

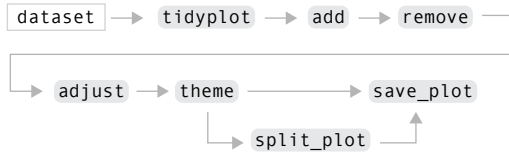


tidyplots cheatsheet

version 0.2.1

@jbengler

Workflow



Dataset

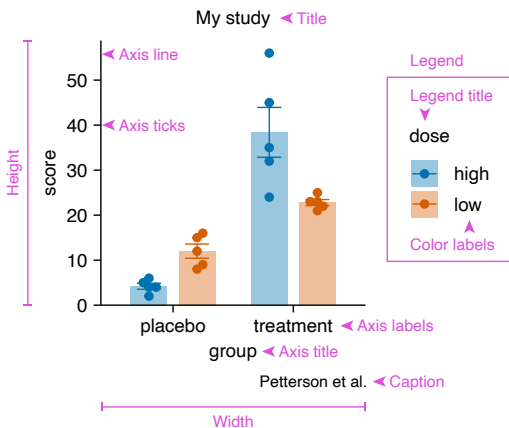
	Variables				
	group	dose	age	sex	score
Observations	<chr>	<chr>	<dbl>	<chr>	<dbl>
A	placebo	high	23	female	2
A	placebo	high	45	male	4
B	placebo	low	23	female	9
B	placebo	low	45	male	8
C	treatment	high	23	female	32
C	treatment	high	45	male	35
D	treatment	low	23	female	23
D	treatment	low	45	male	25
...

Code

```

study |>
  tidyplot(x = group, y = score, color = dose) |>
  add_mean_bar(alpha = 0.4) |>
  add_sem_errorbar() |>
  add_data_points_beeswarm() |>
  add_title("My study") |>
  add_caption("Pettersen et al.")
  
```

Plot





Links

- [website](#)
- [docs](#)
- [help](#)
- [use-cases](#)


Add


Raw data


`add_data_` → `points()`  `labels()` 


Example:
`add_data_points()`

Summary statistics


`add_count_` → `bar()` 


`add_sum_` → `dash()` 

`add_mean_` → `dot()` 


`add_median_` → `value()` 


Examples:
`add_count_bar()`
`add_sum_line()`
`add_mean_value()`

→ `line()` 

→ `area()` 

Dispersion

`add_sem_` → `errorbar()` 


`add_sd_` → `ribbon()` 

Example:
`add_sem_errorbar()`


`add_range_`

`add_ci95_`


Comparison


`add_test_` → `pvalue()` 

Example:
`add_test_pvalue()`


→ `asterisks()` 


Distribution


`add_boxplot()` 

`add_violin()` 

Proportion

`add_barstack()` 

`add_pie()` 

`add_areastack()` 


`add_donut()`

Annotation

`add_title()` → `add_annotation_text()`

`add_caption()` → `add_annotation_rectangle()`

`add_annotation_line()`


`add_reference_lines()` 


ggplot2 code

```

add()
add(ggplot2::geom_point())
  
```

More

`add_heatmap()` 

`add_curvefit()` 

`add_histogram()`

Adjust

Plot

`adjust_size()` → `adjust_description()`

`adjust_colors()` → `adjust_padding()`

`adjust_font()` → `adjust_legend_title()`

→ `adjust_legend_position()`

Axes

`adjust_x_axis()` → `adjust_y_axis()`

`adjust_x_axis_title()` → `adjust_y_axis_title()`

Data labels

`rename_reorder_sort_reverse_` → `color_labels()`

→ `x_axis_labels()`

→ `y_axis_labels()`

Examples:
`rename_color_labels()`
`sort_x_axis_labels()`
`reorder_y_axis_labels()`

Remove

Axes

`remove_` → `x_axis_` → `y_axis_`

→ `line()`

→ `ticks()`

→ `labels()`

→ `title()`

Examples:
`remove_x_axis()`
`remove_x_axis_title()`

More

`remove_title()` → `remove_legend()`




`remove_caption()` → `remove_legend_title()`

`remove_padding()`




More

Color schemes




`colors_discrete_`

- `friendly` 
- `seaside` 
- `apple` 

`colors_continuous_`

- `viridis` 
- `plasma` 
- `mako` 

`colors_diverging_`

- `blue2brown` 
- `blue2red` 
- `spectral` 

Split plot

```
split_plot(by, ncol, nrow, ...)
```

Output

```

save_plot("my_plot.pdf")
view_plot()
  
```

Datasets

- `animals`
- `energy_week`
- `climate`
- `gene_expression`
- `dinosaurs`
- `spendings`
- `distributions`
- `study`
- `energy`
- `time_course`