

Package: catviz (via r-universe)

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Title Visualizing Causal Assignment Trees for CSDiD and DR-DDD Designs

Version 0.1.1

Description Tools for constructing, labeling, and visualizing Causal Assignment Trees (CATs) in settings with staggered adoption. Supports Callaway and Sant'Anna difference-in-differences (CSDiD) and doubly robust difference-in-difference-differences (DR-DDD) designs. The package helps clarify treatment timing, never-treated vs. not-yet-treated composition, and subgroup structure, and produces publication-quality diagrams and summary tables. Current functionality focuses on data-to-node mapping, node counts, cohort-year summaries, and high-quality tree plots suitable for empirical applications prior to estimation. Methods are based on Callaway and Sant'Anna (2021) <[doi:10.1016/j.jeconom.2020.12.001](https://doi.org/10.1016/j.jeconom.2020.12.001)>, Sant'Anna and Zhao (2020) <[doi:10.1016/j.jeconom.2020.06.003](https://doi.org/10.1016/j.jeconom.2020.06.003)>, and Kilanko (2026) <<https://github.com/VictorKilanko/catviz>>.

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URL <https://github.com/VictorKilanko/catviz>

BugReports <https://github.com/VictorKilanko/catviz/issues>

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cat_att_equation	<i>Show ATT contrast implied by CAT nodes and design</i>
------------------	--

Description

Returns LaTeX and plain-text versions of the ATT equation that match the Causal Assignment Tree diagram.

Usage

```
cat_att_equation(
  design = c("drddd", "csdid"),
  subgroup_value = 1,
  include_never_treated = TRUE
)
```

Arguments

design Character; either "drddd" or "csdid".
 subgroup_value Integer; 0 or 1 selecting the subgroup for CSDiD contrast.
 include_never_treated Logical; if TRUE (default), a note about never-treated controls is included in the output.

Value

A named list with four elements:

- text - plain-text representation of the ATT contrast equation.
- tex - LaTeX math string of the ATT contrast equation.
- nodes - character vector naming the CAT nodes involved in the contrast.
- note - plain-text note about the control group composition.

Examples

```

eq <- cat_att_equation(design = "csdid")
cat(eq$text)

eq2 <- cat_att_equation(design = "drddd")
cat(eq2$text)

```

cat_balance_plot *Love plot for balance*

Description

Love plot for balance

Usage

```
cat_balance_plot(balance_tbl)
```

Arguments

balance_tbl A balance table as returned by cat_balance_table(), containing columns covariate, smd, and group.

Value

A ggplot object showing standardized mean differences by covariate.

Examples

```
df <- data.frame(
  id   = rep(1:4, each = 3),
  year = rep(2018:2020, 4),
  g    = c(rep(2019, 6), rep(Inf, 6)),
  age  = c(25, 25, 25, 30, 30, 30, 40, 40, 40, 35, 35, 35)
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
btbl <- cat_balance_table(spec, covariates = "age")
cat_balance_plot(btbl)
```

<code>cat_balance_table</code>	<i>Standardized mean differences across CAT nodes or design groups</i>
--------------------------------	--

Description

Standardized mean differences across CAT nodes or design groups

Usage

```
cat_balance_table(spec, covariates, by = c("node", "design"), weight = NULL)
```

Arguments

<code>spec</code>	A <code>cat_spec</code> object. Must be labeled (via <code>cat_label()</code>) when <code>by = "design"</code> .
<code>covariates</code>	Character vector of covariate names to assess.
<code>by</code>	Character; "node" (default) computes SMDs across CAT nodes; "design" compares Treated vs Never-Treated units.
<code>weight</code>	Optional name of a weight column in <code>spec\$data</code> .

Value

A tibble with one row per covariate-group combination and four columns:

- `covariate` - name of the covariate.
- `group` - CAT node label or design group ("Treated" or "Never-Treated").
- `mean` - weighted mean of the covariate within the group.
- `smd` - standardized mean difference relative to the first (reference) group.

