

# Model Plots

## Table of contents

<b>1</b>	<b>Rename, reorder, subset</b>	<b>2</b>
<b>2</b>	<b>Several models</b>	<b>3</b>
<b>3</b>	<b>Customizing plots</b>	<b>5</b>
3.1	Conditional colors and shape . . . . .	7
3.2	Example: Using facets to compare models . . . . .	7
<b>4</b>	<b>Confidence intervals</b>	<b>9</b>
<b>5</b>	<b>Background annotations</b>	<b>10</b>
<b>6</b>	<b>Raw data and customization</b>	<b>11</b>

`modelplot` is a function from the `modelsummary` package. It allows you to plot model estimates and confidence intervals. It makes it easy to subset, rename, reorder, and customize plots using same mechanics as in `modelsummary`.

To illustrate how the function works, we fit a linear model to data about the [Palmer Penguins](#):

```
url <- 'https://vincentarelbundock.github.io/Rdatasets/csv/palmerpenguins/penguins.csv'
dat <- read.csv(url)

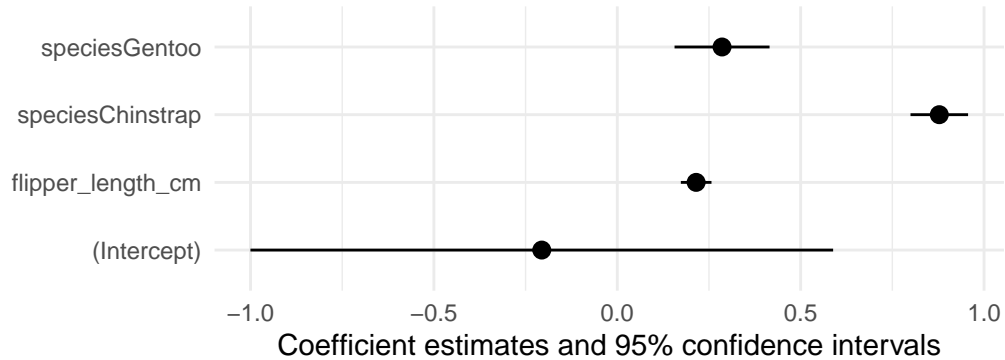
# rescale mm -> cm
dat$bill_length_cm <- dat$bill_length_mm / 10
dat$flipper_length_cm <- dat$flipper_length_mm / 10

mod <- lm(bill_length_cm ~ flipper_length_cm + species, data = dat)
```

Then, we load the `modelsummary` library and call `modelplot`:

```
library(modelsummary)
```

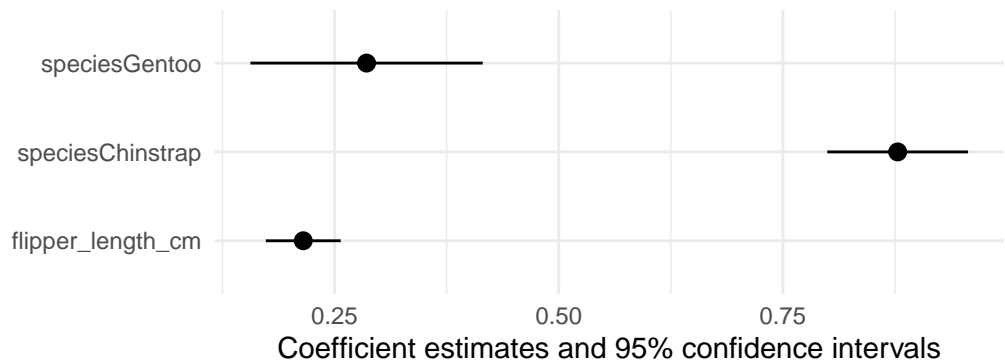
```
modelplot(mod)
```



## 1 Rename, reorder, subset

`modelplot` uses the same mechanics as `modelsummary` to rename, reorder, and subset estimates. First, you can use the `coef_omit` argument. This will omit any coefficient that matches a string or regular expression. To omit the intercept, for example, we can type:

```
modelplot(mod, coef_omit = 'Intercc')
```



