

The facets layer

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2

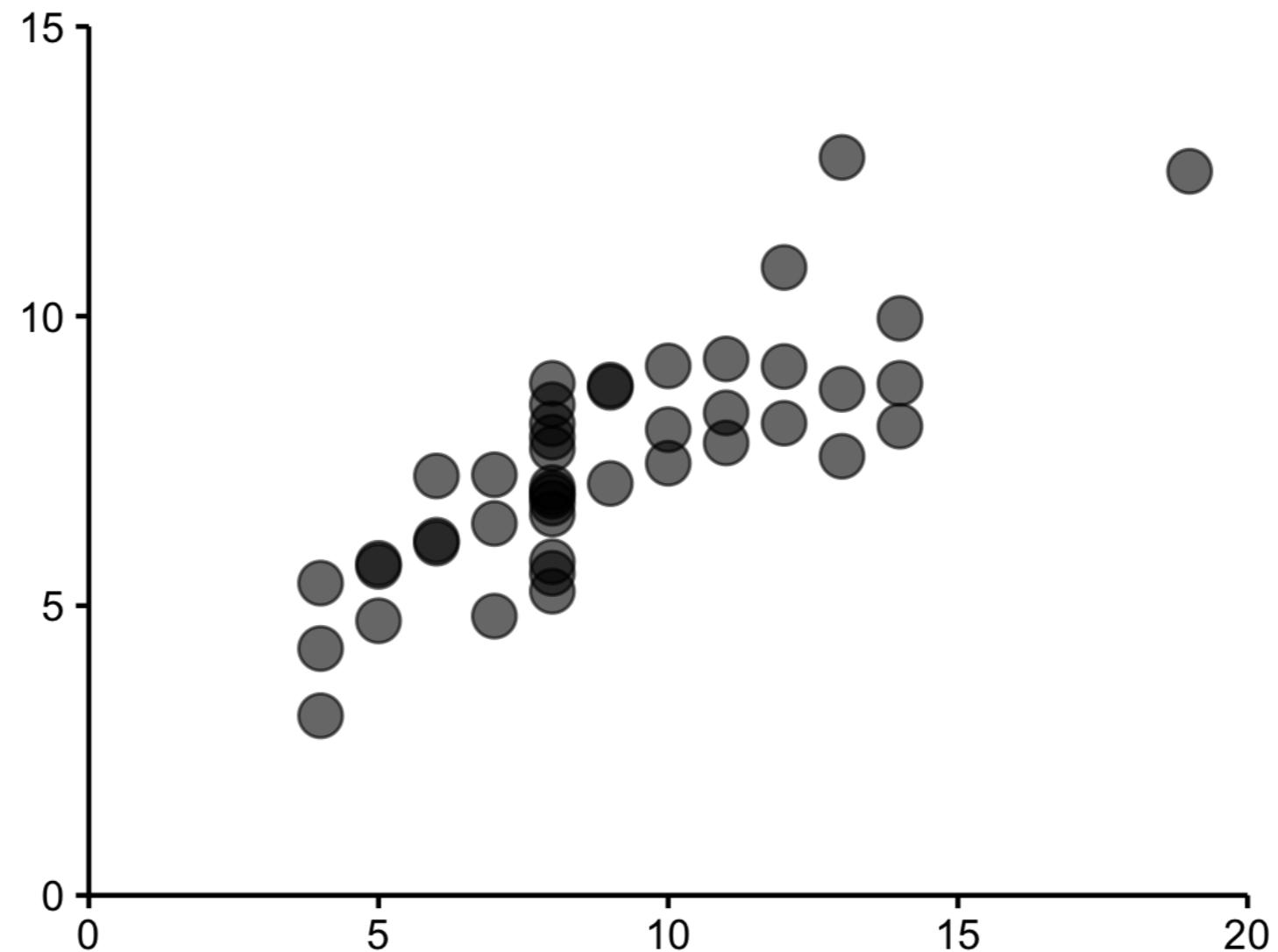


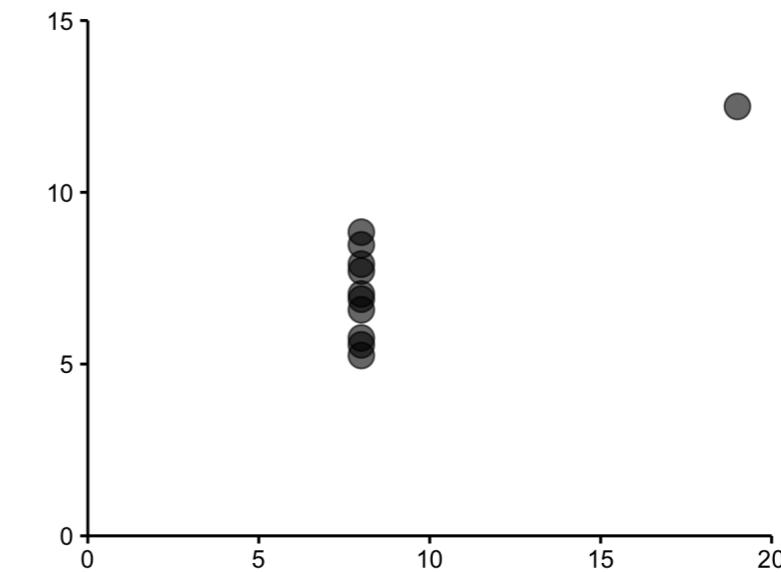
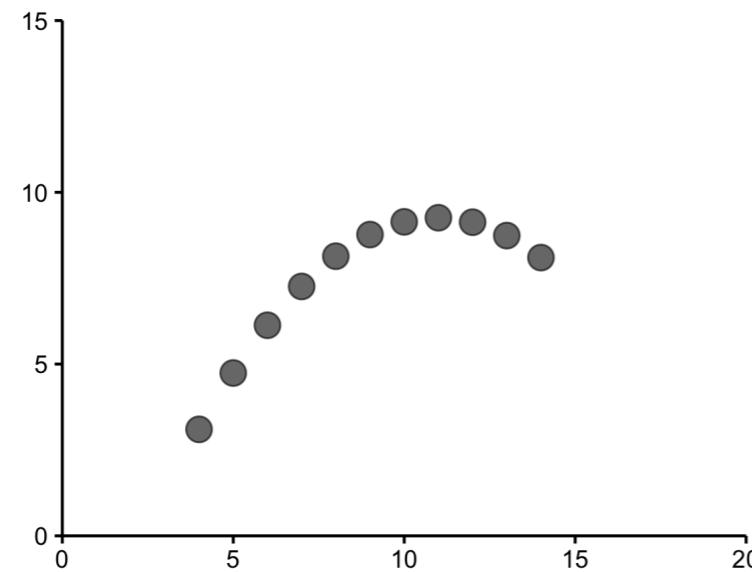
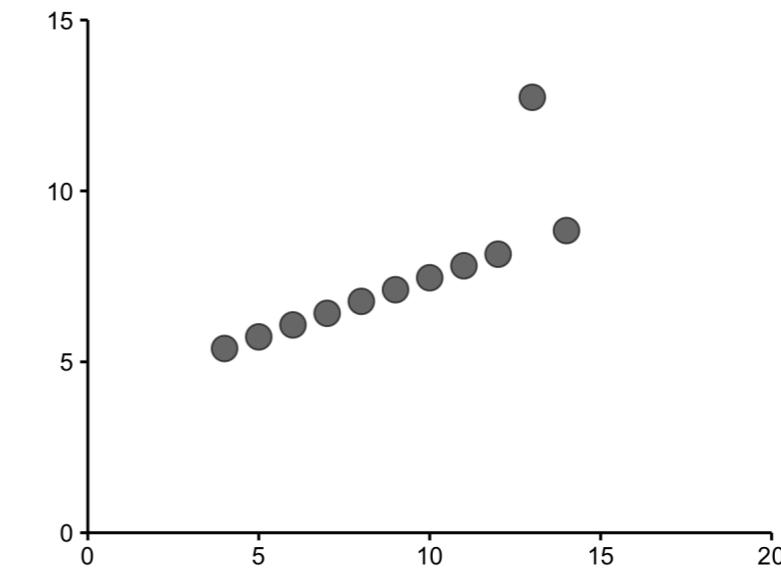
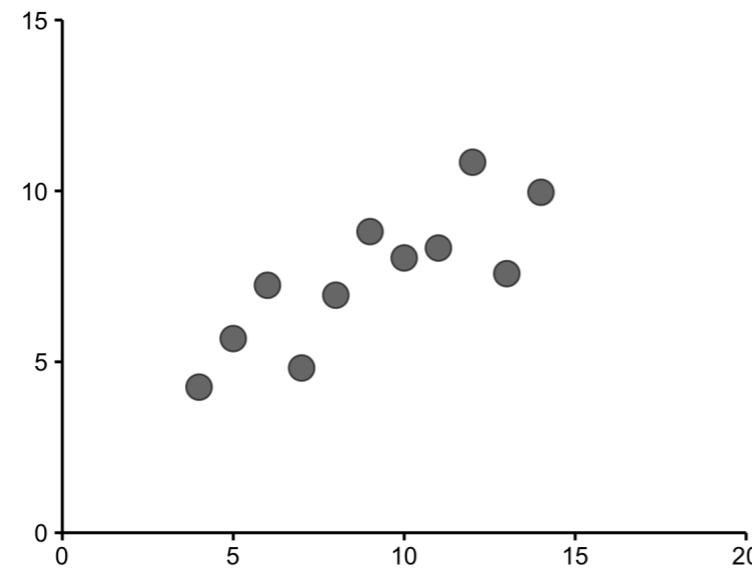
Rick Scavetta