Examples

```
df <- data.frame(
  id   = rep(1:4, each = 3),
  year = rep(2018:2020, 4),
  g    = c(rep(2019, 6), rep(Inf, 6)),
  age  = c(25, 25, 25, 30, 30, 30, 40, 40, 40, 35, 35, 35)
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
cat_balance_table(spec, covariates = "age")
```

cat_counts	<i>Count observations or units per node</i>
------------	---

Description

Count observations or units per node

Usage

```
cat_counts(spec)
```

Arguments

spec A cat_spec or labeled cat_spec object

Value

A tibble with counts per node

Examples

```
df <- data.frame(
  id   = rep(1:4, each = 3),
  year = rep(2018:2020, 4),
  g    = c(rep(2019, 6), rep(Inf, 6))
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
cat_counts(spec)
```

cat_design_csdid	<i>Blueprint for Callaway-Sant'Anna DiD Tree (Staggered Adoption)</i>
------------------	---

Description

Creates the tree structure for CSDiD with multiple treatment cohorts and a never-treated comparison group.

Usage

```
cat_design_csdid(cohort_labels)
```

Arguments

cohort_labels Character vector of cohort labels (e.g., "g = 2015 (A)")

Details

Tree structure: All Units |– Never-Treated (g = Inf) (last letter) +- Treated Cohorts |– g = g1 (A) |– g = g2 (B) |– g = g3 (C) +- ...

Value

A nested list representing the tree structure

Examples

```
tree <- cat_design_csdid(c("g = 2018 (A)", "g = 2019 (B)"))
tree$root
```

cat_design_ddd

Blueprint for Difference-in-Difference-in-Differences Tree

Description

Creates the tree structure for DDD with multiple treatment cohorts, each split into treated (Q=1) and untreated (Q=0) subgroups, plus never-treated subgroups.

Usage

```
cat_design_ddd(cohort_labels)
```

Arguments

cohort_labels Character vector of cohort labels (e.g., "g = 2015")

Details

Tree structure: All Units |– Treated Cohorts ||– g = g1 ||– Q = 1 (A) ||+- Q = 0 (B) |– g = g2 ||– Q = 1 (C) ||+- Q = 0 (D) |+- ... +- Never-Treated (g = Inf) |– Q = 1 (penultimate letter) +- Q = 0 (last letter)

Value

A nested list representing the tree structure

Examples

```
tree <- cat_design_ddd(c("g = 2018", "g = 2019"))
tree$root
```

cat_design_did	<i>Blueprint for 2x2 Difference-in-Differences Tree</i>
----------------	---

Description

Creates the tree structure for standard 2x2 DiD with one treated cohort and one control (never-treated) group.

Usage

```
cat_design_did()
```

Details

Tree structure: All Units |– Treated (g = g*) |– Pre (C) | +- Post (D) +- Control (g = Inf) |– Pre (E) +- Post (F)

Value

A nested list representing the tree structure

Examples

```
tree <- cat_design_did()
tree$root
```

cat_diag	<i>General diagnostic helper for CAT specifications</i>
----------	---

Description

Automatically selects an appropriate diagnostic based on the method argument. Dispatches to:

- "event" -> [cat_event_table\(\)](#) (event-time counts; no outcome needed)
- "drddd" -> [cat_pt_drddd\(\)](#) (subgroup pretrend plot)
- "csdid" -> [cat_pt_csdid\(\)](#) (parallel-gaps plot)

Usage

```
cat_diag(spec, outcome = NULL, method = c("event", "drddd", "csdid"), ...)
```

Arguments

spec	A cat_spec object
outcome	Outcome variable name (required for "drddd" and "csdid")
method	Diagnostic type: "event", "drddd", or "csdid"
...	Additional arguments passed to the specific diagnostic function (e.g., pre_window)

Value

A list with diagnostic results (always includes data; includes plot for "drddd" and "csdid")

Examples

```
df <- data.frame(id=rep(1:10,each=6), year=rep(2015:2020,10),
                 g=c(rep(2018,30),rep(Inf,30)), outcome=rnorm(60))
spec <- cat_spec(df, id="id", time="year", g="g")
result <- cat_diag(spec, method = "event")
```

cat_event_table	<i>Count treated and control observations by event time</i>
-----------------	---

Description

Summarizes the number of treated and control observations by event time $e = t - g$. Works directly with any `cat_spec` object; does not require any additional labeling.