Second, you can use the `coef_map` argument. `coef_map` is a named character vector, where names correspond to the original term names, and values correspond to the names you want to assign. Any variable that is *not* included in `coef_map` will be excluded. Variables will also be drawn in the same order as in `coef_map`:

```
cm <- c('speciesChinstrap' = 'Chinstrap',
       'speciesGentoo' = 'Gentoo',
       'flipper_length_cm' = 'Flipper length (cm)')

modelplot(mod, coef_map = cm)
```



## 2 Several models

The main `modelsummary` functions allows you to create a table with the results of several models side-by-side, by storing them in a (potentially named) list:

```
models <- list(
  "Small model" = lm(bill_length_cm ~ flipper_length_cm, data = dat),
  "Medium model" = lm(bill_length_cm ~ flipper_length_cm + body_mass_g, data = dat),
  "Large model" = lm(bill_length_cm ~ flipper_length_cm + body_mass_g + species, data = dat))

modelsummary(models, statistic = 'conf.int')
```

	Small model	Medium model	Large model
(Intercept)	−0.726 [−1.356, −0.097]	−0.344 [−1.245, 0.557]	0.984 [0.215, 1.752]
flipper_length_cm	0.255 [0.224, 0.286]	0.222 [0.158, 0.285]	0.095 [0.048, 0.142]
body_mass_g		0.000 [0.000, 0.000]	0.000 [0.000, 0.000]
speciesChinstrap			0.939 [0.867, 1.011]
speciesGentoo			0.207 [0.088, 0.326]
Num.Obs.	342	342	342
R2	0.431	0.433	0.817
R2 Adj.	0.429	0.430	0.815
AIC	369.0	369.6	−12.6
BIC	380.5	385.0	10.4
Log.Lik.	−181.499	−180.813	12.313
F	257.092	129.365	375.333
RMSE	0.41	0.41	0.23

modelplot works the same way:

```
modelplot(models, coef_omit = 'Interc')
```



Instead of displaying results with “dodged” side-by-side lines, you can also use **facet**:

```
modelplot(models, facet = TRUE)
```



### 3 Customizing plots

The graphs produced by `modelplot` are simple `ggplot2` objects. You can thus post-process them using the normal suite of functions available for all objects of this type. Here, we change the axis labels, add a title and a caption, and use a color scheme inspired by Wes Anderson's *Darjeeling Limited*:

```
library(wesanderson)
library(ggplot2)

modelplot(models) +
```

```
labs(x = 'Coefficients',
     y = 'Term names',
     title = 'Linear regression models of "Bill Length (cm)"',
     caption = "Data source: Gorman, Williams & Fraser (2014), packaged for R by @apresh.",
     scale_color_manual(values = wes_palette('Darjeeling1'))
```



iams & Fraser (2014), packaged for R by @apreshill and @allison\_horst

In `ggplot2`, some visual choices must be made when calling the “geom”, rather than with post-processing functions. For instance, the `size`, `color`, `fatten`, `linetype` arguments must all be specified inside the `geom_pointrange` function for them to take effect. `modelplot` will pass any unknown argument to `geom_pointrange`, so users can simply call:

```
modelplot(mod, size = 1, fatten = .7, color = 'darkgreen', linetype = 'dotted') +
  theme_classic()
```



### 3.1 Conditional colors and shape

Note: This section requires a version of `modelsummary` greater than 1.2.0 [or the development version](#).

In a [very nice Stack Overflow answer](#), Allan Cameron shows how we can use the `aes()` function from `ggplot2` to add conditional aesthetics. For example, if we want to display statistically significant coefficients in a different color:

```
library(ggplot2)
mod <- lm(hp ~ factor(gear) + factor(cyl), data = mtcars)

modelplot(mod, coef_rename = TRUE) +
  aes(color = ifelse(p.value < 0.001, "Significant", "Not significant")) +
  scale_color_manual(values = c("grey", "black"))
```



### 3.2 Example: Using facets to compare models

Customizing plots with `ggplot2` makes `modelplot` very flexible. For example, imagine you want to compare the coefficients of three models with different dependent variables. First, we

load the packages and estimate our models:

```
library(ggplot2)
library(modelsummary)

models <- list(
  lm(vs ~ carb + mpg + cyl, data = mtcars),
  lm(displ ~ carb + mpg + cyl, data = mtcars),
  lm(hp ~ carb + mpg + cyl, data = mtcars))
```