Founder, Scavetta Academy

Facets

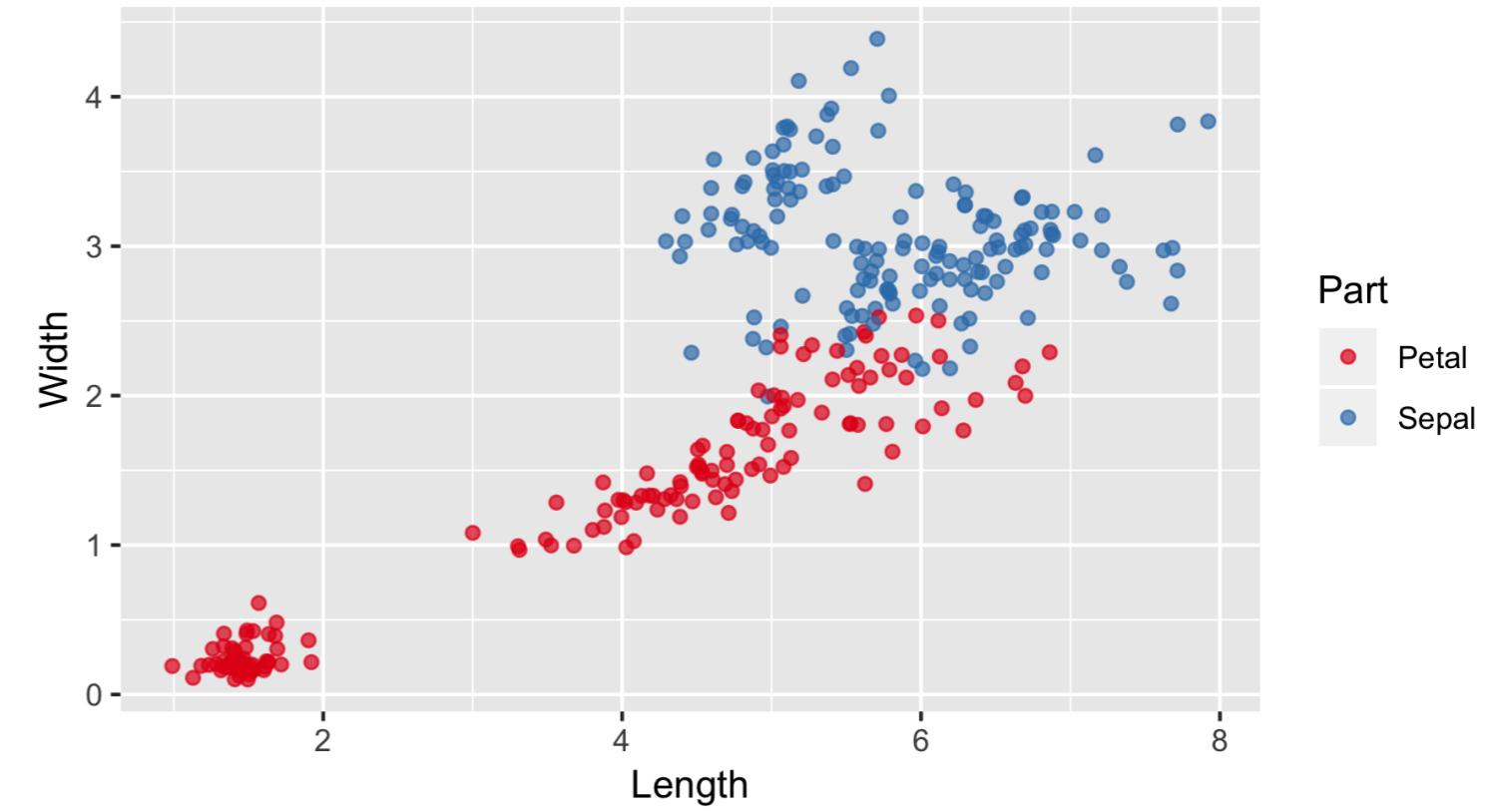
- Straight-forward yet useful
- Concept of Small Multiples
 - Popularized by Edward Tufte
 - Visualization of Quantitative Information, 1983





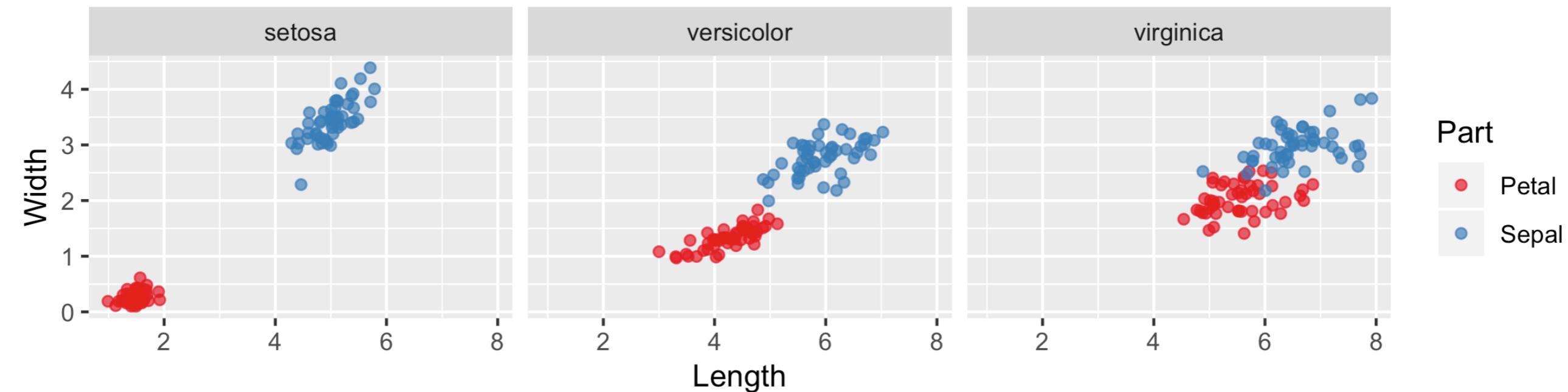
iris.wide

```
p <- ggplot(iris.wide, aes(x = Length,  
                           y = Width,  
                           color = Part)) +  
  geom_jitter(alpha = 0.7) +  
  scale_color_brewer(palette = "Set1") +  
  coord_fixed()  
  
p
```



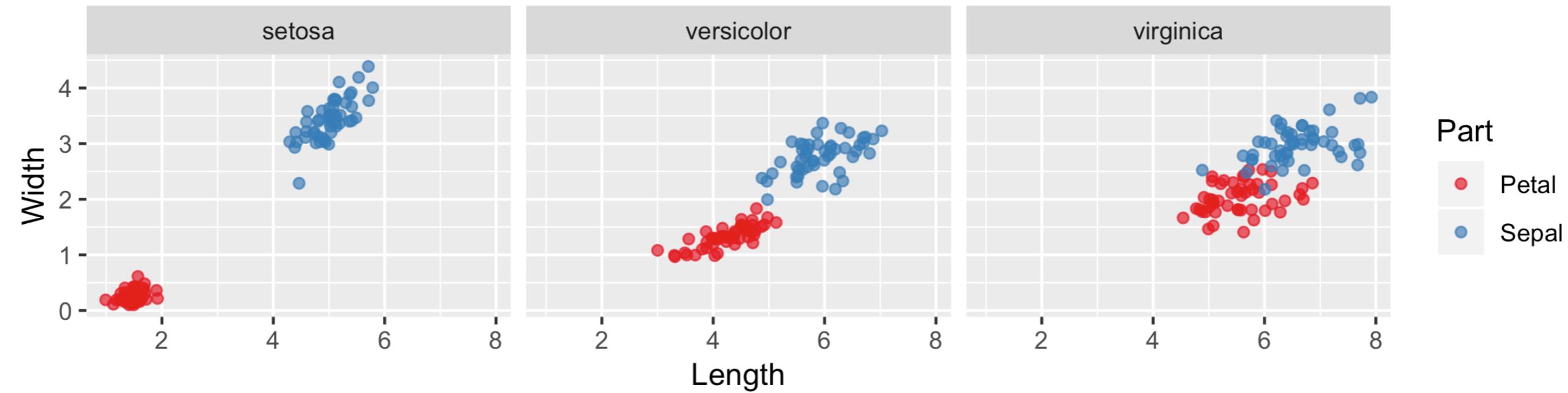
iris.wide & facet_grid()

```
p <- ggplot(iris.wide, aes(x = Length, y = Width, color = Part)) +  
  geom_jitter(alpha = 0.7) +  
  scale_color_brewer(palette = "Set1") +  
  coord_fixed()  
p + facet_grid(cols = vars(Species))
```



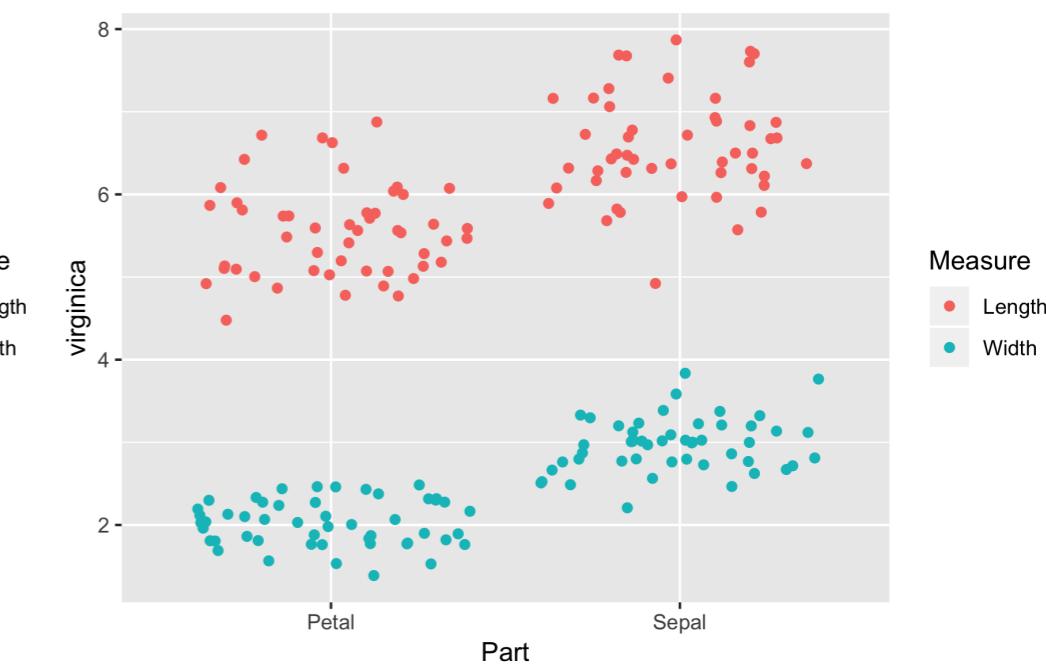
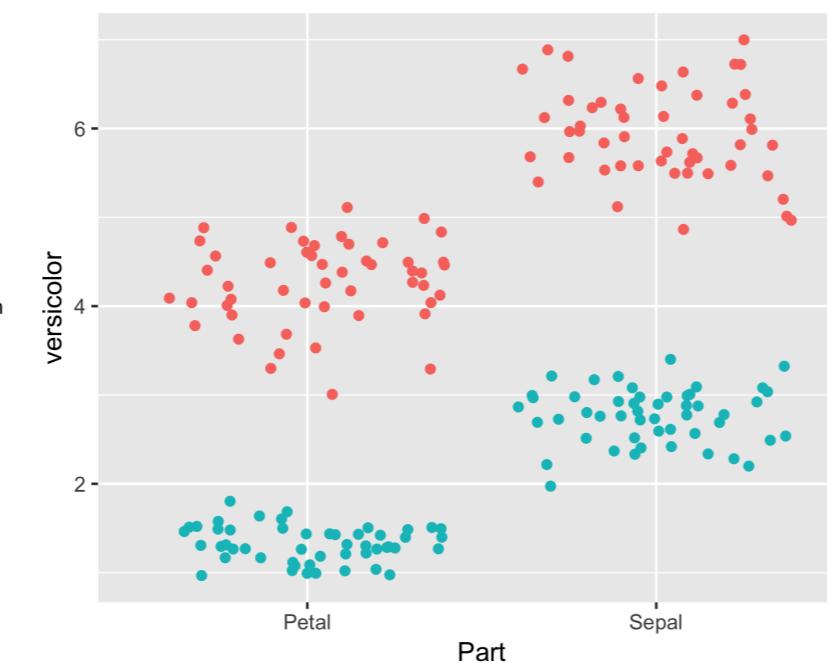
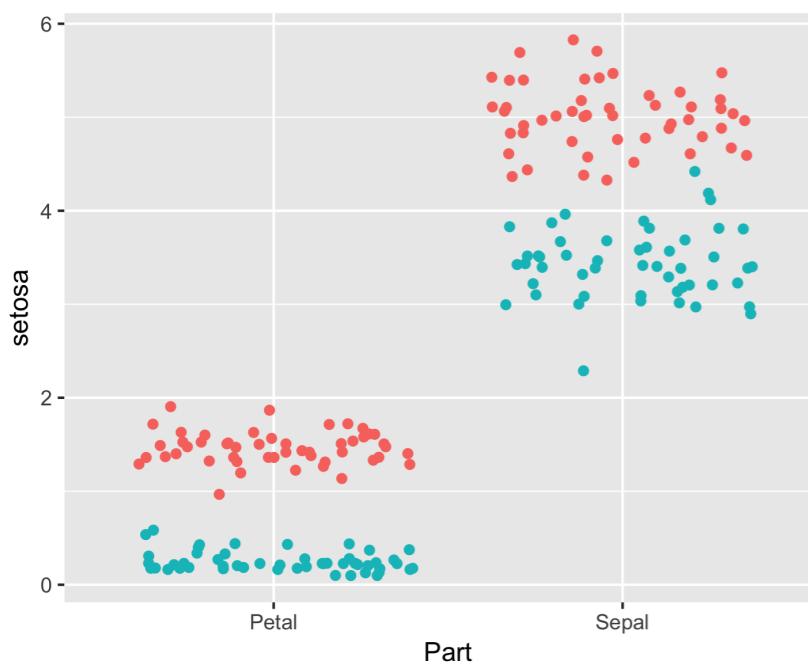
Formula notation

```
p <- ggplot(iris.wide, aes(x = Length, y = Width, color = Part)) +  
  geom_jitter(alpha = 0.7) +  
  scale_color_brewer(palette = "Set1") +  
  coord_fixed()  
p + facet_grid(. ~ Species)
```