Usage

```
cat_event_table(spec, event_window = -10:10)
```

Arguments

`spec` A `cat_spec` object (from `cat_spec()`)

`event_window` Integer vector of event times to include (default `-10:10`)

Value

A tibble with columns `e`, `n_treated`, `n_control`

Examples

```
df <- data.frame(
  id = rep(1:10, each = 6),
  year = rep(2015:2020, 10),
  g = c(rep(2018, 30), rep(Inf, 30))
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
cat_event_table(spec, event_window = -3:2)
```

cat_label	<i>Label CAT nodes with cohort letters and canonical g labels</i>
-----------	---

Description

Adds three columns to `spec$data`:

- `.cohort_letter`: uppercase letter assigned chronologically to each finite g cohort
- `.g_label`: canonical label ("g = 2015" or "g = Inf")
- `.g_pretty`: combined label ("g = 2015 (A)")

Usage

```
cat_label(spec)
```

Arguments

`spec` A `cat_spec` object (from `cat_spec()`)

Details

Never-treated units (g = Inf or g %in% `never_treated_values`) are labeled with the last letter in the sequence.

Value

The same `cat_spec` object with three new columns added to `spec$data`

Examples

```
df <- data.frame(
  id   = rep(1:4, each = 3),
  year = rep(2018:2020, 4),
  g    = c(rep(2019, 6), rep(Inf, 6))
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
spec <- cat_label(spec)
```

cat_plot_csdid	<i>Plot CSDiD Causal Assignment Tree (IMPROVED - No Cut-offs)</i>
----------------	---

Description

Tree structure: All Units |← Treated Cohorts |← g = g1 (A) |← g = g2 (B) |← g = g3 (C) |← ... |← Never-Treated (g = Inf) (last letter)

Usage

```
cat_plot_csdid(spec, counts = TRUE, save_plot = NULL)
```

Arguments

spec	A cat_spec object (CSDID setup: no subgroup).
counts	Logical; include counts in node labels (default TRUE)
save_plot	Optional file path for plot (PNG, PDF, etc.)

Details

Letters A,B,C,... assigned in chronological order of g.

Value

A ggplot object representing the CSDID Causal Assignment Tree.

Examples

```
df <- data.frame(
  id = rep(1:6, each = 4),
  year = rep(2017:2020, 6),
  g = c(rep(2018, 8), rep(2019, 8), rep(Inf, 8))
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
cat_plot_csdid(spec)
```

cat_plot_ddd	<i>Plot DDD-style Causal Assignment Tree (cohorts x subgroup) - IMPROVED VERSION</i>
--------------	--

Description

This version uses optimized spacing to prevent node overlap and create a publication-quality visualization.

Usage

```
cat_plot_ddd(spec, counts = TRUE, save_plot = NULL)
```

Arguments

spec A cat_spec object with a subgroup variable (DDD setup).
 counts Logical; include sample size counts in node labels (default TRUE).
 save_plot Optional file path for saving the plot (PNG, PDF, etc.).

Value

A ggplot object representing the DDD Causal Assignment Tree.