Then, we use the `dvnames` function to rename our list with names matching the dependent variable in each model:

```
models <- dvnames(models)
```

By calling `modelplot` with the `draw=FALSE` argument, we see the raw data used to draw the plot. Here, we see that there is a `model` column:

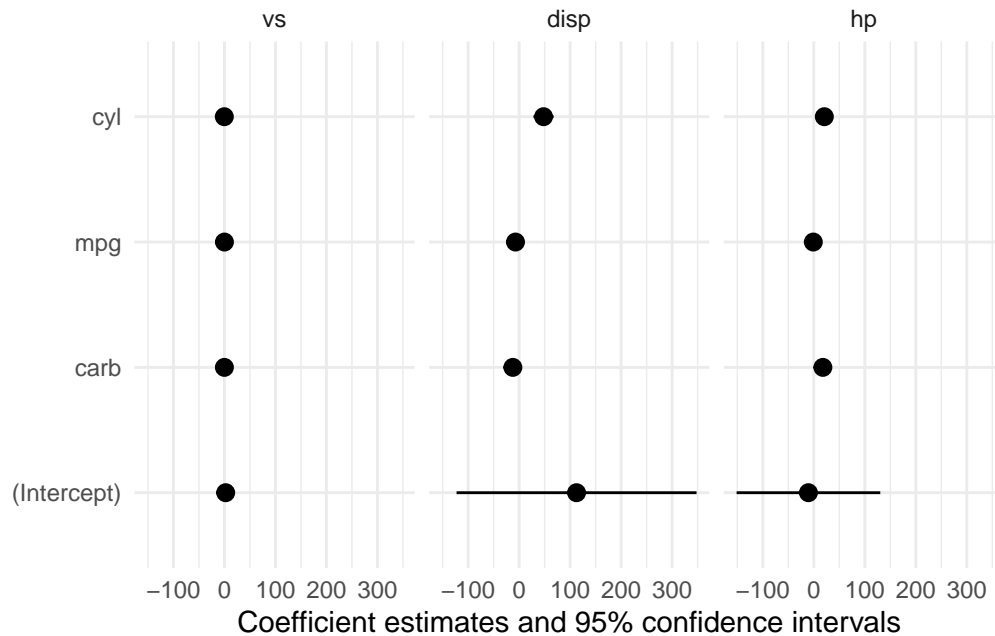
```
modelplot(models, draw = FALSE)
```

	term	model	estimate	std.error	conf.low	conf.high	p.value
1	(Intercept)	vs	2.41742511	0.67622094	1.03224931	3.80260091	1.296718e-03
5	(Intercept)	displ	112.57276339	114.86315481	-122.71374324	347.85927003	3.354494e-01
9	(Intercept)	hp	-10.56116383	68.75946117	-151.40853516	130.28620751	8.790301e-01
2	carb	vs	-0.06945116	0.03943402	-0.15022810	0.01132577	8.912324e-02
6	carb	displ	-12.30144724	6.69827859	-26.02224894	1.41935446	7.692105e-02
10	carb	hp	17.75593287	4.00972816	9.54237706	25.96948867	1.320972e-04
3	mpg	vs	-0.01513960	0.01716410	-0.05029868	0.02001947	3.852593e-01
7	mpg	displ	-7.14964651	2.91550156	-13.12178072	-1.17751230	2.068858e-02
11	mpg	hp	-1.00486469	1.74527956	-4.57990780	2.57017842	5.693755e-01
4	cyl	vs	-0.23926135	0.05687969	-0.35577411	-0.12274859	2.410214e-04
8	cyl	displ	47.90105842	9.66160634	28.11015499	67.69196184	3.111898e-05
12	cyl	hp	20.60581208	5.78363747	8.75856779	32.45305638	1.338485e-03

Finally, we use the `model` column as our identifier in `ggplot2`'s `facet_grid` command to display models side by side:

```
modelplot(models, color = "black") + facet_grid(~model)
```