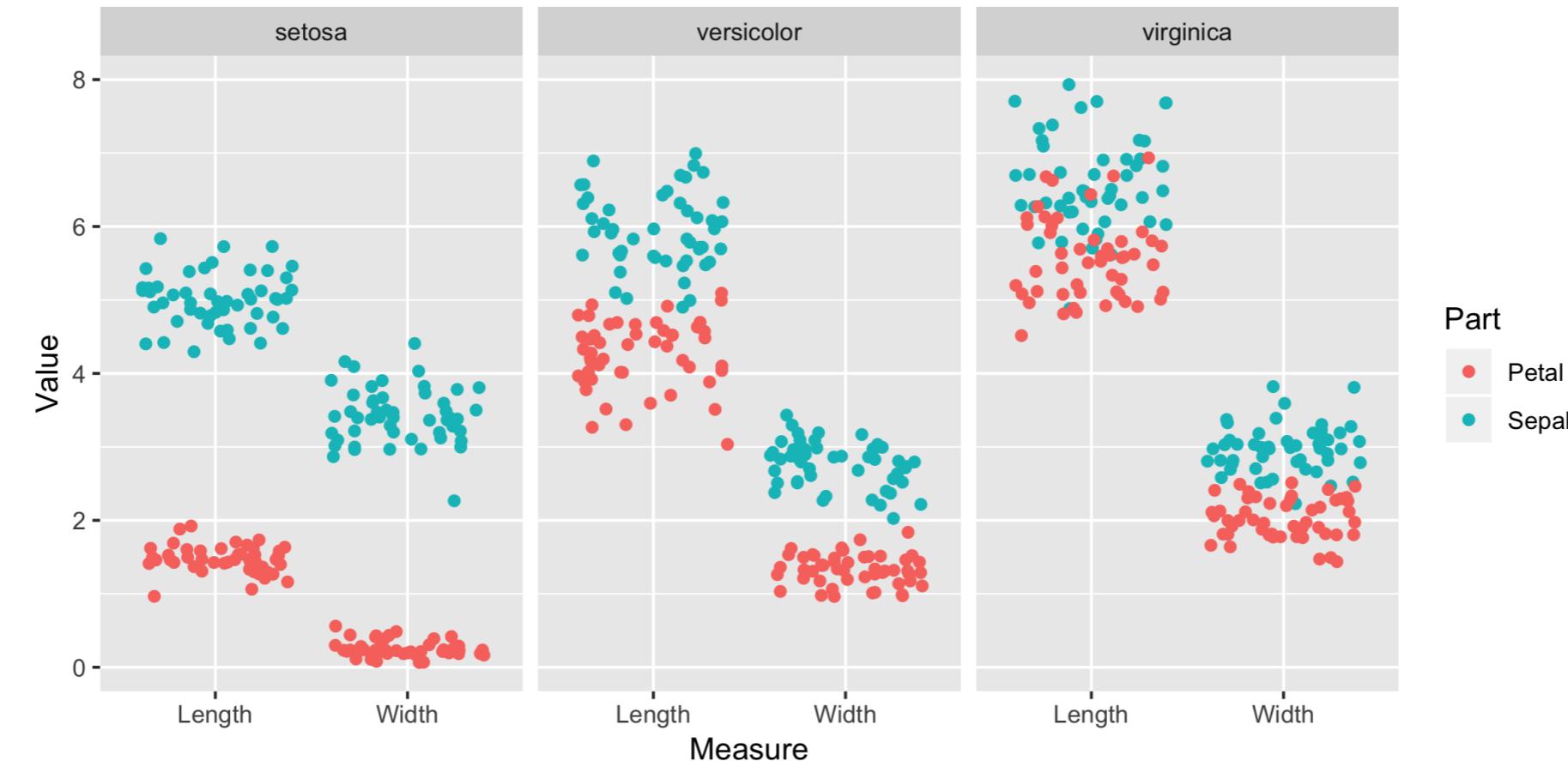
iris.wide2

```
ggplot(iris.wide2, aes(x = Part, y = setosa, color = Measure)) +  
  geom_jitter()  
  
ggplot(iris.wide2, aes(x = Part, y = versicolor, color = Measure)) +  
  geom_jitter()  
  
ggplot(iris.wide2, aes(x = Part, y = virginica, color = Measure)) +  
  geom_jitter()
```



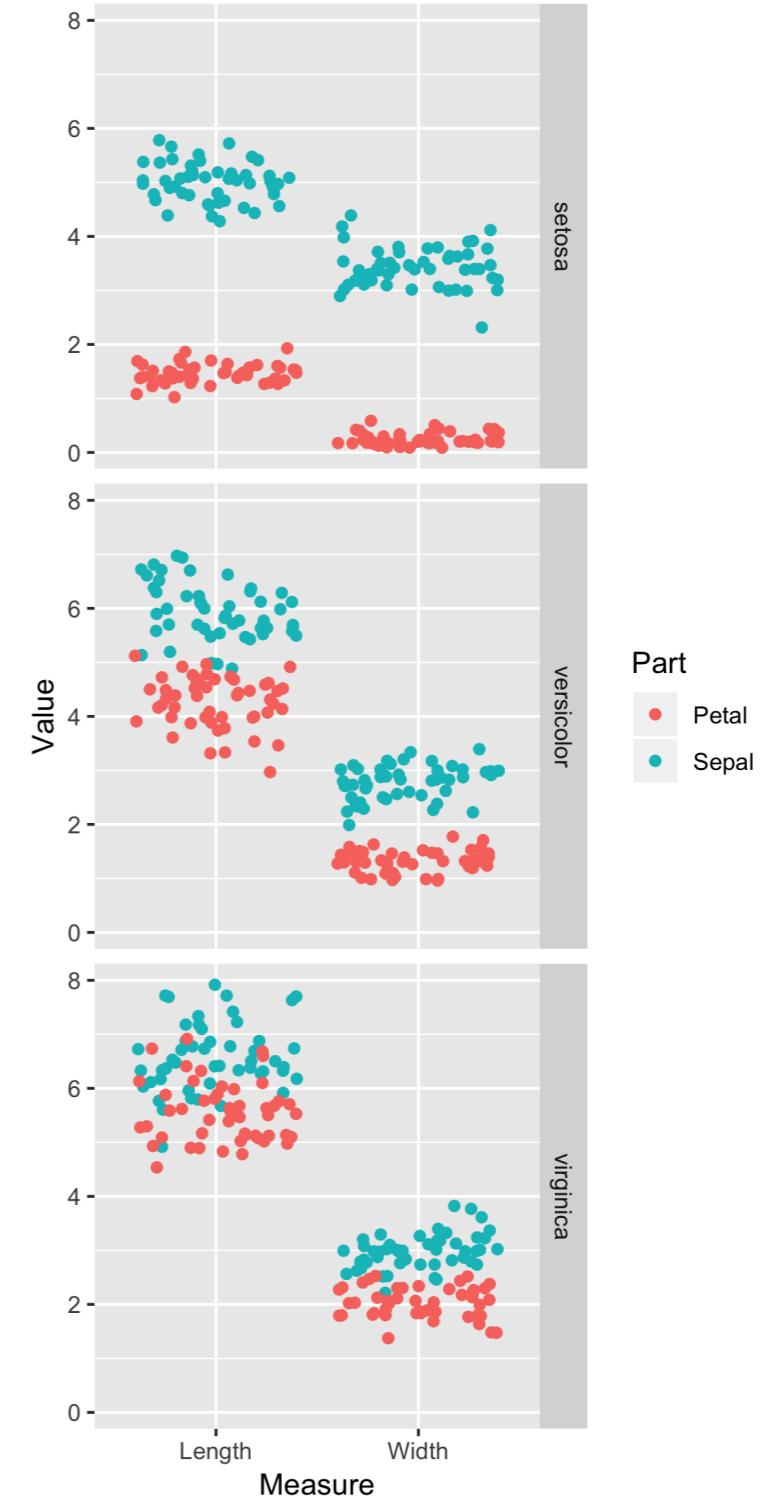
iris.tidy

```
ggplot(iris.tidy, aes(x = Measure, y = Value, color = Part)) +  
  geom_jitter() +  
  facet_grid(cols = vars(Species))
```



iris.tidy faceting done wrong:

```
ggplot(iris.tidy, aes(x = Measure,  
                      y = Value,  
                      color = Part)) +  
  
  geom_jitter() +  
  
  facet_grid(rows = vars(Species))
```



Other options

- Split according to rows and columns

Let's practice!

