

# Package ‘tidysmd’

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**Title** Tidy Standardized Mean Differences

**Version** 0.2.0

**Description** Tidy standardized mean differences ('SMDs'). 'tidysmd' uses the 'smd' package to calculate standardized mean differences for variables in a data frame, returning the results in a tidy format.

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**URL** <https://github.com/r-causal/tidysmd>,  
<https://r-causal.github.io/tidysmd/>

**BugReports** <https://github.com/r-causal/tidysmd/issues>

**Depends** R (>= 2.10)

**Imports** dplyr, purrr, rlang, smd, stats, tidyr, tidymodels, utils

**Suggests** covr, ggplot2, MatchIt, spelling, testthat (>= 3.0.0), vdiff

**Config/testthat/edition** 3

**Encoding** UTF-8

**Language** en-US

**LazyData** true

**RoxygenNote** 7.2.3

**NeedsCompilation** no

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bind_matches	<i>Bind Match Indicator Columns to a Data Frame</i>
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### Description

Given a data frame `.df`, the function `bind_matches` creates binary indicator variables for each match returned by the `MatchIt` library and binds the resulting columns to `.df`. In other words, the result is the original data frame plus a column for however many matches you want to bind.

### Usage

```
bind_matches(.df, ...)
```

### Arguments

<code>.df</code>	A data frame.
<code>...</code>	<code>matchit</code> objects returned by the <code>MatchIt</code> package. They can be named or unnamed.

### Value

`.df` with addition columns for every element of `...`

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geom_love	<i>Create a Love plot</i>
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### Description

`geom_love()` and `love_plot()` are helper functions to create Love plots in `ggplot2`. Love plots are a diagnostic approach to assessing balance before and after weighting. Many researchers use 0.1 on the absolute SMD scale to evaluate if a variable is well-balanced between groups, although this is just a rule of thumb. `geom_love()` is a simple wrapper around `ggplot2::geom_point()`, `ggplot2::geom_line()`, and `ggplot2::geom_vline()`. It also adds default aesthetics via `ggplot2::aes()`. `love_plot()` is a quick plotting function that further wraps `geom_love()`. For more complex Love plots, we recommend using `ggplot2` directly.

### Usage

```
geom_love(
  linewidth = 0.8,
  line_size = NULL,
  point_size = 1.85,
  vline_xintercept = 0.1,
  vline_color = "grey70",
  vlinewidth = 0.6,
```

```

    vline_size = NULL
  )

love_plot(
  .df,
  linewidth = 0.8,
  line_size = NULL,
  point_size = 1.85,
  vline_xintercept = 0.1,
  vline_color = "grey70",
  vlinewidth = 0.6,
  vline_size = NULL
)

```

### Arguments

linewidth	The line size, passed to <code>ggplot2::geom_line()</code> .
line_size	Deprecated. Please use linewidth.
point_size	The point size, passed to <code>ggplot2::geom_point()</code> .
vline_xintercept	The X intercept, passed to <code>ggplot2::geom_vline()</code> .
vline_color	The vertical line color, passed to <code>ggplot2::geom_vline()</code> .
vlwidth	The vertical line size, passed to <code>ggplot2::geom_vline()</code> .
vline_size	Deprecated. Please use vlinewidth.
.df	a data frame produced by <code>tidy_smd()</code>

### Value

a list of geoms or a ggplot

### Examples

```

plot_df <- tidy_smd(
  nhefs_weights,
  race:active,
  .group = qsmk,
  .wts = starts_with("w_")
)

love_plot(plot_df)

# or use ggplot2 directly
library(ggplot2)
ggplot(
  plot_df,
  aes(
    x = abs(smd),
    y = variable,
    group = method,

```

```
    color = method,  
    fill = method  
  )  
) +  
  geom_love()
```

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nhefs\_weights

*NHEFS with various propensity score weights*

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### Description

A dataset containing various propensity score weights for `causaldata::nhefs_complete`.

### Usage

```
nhefs_weights
```

### Format

A data frame with 1566 rows and 14 variables:

**qsmk** Quit smoking

**race** Race

**age** Age

**education** Education level

**smokeintensity** Smoking intensity

**smokeyrs** Number of smoke-years

**exercise** Exercise level

**active** Daily activity level

**wt71** Participant weight in 1971 (baseline)

**w\_ate** ATE weight

**w\_att** ATT weight

**w\_atc** ATC weight

**w\_atm** ATM weight

**w\_ato** ATO weight

tidy\_smd

*Tidy Standardized Mean Differences***Description**

`tidy_smd()` calculates the standardized mean difference (SMD) for variables in a dataset between groups. Optionally, you may also calculate weighted SMDs. `tidy_smd()` wraps `smd::smd()`, returning a tidy dataframe with the columns `variable`, `method`, and `smd`, as well as fourth column the contains the level of `.group` the SMD represents. You may also supply multiple weights to calculate multiple weighted SMDs, useful when comparing different types of weights. Additionally, the `.wts` argument supports matched datasets where the variable supplied to `.wts` is a binary variable indicating whether the row was included in the match. If you're using `MatchIt`, the helper function `bind_matches()` will bind these indicators to the original dataset, making it easier to compare across matching specifications.

**Usage**

```
tidy_smd(
  .df,
  .vars,
  .group,
  .wts = NULL,
  include_observed = TRUE,
  include_unweighted = NULL,
  na.rm = FALSE,
  gref = 1L,
  std.error = FALSE,
  make_dummy_vars = FALSE
)
```

**Arguments**

<code>.df</code>	A data frame
<code>.vars</code>	Variables for which to calculate SMD
<code>.group</code>	Grouping variable
<code>.wts</code>	Variables to use for weighting the SMD calculation. These can be, for instance, propensity score weights or a binary indicator signaling whether or not a participant was included in a matching algorithm.
<code>include_observed</code>	Logical. If using <code>.wts</code> , also calculate the unweighted SMD?
<code>include_unweighted</code>	Deprecated. Please use <code>include_observed</code> .
<code>na.rm</code>	Remove NA values from <code>x</code> ? Defaults to <code>FALSE</code> .
<code>gref</code>	an integer indicating which level of <code>g</code> to use as the reference group. Defaults to 1.

`std.error` Logical indicator for computing standard errors using `compute_smd_var`. Defaults to FALSE.

`make_dummy_vars` Logical. Transform categorical variables to dummy variables using `model.matrix()`? By default, `smd::smd` uses a summary value based on the Mahalanobis distance to approximate the SMD of categorical variables. An alternative approach is to transform categorical variables to a set of dummy variables.

### Value

a tibble

### Examples

```
tidy_smd(nhefs_weights, c(age, education, race), .group = qsmk)
tidy_smd(nhefs_weights, c(age, education), .group = qsmk, std.error = TRUE)

tidy_smd(
  nhefs_weights,
  c(age, race, education),
  .group = qsmk,
  .wts = c(w_ate, w_att, w_atm)
)
```

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