

# Package ‘prettyPanelMatch’

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**Title** 'ggplot2'-Based Visualization for 'PanelMatch' (Imai, Kim, Wang 2023) Results

**Version** 0.2.0

**Description** Provides 'ggplot2'-based plotting functions for 'PanelMatch' (Imai, Kim, Wang (2023) <[doi:10.1111/ajps.12685](https://doi.org/10.1111/ajps.12685)>) results. Tidy-and-plot function pairs for three 'PanelMatch' outputs: treatment effect estimates (PanelEstimate()), placebo test diagnostics (placebo\_test()), and covariate balance checks (get\_covariate\_balance()). Supports multiple models, significance indicators, faceted balance grids, and full 'ggplot2' extensibility.

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**URL** <https://github.com/jacqpark/prettyPanelMatch>

**BugReports** <https://github.com/jacqpark/prettyPanelMatch/issues>

**Encoding** UTF-8

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**Imports** ggplot2 (>= 3.4.0), dplyr, rlang

**Suggests** PanelMatch, testthat (>= 3.0.0)

**NeedsCompilation** no

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ggplot\_panel\_estimate *Create a ggplot2 Coefficient Plot from PanelEstimate Results*

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## Description

Produces a customizable ggplot2 coefficient plot showing point estimates and confidence intervals across lead periods. Supports multiple models with dodged positions and significance-based shape coding (hollow = not significant, filled = significant). A footnote is added by default.

## Usage

```
ggplot_panel_estimate(
  data,
  dodge_width = 0.5,
  point_size = 2.2,
  errorbar_alpha = 0.5,
  errorbar_width = 0,
  shapes = NULL,
  show_signif_shapes = TRUE,
  legend_labels = NULL,
  footnote = "Filled markers denote statistical significance (CI excludes zero).",
  footnote_size = NULL,
  xlab = "Time",
  ylab = "ATT",
  title = NULL,
  subtitle = NULL,
  hline = 0,
  facet_by = NULL,
  theme_fn = ggplot2::theme_minimal
)

## S3 method for class 'ppm_tidy'
autoplot(object, ...)
```

## Arguments

data	A ppm_tidy data frame from <a href="#">tidy_panel_estimate</a> .
dodge_width	Width of position dodge for multiple models. Default 0.5.
point_size	Size of point estimates. Default 2.2.
errorbar_alpha	Alpha transparency for error bars. Default 0.5.
errorbar_width	Width of error bar caps. Default 0 (no caps).
shapes	A character vector of hollow shape names, one per model. Filled counterparts are paired automatically. If NULL (default), shapes cycle through: "circle", "diamond", "triangle", "square", "triangle_down". Available names: "circle", "square", "triangle", "diamond", "triangle_down". Numeric codes (0-14) are also accepted for advanced users.

show_signif_shapes	Logical. If TRUE (default), uses different shapes for significant vs. non-significant estimates. If FALSE, uses uniform shapes per model.
legend_labels	Optional character vector to override legend labels (one per model, in input order).
footnote	Character string for the significance footnote. Set to NULL to suppress. Default explains hollow vs. filled convention.
footnote_size	Font size for the footnote. Default NULL, which matches the axis title size from the active theme.
xlab	X-axis label. Default "Time".
ylab	Y-axis label. Default "ATT".
title	Optional plot title.
subtitle	Optional plot subtitle.
hline	Intercept for reference line. Default 0. Set to NULL to remove.
facet_by	Optional variable name to facet by (e.g., "label"). Default NULL (no faceting).
theme_fn	A ggplot2 theme function. Default theme_minimal.
object	A ppm_tidy data frame.
...	Additional arguments passed to ggplot_panel_estimate.

### Details

The returned object is a standard ggplot object, so you can add any ggplot2 layers, scales, or themes on top of it.

### Value

A ggplot object that can be further customized with standard ggplot2 syntax.

### See Also

[tidy\\_panel\\_estimate](#) to prepare the input data, [gg\\_placebo\\_test](#) for placebo test plots, [gg\\_covariate\\_balance](#) for covariate balance plots.