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2

Facet labels and order

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2

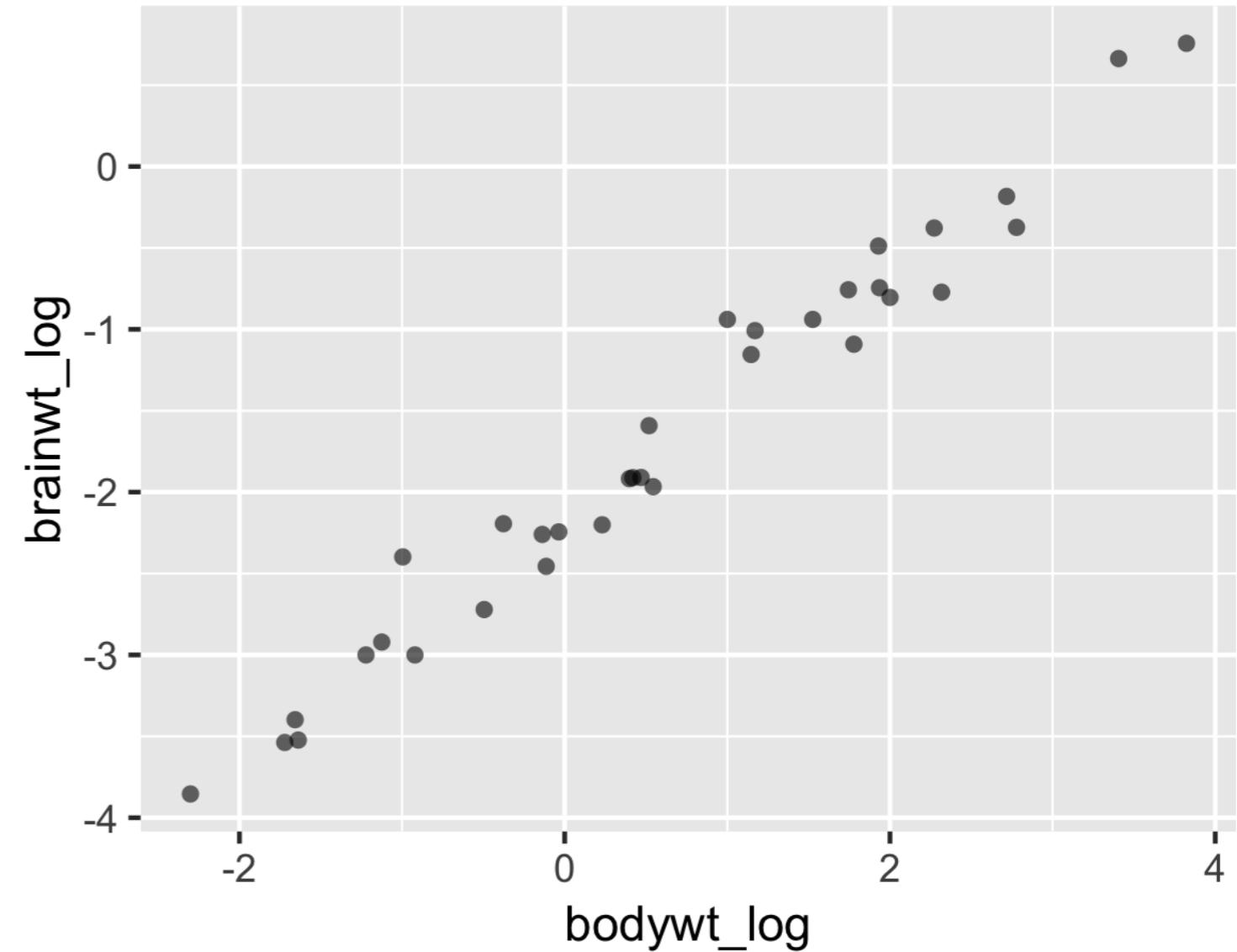


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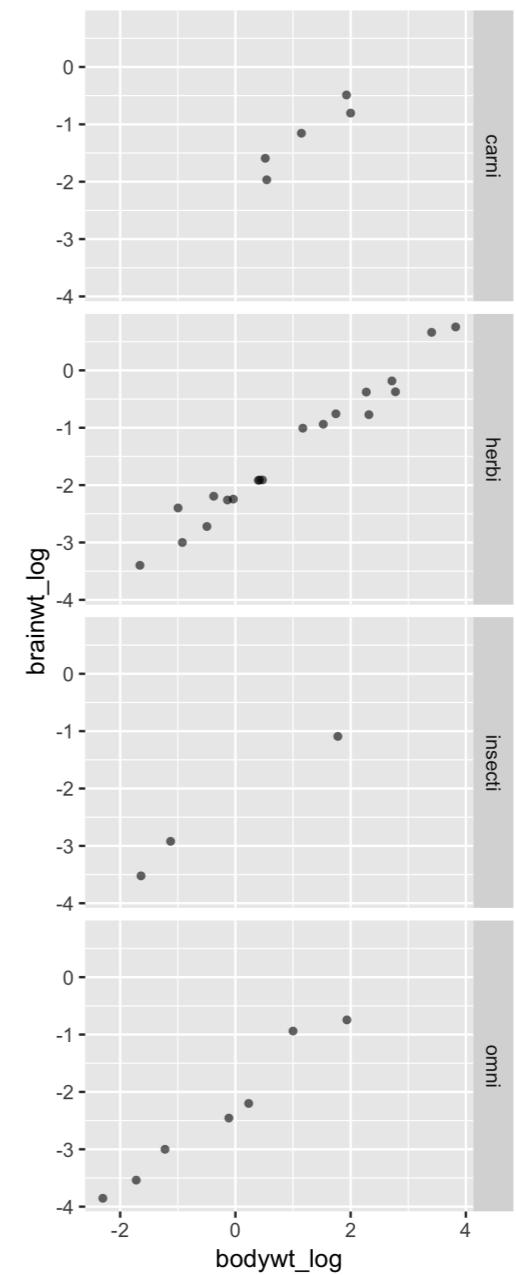
A new dataframe

```
# Plot  
p <- ggplot(msleep2, aes(bodywt_log,  
                           brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  coord_fixed()  
  
p
```



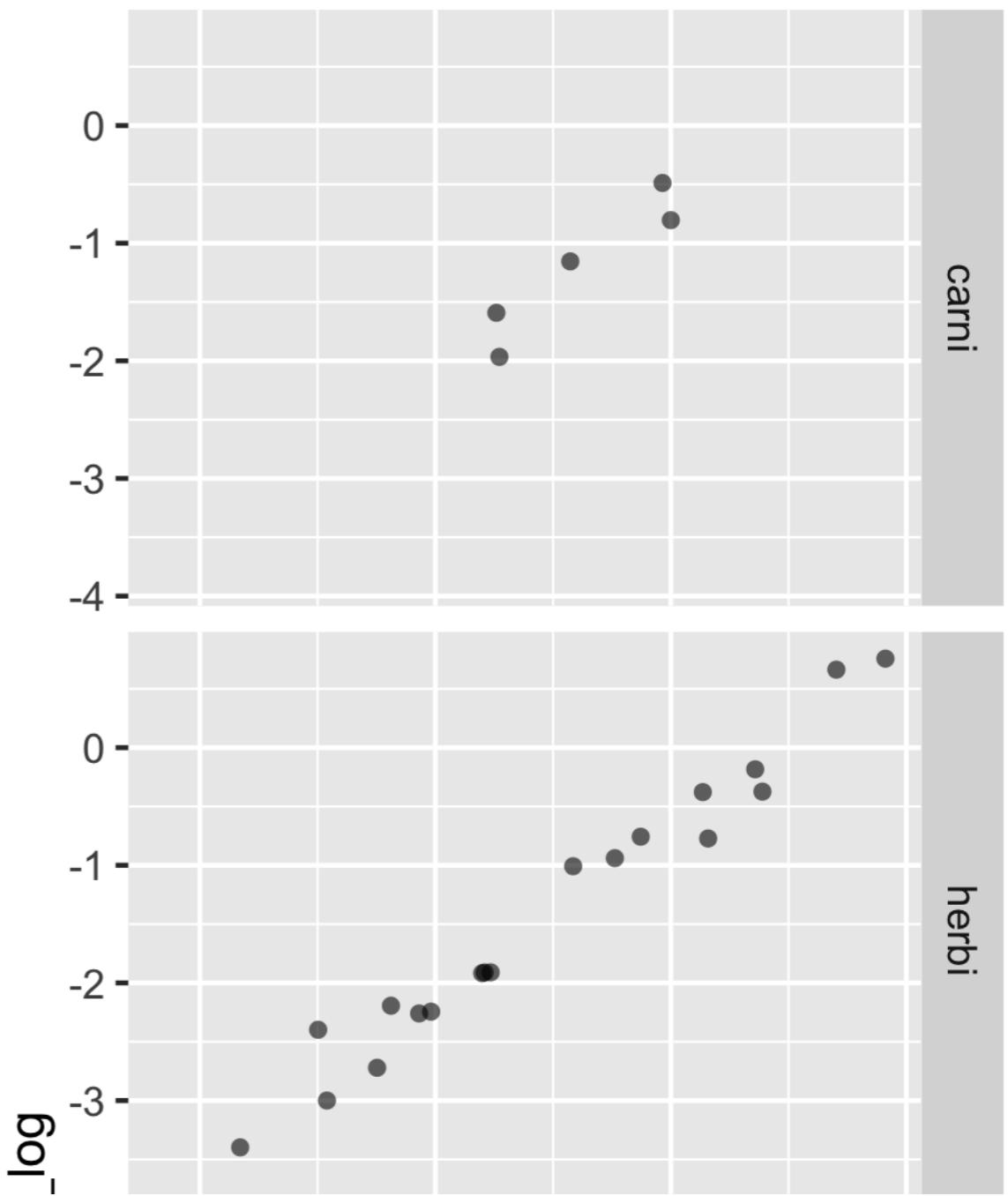
A new dataframe, with facets

```
p +  
  facet_grid(rows = vars(vore))
```



A new dataframe, with facets

```
p +  
  facet_grid(rows = vars(vore))
```

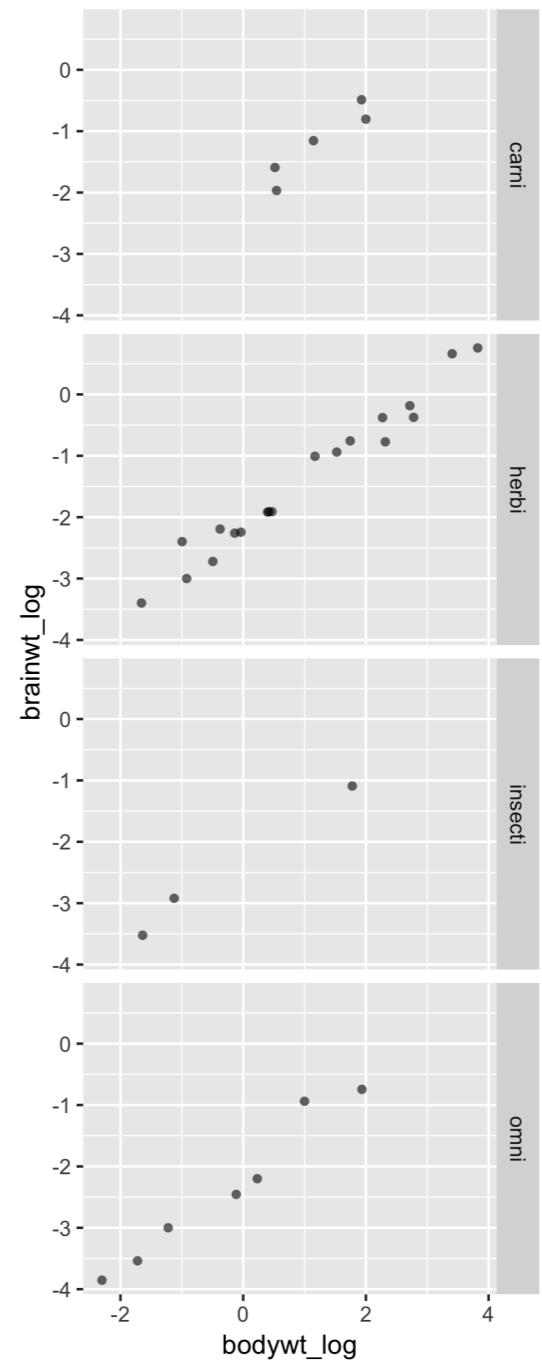


Poor labels and order

```
p +  
  facet_grid(rows = vars(vore))
```

Two typical problems with facets:

- Poorly labeled (e.g. non descriptive)
- Wrong or inappropriate order

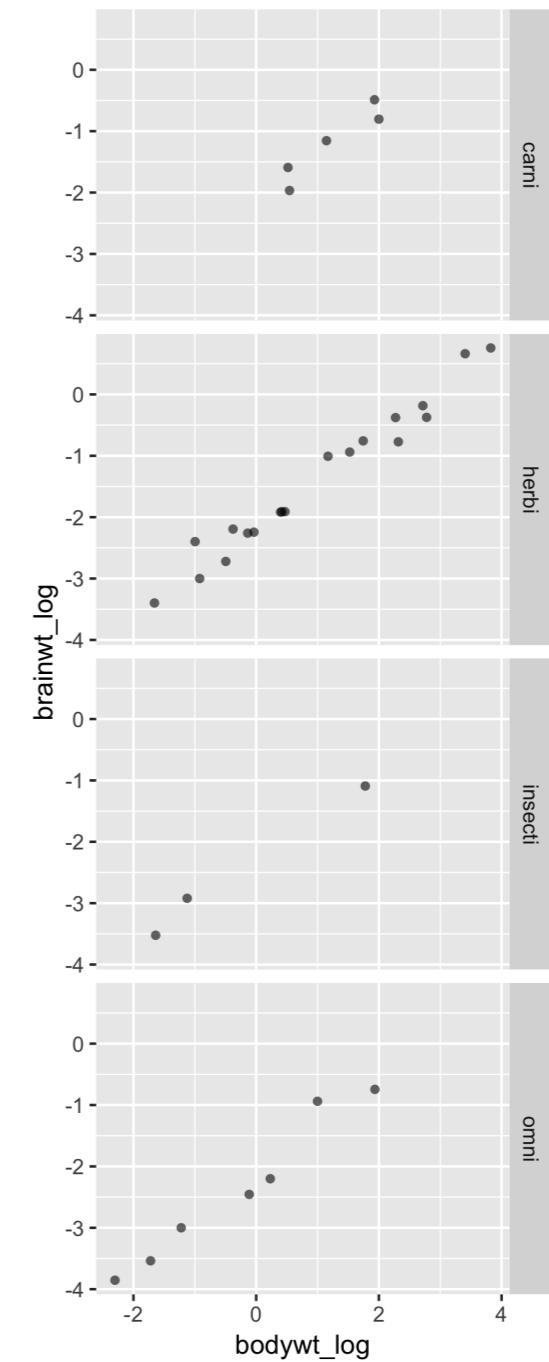


Poor labels and order

```
p +  
  facet_grid(rows = vars(vore))
```

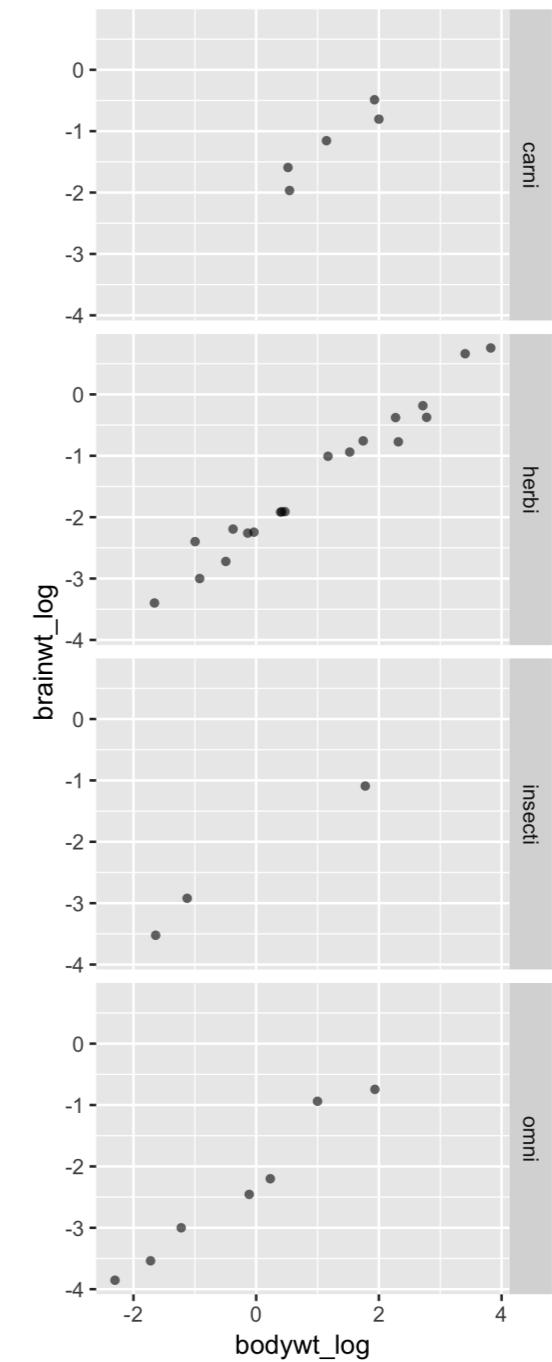
Solutions:

- Easy: Add labels in ggplot
- Better: Relabel and rearrange factor variables in your dataframe



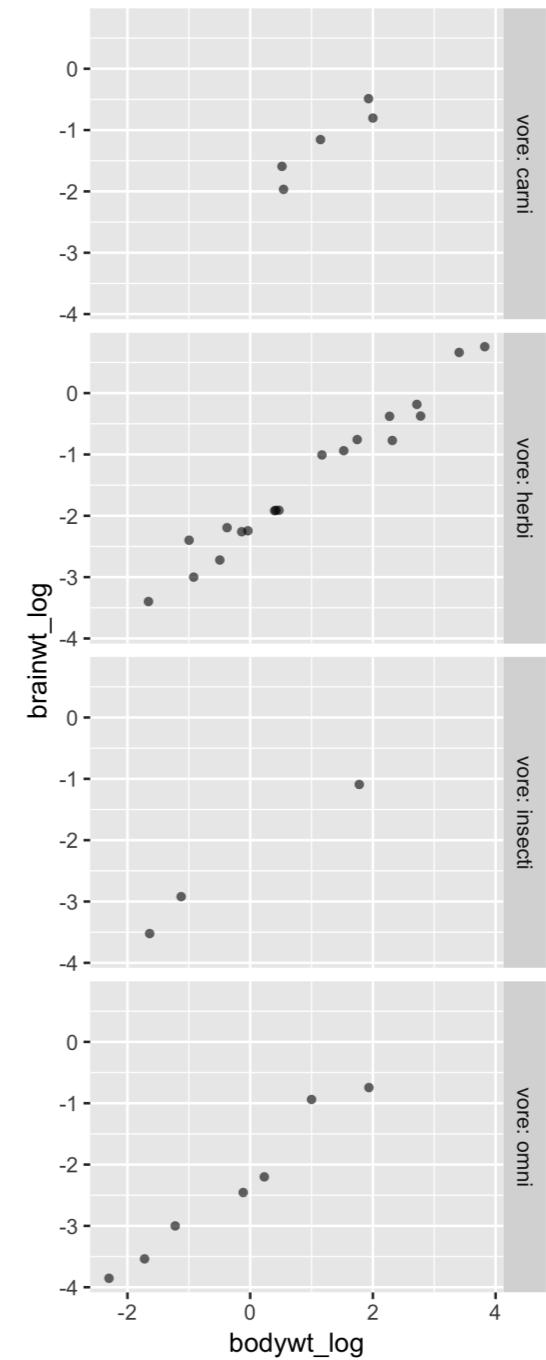
The labeller argument

```
# Default is to label the value  
p +  
  facet_grid(rows = vars(vore),  
             labeller = label_value)
```



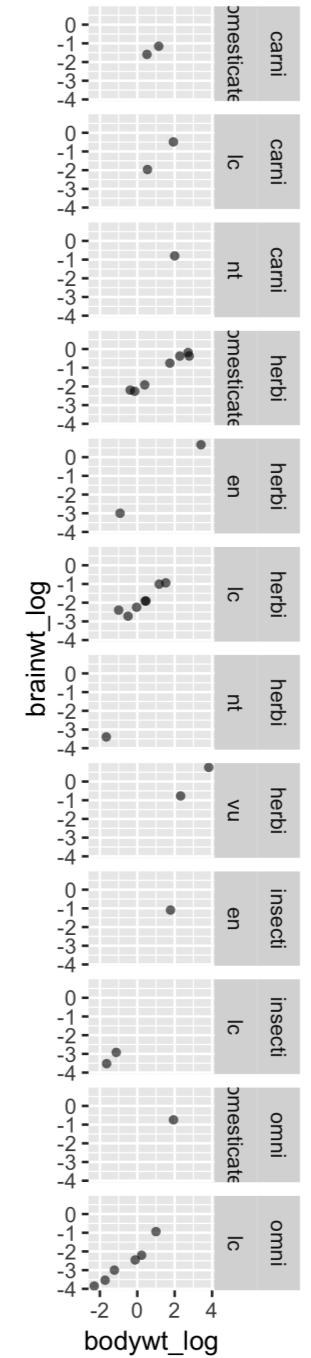
Using `label_both` adds the variable name

```
# Print variable name also  
p +  
  facet_grid(rows = vars(vore),  
             labeller = label_both)
```



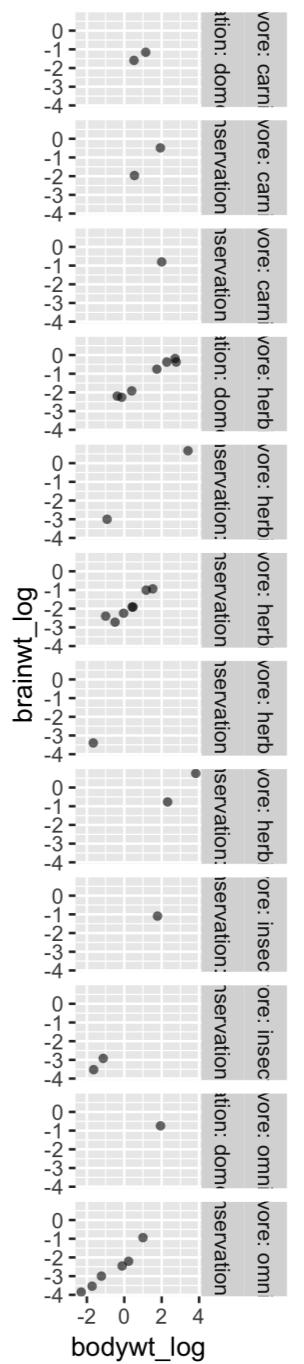
Two variables on one side

```
p +  
  facet_grid(rows = vars(vore,  
                         conservation))
```