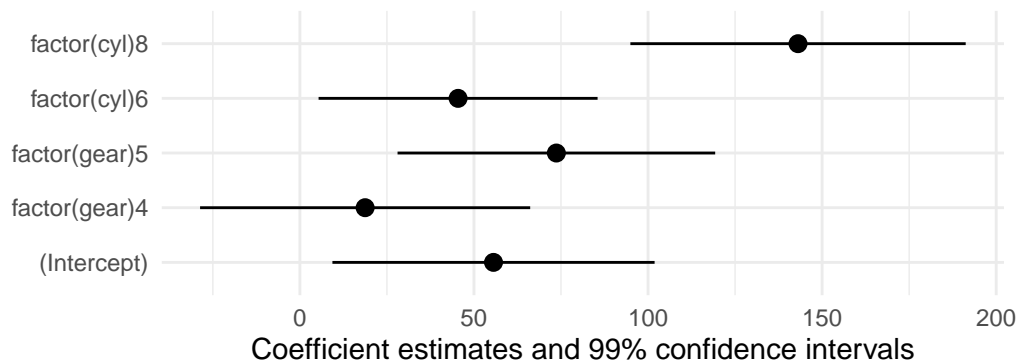




## 4 Confidence intervals

You can change the  $\alpha$  level of your confidence intervals by changing the `conf_level` argument:

```
modelplot(mod, conf_level = .99)
```



```
modelplot(mod, conf_level = NULL)
```



## 5 Background annotations

Sometimes, you want to display annotations on a plot, but you would like to draw these annotations *behind* the `geom_pointrange` which displays the estimates. Since `modelplot` draws the `geom_pointrange` automatically, any `ggplot2` annotation you add to the plot using `+` will be added on *top* of the existing ones.

To add your annotations in the background, you can pass them as a list of `ggplot2` “geoms”:

```
library(ggplot2)

b <- list(geom_vline(xintercept = 0, color = 'orange'),
  annotate("rect", alpha = .1,
    xmin = -.5, xmax = .5,
    ymin = -Inf, ymax = Inf),
  geom_point(aes(y = term, x = estimate), alpha = .3,
    size = 10, color = 'red'))

modelplot(mod, background = b)
```



## 6 Raw data and customization

If you would like to customize the plots even more than what `modelplot` allows, you can obtain the raw data used to draw the plots by setting `draw=FALSE`:

```
modelplot(models, draw = FALSE)
```

	term	model	estimate	std.error	conf.low	conf.high	p.value
1	(Intercept)	vs	2.41742511	0.67622094	1.03224931	3.80260091	1.296718e-03
5	(Intercept)	disp	112.57276339	114.86315481	-122.71374324	347.85927003	3.354494e-01
9	(Intercept)	hp	-10.56116383	68.75946117	-151.40853516	130.28620751	8.790301e-01
2	carb	vs	-0.06945116	0.03943402	-0.15022810	0.01132577	8.912324e-02
6	carb	disp	-12.30144724	6.69827859	-26.02224894	1.41935446	7.692105e-02
10	carb	hp	17.75593287	4.00972816	9.54237706	25.96948867	1.320972e-04
3	mpg	vs	-0.01513960	0.01716410	-0.05029868	0.02001947	3.852593e-01
7	mpg	disp	-7.14964651	2.91550156	-13.12178072	-1.17751230	2.068858e-02
11	mpg	hp	-1.00486469	1.74527956	-4.57990780	2.57017842	5.693755e-01
4	cyl	vs	-0.23926135	0.05687969	-0.35577411	-0.12274859	2.410214e-04
8	cyl	disp	47.90105842	9.66160634	28.11015499	67.69196184	3.111898e-05
12	cyl	hp	20.60581208	5.78363747	8.75856779	32.45305638	1.338485e-03

This allows users to use external tools such as [the powerful ggdist package](#). In this example, we use the `purrr::map_dfr` function to call `modelplot` several times with different confidence levels. Then, we draw a plot where the different confidence intervals are drawn with different thicknesses:

```
library(tidyverse)
library(modelsummary)
library(ggdist)

# fit
models <- list(
  lm(mpg ~ am, mtcars),
  lm(mpg ~ am + cyl, mtcars))

# summarize
dat <- map_dfr(c(.8, .9, .99), function(x) {
  modelplot(models, conf_level = x, draw = FALSE) %>%
  mutate(.width = x)
})

# plot
ggplot(dat, aes(
  y = term, x = estimate,
  xmin = conf.low, xmax = conf.high,
  color = model)) +
ggdist::geom_pointinterval(
  position = "dodge",
  interval_size_range = c(1, 3),
  fatten_point = .1)
```