### Examples

```
# Toy example (runs without PanelMatch)
toy <- data.frame(
  term      = factor(paste0("t+", 0:2), levels = paste0("t+", 0:2), ordered = TRUE),
  estimate  = c(0.5, 0.8, 1.2),
  std.error = c(0.2, 0.3, 0.25),
  conf.low  = c(0.1, 0.2, 0.7),
  conf.high = c(0.9, 1.4, 1.7),
  label     = factor("Model", ordered = TRUE),
  signif    = c("Non-signif", "Signif", "Signif"),
  stringsAsFactors = FALSE
)
class(toy) <- c("ppm_tidy", "data.frame")
```

```
ggplot_panel_estimate(toy)
```

---

gg\_covariate\_balance *Create a ggplot2 Covariate Balance Plot*

---

## Description

Produces a faceted covariate balance plot showing standardized mean differences across matching stages. Dependent variables are drawn as black solid lines; covariates as grey lines with distinct linetypes.

## Usage

```
gg_covariate_balance(
  data,
  dv_color = "black",
  cov_color = "grey70",
  dv_linetype = "solid",
  cov_linetypes = NULL,
  hline = 0,
  ylim = c(-2, 2),
  xlab = "Time",
  ylab = "SD",
  title = NULL,
  subtitle = NULL,
  show_legend = FALSE,
  strip_text_y_size = 8.5,
  theme_fn = ggplot2::theme_bw
)

## S3 method for class 'ppm_cov_tidy'
autoplot(object, ...)
```

## Arguments

data	A ppm_cov_tidy data frame from <a href="#">pretty_covariate_balance</a> .
dv_color	Color for DV lines. Default "black".
cov_color	Color for covariate lines. Default "grey70".
dv_linetype	Linetype for DV lines. Default "solid".
cov_linetypes	Character vector of linetypes for covariates. If NULL (default), cycles through "dashed", "twodash", "dotted", "dotdash", "longdash".
hline	Y-intercept for reference line. Default 0. Set to NULL to remove.
ylim	Y-axis limits as a length-2 numeric vector. Default c(-2, 2). Set to NULL for automatic limits.

xlab	X-axis label. Default "Time".
ylab	Y-axis label. Default "SD".
title	Optional plot title.
subtitle	Optional plot subtitle.
show_legend	Logical. Show legend? Default FALSE.
strip_text_y_size	Font size for row strip labels. Default 8.5. Set to NULL to use the theme default.
theme_fn	A ggplot2 theme function. Default theme_bw.
object	A ppm_cov_tidy data frame.
...	Additional arguments passed to gg_covariate_balance.

## Details

The default layout uses `facet_grid(model ~ stage)`, where models (different DVs / subsamples) form the rows and matching stages form the columns, reproducing the standard PanelMatch covariate-balance diagnostic.

## Value

A ggplot object that can be further customized with standard ggplot2 syntax.

## See Also

[pretty\\_covariate\\_balance](#) to prepare the input data, [ggplot\\_panel\\_estimate](#) for treatment effect plots, [gg\\_placebo\\_test](#) for placebo test plots.

## Examples

```
# Toy example (runs without PanelMatch)
toy <- data.frame(
  model = factor("Model A", ordered = TRUE),
  stage = factor("Before matching", ordered = TRUE),
  time = factor(rep(paste0("t-", 3:1), 2),
                levels = paste0("t-", 3:1), ordered = TRUE),
  variable = factor(rep(c("outcome", "covar1"), each = 3), ordered = TRUE),
  estimate = c(0.3, 0.5, 0.8, -0.1, 0.2, 0.1),
  is_dv = rep(c(TRUE, FALSE), each = 3),
  stringsAsFactors = FALSE
)
class(toy) <- c("ppm_cov_tidy", "data.frame")
gg_covariate_balance(toy)
```

---

gg\_placebo\_test      *Create a ggplot2 Coefficient Plot from Placebo Test Results*

---

## Description

Produces a customizable ggplot2 coefficient plot for placebo test estimates from the PanelMatch package. This is a convenience wrapper around `ggplot_panel_estimate` with defaults tailored for placebo tests (e.g., y-axis label set to "Placebo estimate").