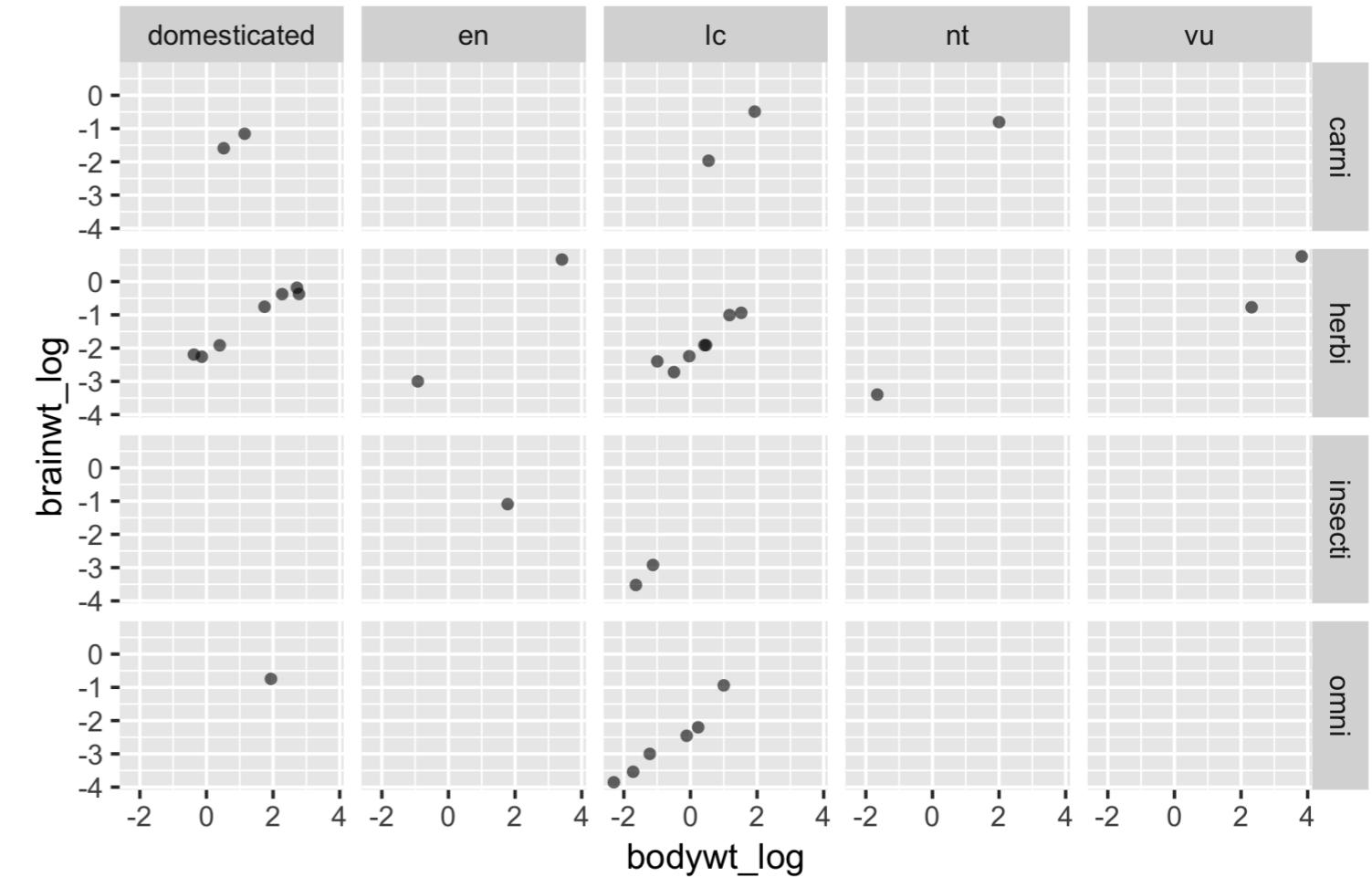
Using `label_context` avoids ambiguity

```
p +  
  facet_grid(rows = vars(vore,  
                         conservation),  
             labeller = label_context)
```



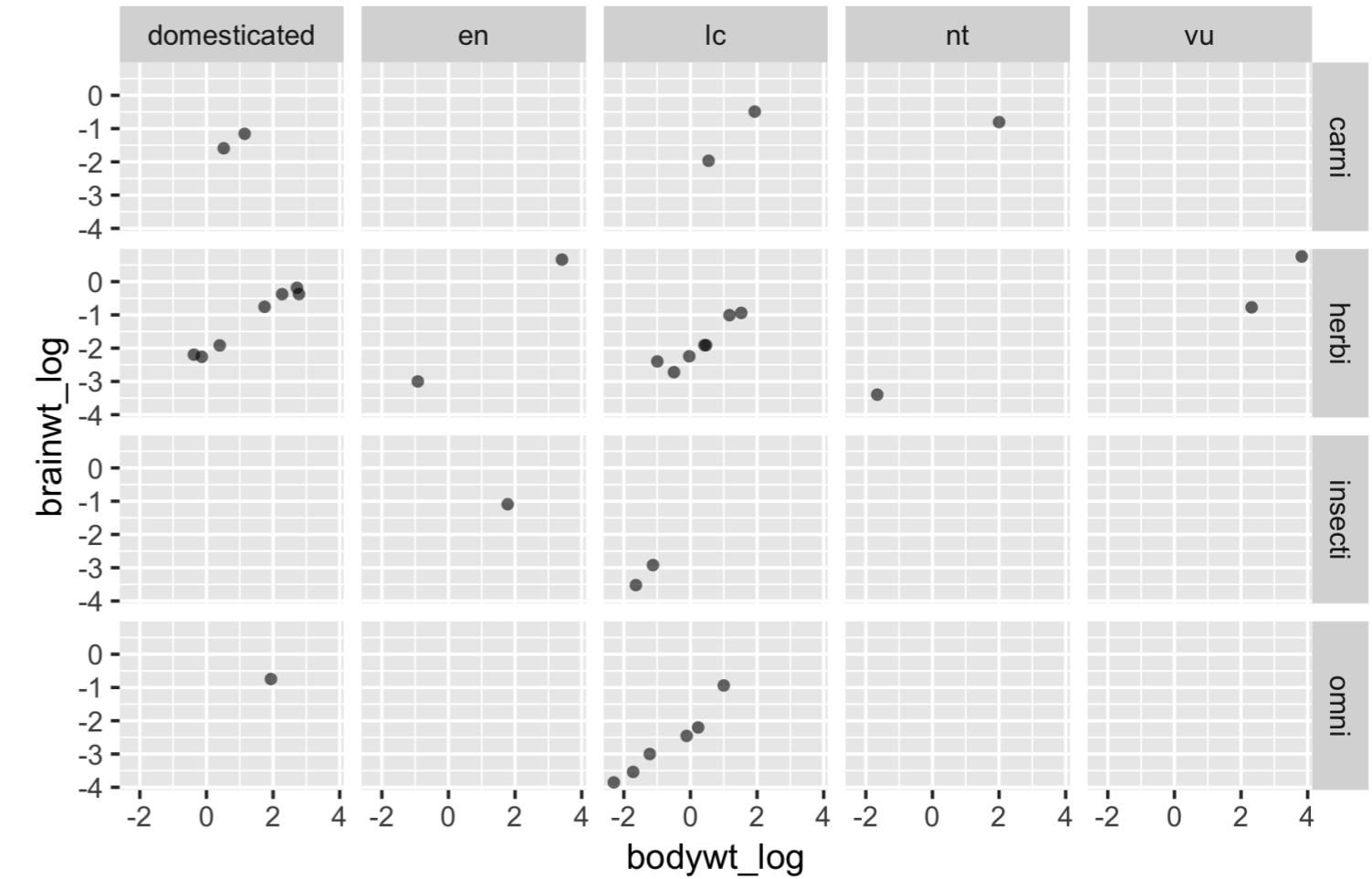
Use rows and columns when appropriate

```
p +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation),  
             labeller = label_context)
```

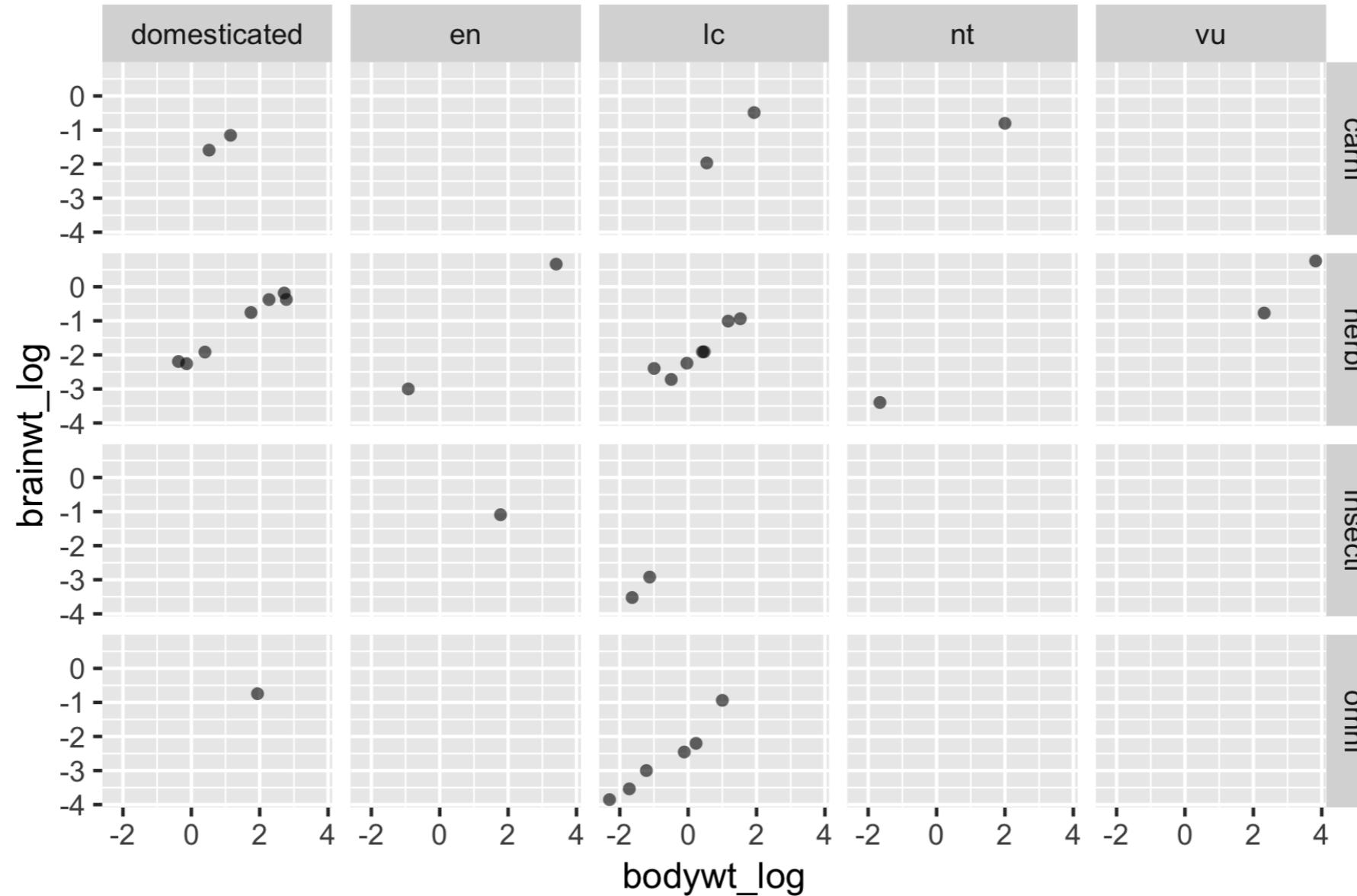


Use rows and columns when appropriate

```
p +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation))
```



