design.
- **...**: Arguments to redesign e.g., n = 100. If redesigning multiple arguments, they must be specified as a named list.
- **expand**: If TRUE, redesign using the crossproduct of . . . , otherwise recycle them.
**Details**

Warning: redesign will edit any symbol in your design, but if the symbol you attempt to change does not exist in a step's environment no changes will be made and no error or warning will be issued.

Please note that redesign functionality is experimental and may be changed in future versions.

**Value**

A design, or, in the case of multiple values being passed onto . . . , a 'by'-list of designs.

**Examples**

```r
n <- 500
population <- declare_population(N = 1000)
sampling <- declare_sampling(n = n)
design <- population + sampling

# returns a single, modified design
modified_design <- redesign(design, n = 200)

# returns a list of six modified designs
design_vary_N <- redesign(design, n = seq(400, 900, 100))

# When redesigning with arguments that are vectors, use list() in redesign, with each list item representing a design you wish to create
prob_each <- c(.1, .5, .4)
assignment <- declare_assignment(prob_each = prob_each)
design <- population + assignment

# returns two designs

designs_vary_prob_each <- redesign(
  design,
  prob_each = list(c(.2, .5, .3), c(0, .5, .5)))

# To illustrate what does and does not get edited by redesign, consider the following three designs. In the first two, argument X is called from the step's environment; in the third it is not. Using redesign will alter the role of X in the first two designs but not the third one.

X <- 3
f <- function(b, X) b*X
g <- function(b) b*X
```
design1 <- declare_population(N = 1, A = X) + NULL
design2 <- declare_population(N = 1, A = f(2, X)) + NULL
design3 <- declare_population(N = 1, A = g(2)) + NULL

draw_data(design1)
draw_data(design2)
draw_data(design3)
draw_data(redesign(design1, X=0))
draw_data(redesign(design2, X=0))
draw_data(redesign(design3, X=0))

---

**reshape_diagnosis**

Clean up a diagnosis object for printing

**Description**

If diagnosands are bootstrapped, se’s are put in parentheses on a second line and rounded to digits.

**Usage**

```
reshape_diagnosis(diagnosis, digits = 2, select = NULL)
```

**Arguments**

- **diagnosis**: An object from `diagnose_design`, either a diagnosand dataframe or a list containing a diagnosand dataframe.
- **digits**: Number of digits.
- **select**: List of columns to include in output. Defaults to all.

**Value**

A formatted text table with bootstrapped standard errors in parentheses.

**Examples**

```
# library(DesignLibrary)
# diagnosis <- diagnose_design(two_arm_designer(), sims = 3)
# reshape_diagnosis(diagnosis)
# reshape_diagnosis(diagnosis, select = c("Bias", "Power"))
```
run_design

Execute a design

Description

Execute a design

Usage

run_design(design)

Arguments

design  a DeclareDesign object

set_citation

Set the citation of a design

Description

Set the citation of a design

Usage

set_citation(design, title = NULL, author = NULL, year = NULL,
             description = "Unpublished research design declaration",
             citation = NULL)

Arguments

design  A design typically created using the + operator
title   The title of the design, as a character string.
author  The author(s) of the design, as a character string.
year    The year of the design, as a character string.
description  A description of the design in words, as a character string.
citation (optional) The preferred citation for the design, as a character string, in which
case title, author, year, and description may be left unspecified.

Value

a design object with a citation attribute
Examples

```r
design <-
design <-
```

```r
design <-
design <-
```

```r
cite_design(design)
cite_design(design)
```

set_diagnosands

Set the diagnosands for a design

Description

A researcher often has a set of diagnosands in mind to appropriately assess the quality of a design. `set_diagnosands` sets the default diagnosands for a design, so that later readers can assess the design on the same terms as the original author. Readers can also use `diagnose_design` to diagnose the design using any other set of diagnosands.

Usage

```r
set_diagnosands(x, diagnosands = default_diagnosands)
```

Arguments

- `x`: A design typically created using the `+` operator, or a simulations data.frame created by `simulate_design`.
- `diagnosands`: A set of diagnosands created by `declare_diagnosands`.

Value

A design object with a diagnosand attribute.

Examples

```r
design <-
design <-
```

```r
design <-
design <-
```

```r
cite_design(design)
cite_design(design)
```

```r
cite_design(design)
cite_design(design)
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```r
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```
term = '(Intercept)', model = lm_robust)

diagnostics <- declare_diagnostics(
    median_bias = median(estimate - estimand), keep_defaults = FALSE)

design <- set_diagnostics(design, diagnostics)

## Not run:

diagnose_design(design)

simulations_df <- simulate_design(design)
simulations_df <- set_diagnostics(simulations_df, design)

diagnose_design(simulations_df)

## End(Not run)

---

**simulate_design** Simulate a design

**Description**

Runs many simulations of a design and returns a simulations data.frame.

**Usage**

`simulate_design(..., sims = 500)`

`simulate_designs(..., sims = 500)`

**Arguments**

`...` A design created using the + operator, or a set of designs. You can also provide a single list of designs, for example one created by `expand_design`.

`sims` The number of simulations, defaulting to 500. If sims is a vector of the form c(10, 1, 2, 1) then different steps of a design will be simulated different numbers of times.

**Details**

Different steps of a design may each be simulated different a number of times, as specified by sims. In this case simulations are grouped into "fans". The nested structure of simulations is recorded in the dataset using a set of variables named "step_x_draw." For example if sims = c(2,1,1,3) is passed to simulate_design, then there will be two distinct draws of step 1, indicated in variable "step_1_draw" (with values 1 and 2) and there will be three draws for step 4 within each of the step 1 draws, recorded in "step_4_draw" (with values 1 to 6).
Examples

```r
my_population <- declare_population(N = 500, noise = rnorm(N))

my_potential_outcomes <- declare_potential_outcomes(
  Y_Z_0 = noise, Y_Z_1 = noise +
  rnorm(N, mean = 2, sd = 2))

my_assignment <- declare_assignment()

my_estimand <- declare_estimand(ATE = mean(Y_Z_1 - Y_Z_0))

my_estimator <- declare_estimator(Y ~ Z, estimand = my_estimand)

my_reveal <- declare_reveal()

design <- my_population +
  my_potential_outcomes +
  my_estimand +
  my_assignment +
  my_reveal +
  my_estimator
```

## Not run:
simulations <- simulate_design(designs = c(1, 1, 1, 100, 1))
diagnosis <- diagnose_design(simulations)

## End(Not run)

## Not run:
# A fixed population with simulations over assignment only
head(simulate_design(design, sims = c(1, 1, 1, 100, 1)))

## End(Not run)
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