Examples

```
df <- data.frame(
  id   = rep(1:6, each = 4),
  year = rep(2017:2020, 6),
  g    = c(rep(2018, 8), rep(2019, 8), rep(Inf, 8)),
  p    = rep(c(0L, 1L), 12)
)
spec <- cat_spec(df, id = "id", time = "year", g = "g", subgroup = "p")
cat_plot_ddd(spec)
```

 cat_plot_did

Plot 2x2 DID Causal Assignment Tree (IMPROVED - No Cut-offs)

Description

Structure: All Units |– Treated (A) |– Pre (C) |– Post (D) +– Control (B) |– Pre (E) +– Post (F)

Usage

```
cat_plot_did(spec, counts = TRUE, save_plot = NULL)
```

Arguments

spec A cat_spec object (standard DID with no staggered timing).
 counts Logical; include sample size counts in node labels.
 save_plot Optional path to save.

Value

A ggplot object.

Examples

```
df <- data.frame(
  id   = rep(1:4, each = 2),
  year = rep(2019:2020, 4),
  g    = c(rep(2020, 4), rep(Inf, 4))
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
cat_plot_did(spec)
```

cat_plot_tree

Plot a Causal Assignment Tree (unified interface)

Description

cat_plot_tree() is the recommended high-level function for visualizing any CAT design. It inspects the cat_spec object and automatically dispatches to the correct underlying plot function:

Usage

```
cat_plot_tree(spec, counts = TRUE, grayscale = FALSE, save_plot = NULL, ...)
```

Arguments

spec	A cat_spec object (from <code>cat_spec()</code>).
counts	Logical; include sample-size counts in node labels (default TRUE).
grayscale	Logical; use a grayscale color palette suitable for black-and-white publications (default FALSE). When TRUE, treated nodes are shown in dark gray and control nodes in light gray.
save_plot	Optional file path to save the plot (e.g. "tree.png"). Passed to <code>ggplot2::ggsave()</code> .
...	Additional arguments passed to the underlying plot function.

Details

Design	Condition	Underlying function
DDD / DR-DDD	subgroup column provided, multiple g values	cat_plot_ddd()
CSDiD	No subgroup, multiple g values	cat_plot_csdid()
2x2 DiD	No subgroup, exactly one finite g value	cat_plot_did()

Value

A ggplot object.

Examples

```
df <- data.frame(
  id   = rep(1:6, each = 4),
  year = rep(2017:2020, 6),
  g    = c(rep(2018, 8), rep(2019, 8), rep(Inf, 8))
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
cat_plot_tree(spec)

df$p <- rep(c(0L, 1L), 12)
spec_ddd <- cat_spec(df, id = "id", time = "year", g = "g", subgroup = "p")
cat_plot_tree(spec_ddd)

cat_plot_tree(spec, grayscale = TRUE)
```

cat_pt_csdid

CSDiD parallel-gaps diagnostic

Description

Checks whether treated cohorts and the never-treated group have parallel pre-treatment trends. Plots the gap $\text{mean}(\text{treated}) - \text{mean}(\text{never-treated})$ across pre-treatment event-time periods.

Usage

```
cat_pt_csdid(spec, y, pre_window = -8:-1)
```

Arguments

spec	A cat_spec object
y	Outcome variable name
pre_window	Integer vector of pre-periods (default -8:-1)

Value

A list with data (tibble) and plot (ggplot)

Examples

```
set.seed(42)
df <- data.frame(
  id     = rep(1:10, each = 6),
  year   = rep(2015:2020, 10),
  g      = c(rep(2018, 30), rep(Inf, 30)),
  outcome = rnorm(60)
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
result <- cat_pt_csdid(spec, y = "outcome", pre_window = -3:-1)
```

cat_pt_drddd	<i>DR-DDD pretrend diagnostic: subgroup means in pre-periods</i>
--------------	--

Description

Plots mean outcomes for the treated subgroup (subgroup = 1) vs. the control subgroup (subgroup = 0) across pre-treatment event-time periods. Requires a subgroup variable in the `cat_spec`.