Use rows and columns when appropriate

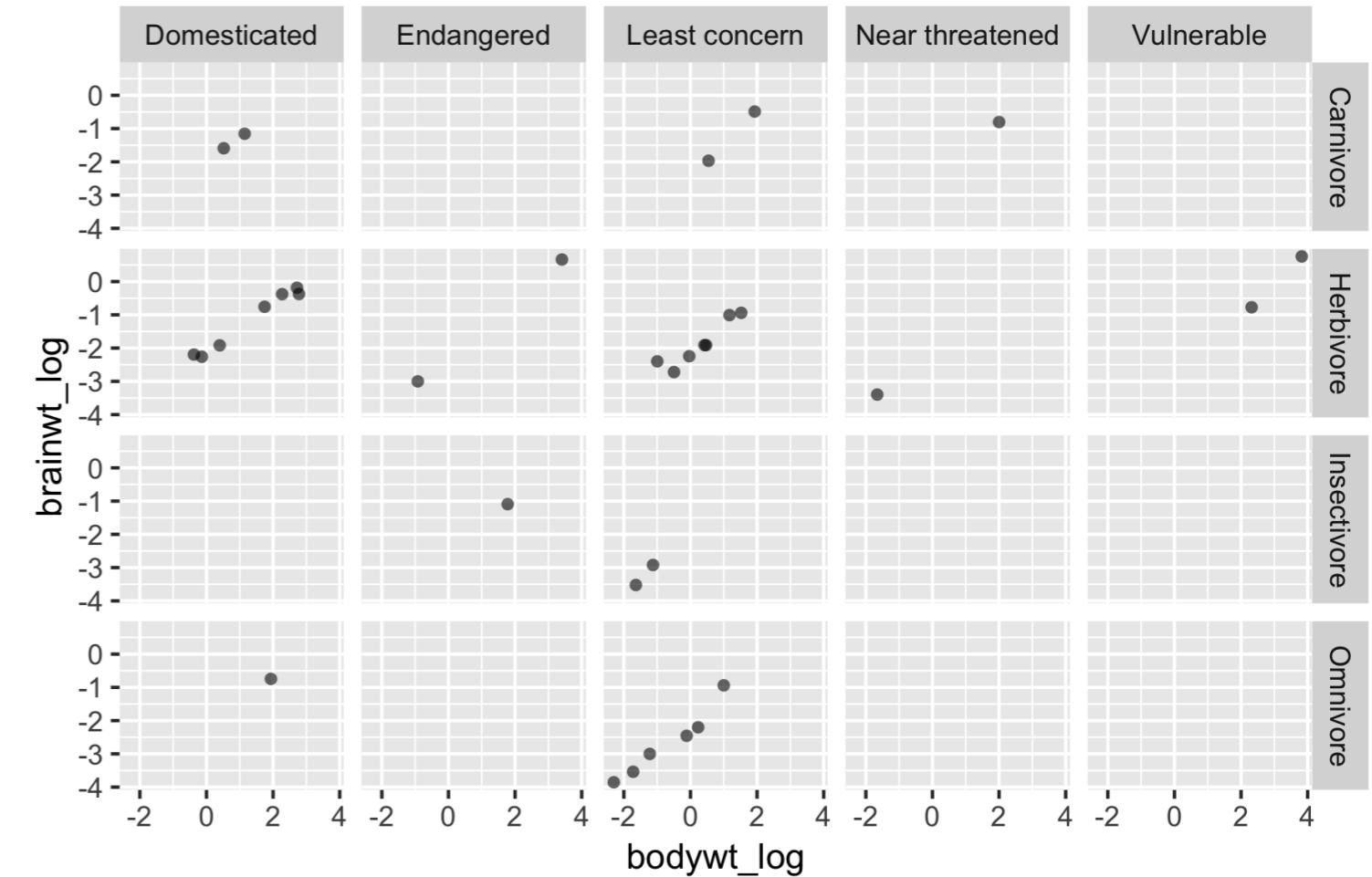


Relabeling and reordering factors

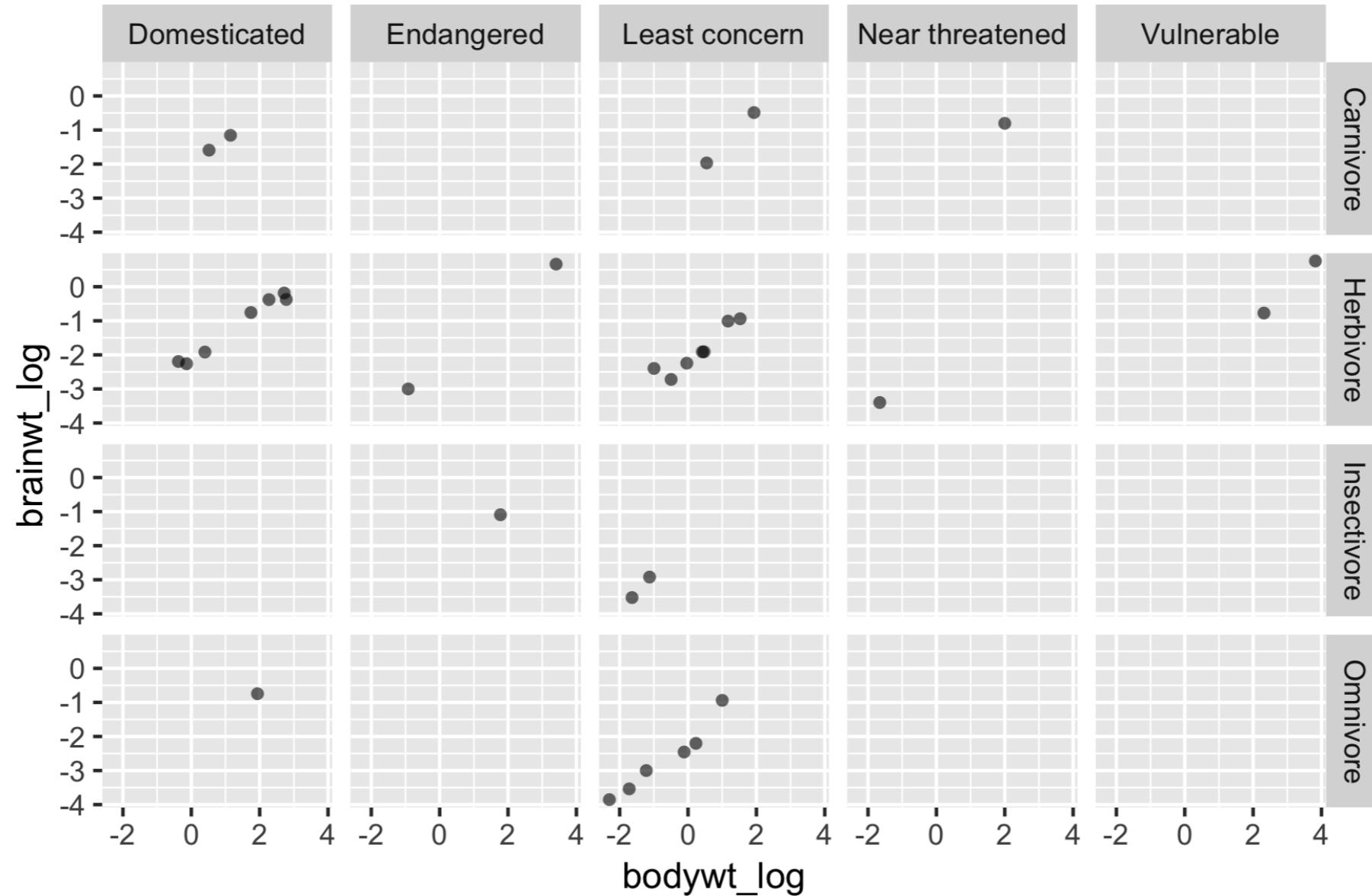
```
msleep2$conservation <- fct_recode(msleep2$conservation,  
                                     Domesticated = "domesticated",  
                                     `Least concern` = "lc",  
                                     `Near threatened` = "nt",  
                                     Vulnerable = "vu",  
                                     Endangered = "en")  
  
msleep2$vore = fct_recode(msleep2$vore,  
                           Carnivore = "carni",  
                           Herbivore = "herbi",  
                           Insectivore = "insecti",  
                           Omnivore = "omni")
```

Reinitialize plot with new labels

```
# Plot  
p <- ggplot(msleep2, aes(bodywt_log,  
                           brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  coord_fixed()  
  
p +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation))
```