## Usage

```
gg_placebo_test(data, ylab = "Placebo estimate", ...)

## S3 method for class 'ppm_placebo_tidy'
autoplot(object, ...)
```

## Arguments

<code>data</code>	A <code>ppm_placebo_tidy</code> data frame from <code>pretty_placebo_test</code> .
<code>ylab</code>	Y-axis label. Default "Placebo estimate".
<code>...</code>	Additional arguments passed to <code>gg_placebo_test</code> .
<code>object</code>	A <code>ppm_placebo_tidy</code> data frame.

## Details

All arguments are passed through to `ggplot_panel_estimate()`, so the full range of customization (shapes, dodging, significance coding, faceting, themes) is available.

## Value

A ggplot object.

## See Also

`pretty_placebo_test` to prepare the input data, `ggplot_panel_estimate` for treatment effect plots.

## Examples

```
# Toy example (runs without PanelMatch)
toy <- data.frame(
  term      = factor(paste0("t-", 3:1), levels = paste0("t-", 3:1), ordered = TRUE),
  estimate  = c(0.1, -0.05, 0.02),
  std.error = c(0.15, 0.12, 0.10),
  conf.low  = c(-0.19, -0.29, -0.18),
  conf.high = c(0.39, 0.19, 0.22),
  label     = factor("Model", ordered = TRUE),
  signif    = c("Non-signif", "Non-signif", "Non-signif"),
```

```

  stringsAsFactors = FALSE
)
class(toy) <- c("ppm_placebo_tidy", "data.frame")
gg_placebo_test(toy)

```

---

pretty\_covariate\_balance

*Tidy Covariate Balance Matrices into a Data Frame*


---

## Description

Converts `get_covariate_balance()` matrices from the `PanelMatch` package into a single tidy data frame suitable for `ggplot2` plotting.

## Usage

```

pretty_covariate_balance(
  ...,
  stage_labels = c("Before matching", "Matched, pre-refinement", "Post-refinement"),
  dv = NULL
)

```

## Arguments

...	Named arguments where each value is a list of matrices from <code>get_covariate_balance()</code> , one per matching stage. Names become model labels (row facet labels). A single matrix can be passed directly instead of wrapping in a list.
stage_labels	Character vector naming the matching stages, in order. Must be at least as long as the longest list of matrices provided. Default: <code>c("Before matching", "Matched, pre-refinement", "Post-refinement")</code> .
dv	Character vector of variable names that are dependent variables. These are styled differently (black solid lines) in the plot. Variables not listed here are treated as covariates (grey, varied linetypes).

## Details

Each named argument should be a list of 1–3 matrices (one per matching stage, e.g., before matching, after matching pre-refinement, post-refinement). The argument names become model/row facet labels.

## Value

A data frame (with class `"ppm_cov_tidy"`) containing:

**model** Model label (ordered factor, row facet)  
**stage** Matching stage label (ordered factor, column facet)

**time** Pre-treatment period label (ordered factor, e.g., "t-3")

**variable** Covariate or DV name (ordered factor)

**estimate** Standardized mean difference

**is\_dv** Logical; TRUE for dependent variables

### See Also

[gg\\_covariate\\_balance](#) to plot the result, [tidy\\_panel\\_estimate](#) for treatment effect estimates, [pretty\\_placebo\\_test](#) for placebo test results.

### Examples

```
# Create a mock covariate balance matrix (rows = time, cols = variables)
mat <- matrix(
  c(0.3, -0.1, 0.5, 0.2, 0.8, 0.1),
  nrow = 3,
  dimnames = list(NULL, c("outcome", "covar1"))
)
pretty_covariate_balance(
  "My Model" = mat,
  stage_labels = "Before matching",
  dv = "outcome"
)
```

---

pretty\_placebo\_test *Tidy placebo\_test Results into a Data Frame*

---

### Description

Converts one or more placebo\_test() results from the PanelMatch package into a single tidy data frame suitable for ggplot2 plotting.