Usage

```
cat_pt_drddd(spec, y, pre_window = -8:-1)
```

Arguments

<code>spec</code>	A <code>cat_spec</code> object with a subgroup variable
<code>y</code>	Name of the outcome variable
<code>pre_window</code>	Integer vector of pre-periods (default <code>-8:-1</code>)

Value

A list with elements `data` (tibble) and `plot` (ggplot)

Examples

```
set.seed(42)
df <- data.frame(
  id      = rep(1:10, each = 6),
  year    = rep(2015:2020, 10),
  g       = c(rep(2018, 30), rep(Inf, 30)),
  p       = rep(c(0L, 1L), 30),
  outcome = rnorm(60)
)
spec <- cat_spec(df, id = "id", time = "year", g = "g", subgroup = "p")
result <- cat_pt_drddd(spec, y = "outcome", pre_window = -3:-1)
```

cat_save_png	<i>Save a CAT ggplot as a high-quality PNG</i>
--------------	--

Description

Save a CAT ggplot as a high-quality PNG

Usage

```
cat_save_png(
  plot,
  filename = "CAT_plot.png",
  width = 10,
  height = 6,
  dpi = 400
)
```

Arguments

plot	A ggplot object (e.g., from cat_plot_tree())
filename	Path to save the PNG (e.g., "CAT_plot.png")
width	Width in inches (default = 10)
height	Height in inches (default = 6)
dpi	Resolution in dots per inch (default = 400)

Value

Invisibly returns the file path

Examples

```
## Not run:
df <- data.frame(
  id   = rep(1:4, each = 3),
  year = rep(2018:2020, 4),
  g    = c(rep(2019, 6), rep(Inf, 6))
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")
p <- cat_plot_tree(spec)
cat_save_png(p, filename = tempfile(fileext = ".png"))

## End(Not run)
```

cat_spec

Build a Causal Assignment Tree specification

Description

cat_spec() is the entry point for catviz. It attaches internal standardised columns (.id, .time, .g, .subgroup, .NT, .NYT, .node) to your panel data and records the variable mapping so that all downstream functions know where to look.

Usage

```
cat_spec(
  data,
  id,
  time,
  g,
  subgroup = NULL,
  group_id = NULL,
  never_treated_values = c(0, Inf)
)
```

Arguments

<code>data</code>	A data frame (panel structure: one row per unit x time period).
<code>id</code>	Name of the unit identifier column (e.g. "hospital_id").
<code>time</code>	Name of the time column (e.g. "year" or "date").
<code>g</code>	Name of the first treatment period column. Units that never receive treatment should have <code>g = Inf</code> (or another value listed in <code>never_treated_values</code>).
<code>subgroup</code>	<i>(optional)</i> Name of a binary subgroup column (0/1), used for DR-DDD designs. Omit or set <code>NULL</code> for pure CSDID .
<code>group_id</code>	<i>(optional)</i> Name of a higher-level grouping column (e.g. "state") when treatment is assigned at a level above the unit.
<code>never_treated_values</code>	Numeric vector of <code>g</code> values that indicate never-treated status. Default: <code>c(0, Inf)</code> .

Value

A `cat_spec` object: a list with elements

- `$data` - the augmented data frame
- `$meta` - a list of variable names and settings

Examples

```
df <- data.frame(
  id = rep(1:4, each = 3),
  year = rep(2018:2020, 4),
  g = c(rep(2019, 6), rep(Inf, 6))
)
spec <- cat_spec(df, id = "id", time = "year", g = "g")

df$p <- rep(c(0, 1), 6)
spec_ddd <- cat_spec(df, id = "id", time = "year", g = "g", subgroup = "p")
```

`generate_cohort_labels`*Generate cohort labels with letters*

Description

Creates labeled cohort identifiers in the format "g = YYYY (A)" where letters are assigned chronologically.

Usage

```
generate_cohort_labels(g_values, start_letter = "A")
```

Arguments

<code>g_values</code>	Numeric vector of treatment years/periods
<code>start_letter</code>	Starting letter (default "A")

Value

Character vector of labeled cohorts

Examples

```
generate_cohort_labels(c(2015, 2016, 2019))
```

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