### Usage

```
pretty_placebo_test(..., labels = NULL, confidence_level = 0.95)
```

### Arguments

...	One or more placebo_test() result objects. Can also be a single named list of results. Named arguments become model labels automatically.
labels	A character vector of labels, one per result. If NULL and inputs are named, the names are used. Otherwise defaults to "Model" (single) or "Model 1", "Model 2", etc.
confidence_level	Confidence level for constructing intervals. Default 0.95.

**Value**

A data frame (with class "ppm\_placebo\_tidy") containing:

**term** Lag period label (e.g., "t-3", "t-2")

**estimate** Point estimate

**std.error** Standard error

**conf.low** Lower confidence bound

**conf.high** Upper confidence bound

**label** Model label (ordered factor preserving input order)

**signif** Whether the CI excludes zero ("Signif" or "Non-signif")

**See Also**

[gg\\_placebo\\_test](#) to plot the result, [tidy\\_panel\\_estimate](#) for treatment effect estimates, [pretty\\_covariate\\_balance](#) for covariate balance.

**Examples**

```
# Create a mock placebo_test result
pt <- list(
  estimates = c("t-3" = 0.10, "t-2" = -0.05, "t-1" = 0.02),
  standard.errors = c("t-3" = 0.15, "t-2" = 0.12, "t-1" = 0.10)
)
pretty_placebo_test(pt, labels = "My Model")

# Custom confidence level
pretty_placebo_test(pt, confidence_level = 0.90)
```

---

tidy\_panel\_estimate    *Tidy PanelEstimate Summaries into a Data Frame*

---

**Description**

Converts one or more summary(PanelEstimate(...)) objects into a single tidy data frame suitable for ggplot2 plotting.

**Usage**

```
tidy_panel_estimate(..., labels = NULL)
```

**Arguments**

...	One or more PanelEstimate summary objects (or raw PanelEstimate objects, which will be summarized automatically). Can also be a single named list of summaries.
labels	A character vector of labels, one per summary. Used to distinguish models in the plot legend. If NULL and inputs are named (either as named arguments or a named list), the names are used. Otherwise defaults to "Model 1", "Model 2", etc.

**Value**

A data frame (with class "ppm\_tidy") containing columns:

<b>term</b>	Lead period label (e.g., "t+0", "t+1", ...)
<b>estimate</b>	Point estimate (ATT)
<b>std.error</b>	Standard error
<b>conf.low</b>	Lower confidence bound
<b>conf.high</b>	Upper confidence bound
<b>label</b>	Model label (ordered factor preserving input order)
<b>signif</b>	Whether the CI excludes zero ("Signif" or "Non-signif")

**See Also**

[ggplot\\_panel\\_estimate](#) to plot the result, [pretty\\_placebo\\_test](#) for placebo test results, [pretty\\_covariate\\_balance](#) for covariate balance.

**Examples**

```
# Create a mock PanelEstimate summary (matrix with 4 columns)
pe_sum <- matrix(
  c(0.5, 0.2, 0.1, 0.9,
    0.8, 0.3, 0.2, 1.4,
    1.2, 0.25, 0.7, 1.7),
  nrow = 3, byrow = TRUE,
  dimnames = list(NULL, c("Estimate", "Std.Error", "lower", "upper"))
)
tidy_panel_estimate(pe_sum, labels = "My Model")

# Multiple models with named arguments
pe_sum2 <- matrix(
  c(0.3, 0.15, 0.0, 0.6,
    0.6, 0.20, 0.2, 1.0,
    0.9, 0.18, 0.5, 1.3),
  nrow = 3, byrow = TRUE,
  dimnames = list(NULL, c("Estimate", "Std.Error", "lower", "upper"))
)
tidy_panel_estimate("Model A" = pe_sum, "Model B" = pe_sum2)
```

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