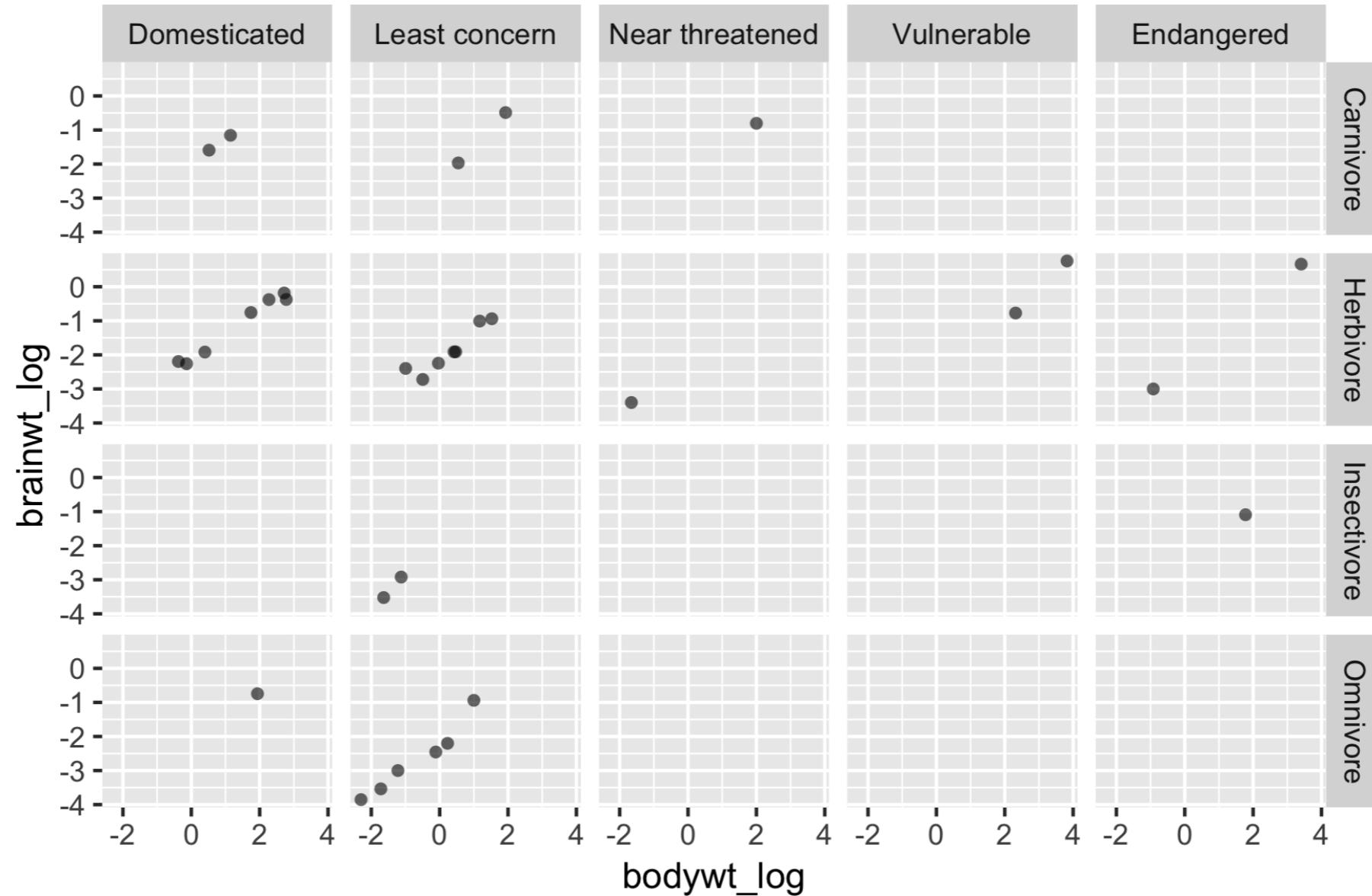
Reinitialize plot with new labels



Changing the order of levels

```
# Change order of levels:  
msleep2$conservation = fct_relevel(msleep2$conservation,  
                                     c("Domesticated",  
                                       "Least concern",  
                                       "Near threatened",  
                                       "Vulnerable",  
                                       "Endangered"))
```

Reinitialize plot with new order



Let's practice!

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2

Facet plotting spaces

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2



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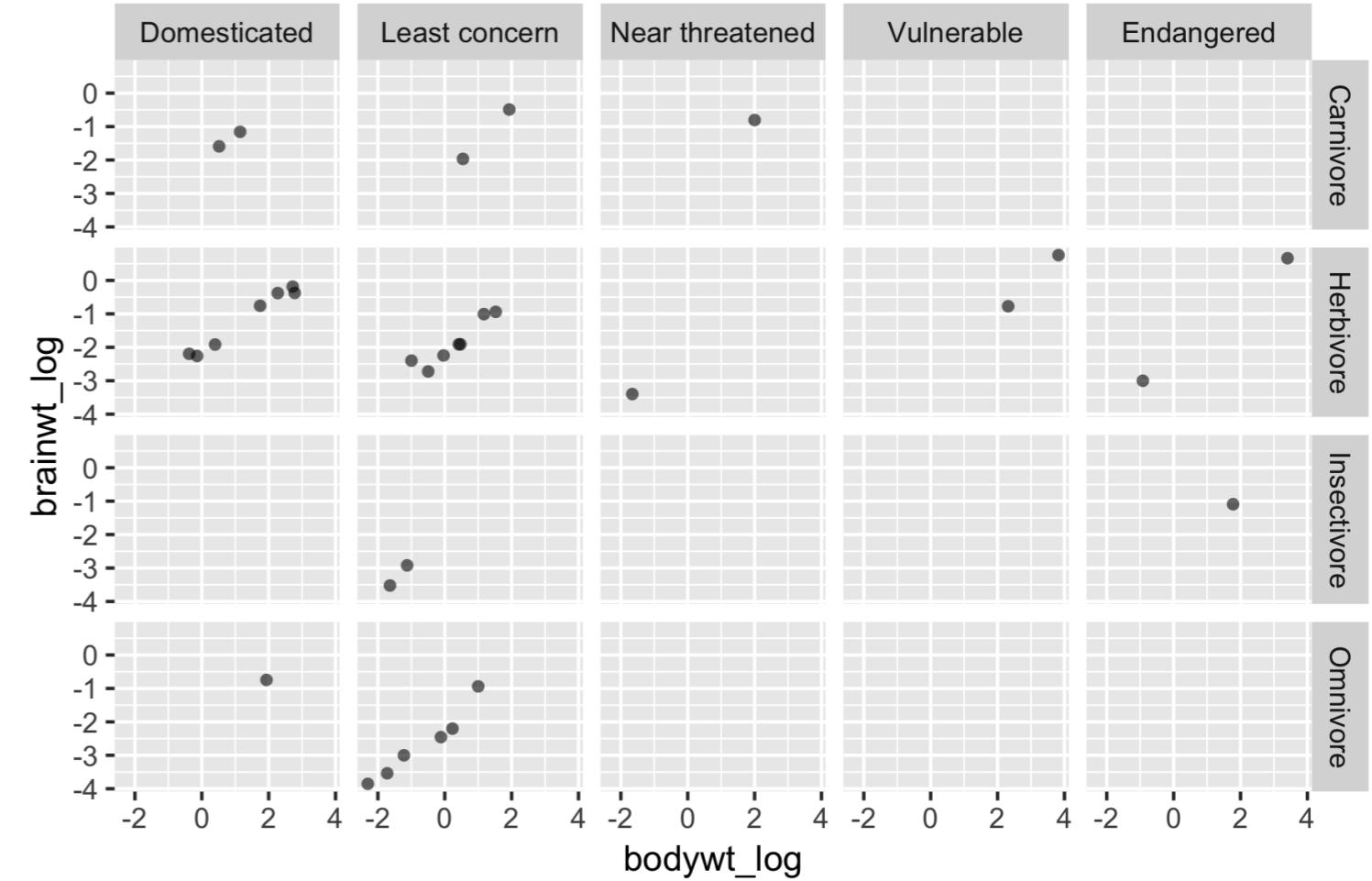
Facets and variable plotting spaces

Reasons to not use consistent plotting spaces:

Variable type	Subsets contains
Continuous	Wildly different ranges
Categorical	Different groups

Adjusting the plotting space...

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  coord_fixed() +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation))
```



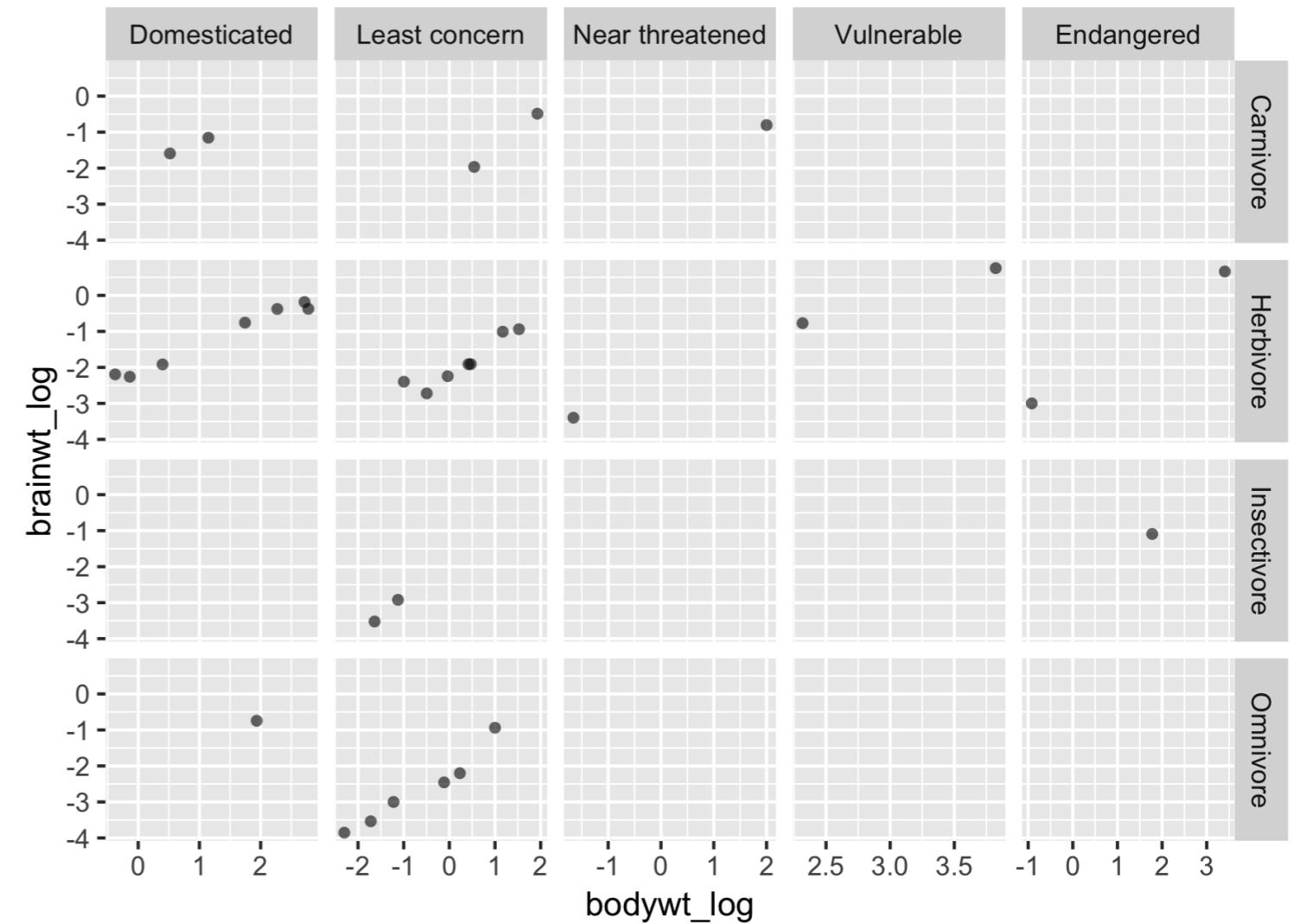
... but not with fixed scales

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  coord_fixed() +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation),  
             scales = "free_x")
```

Error: coord_fixed doesn't support free scales

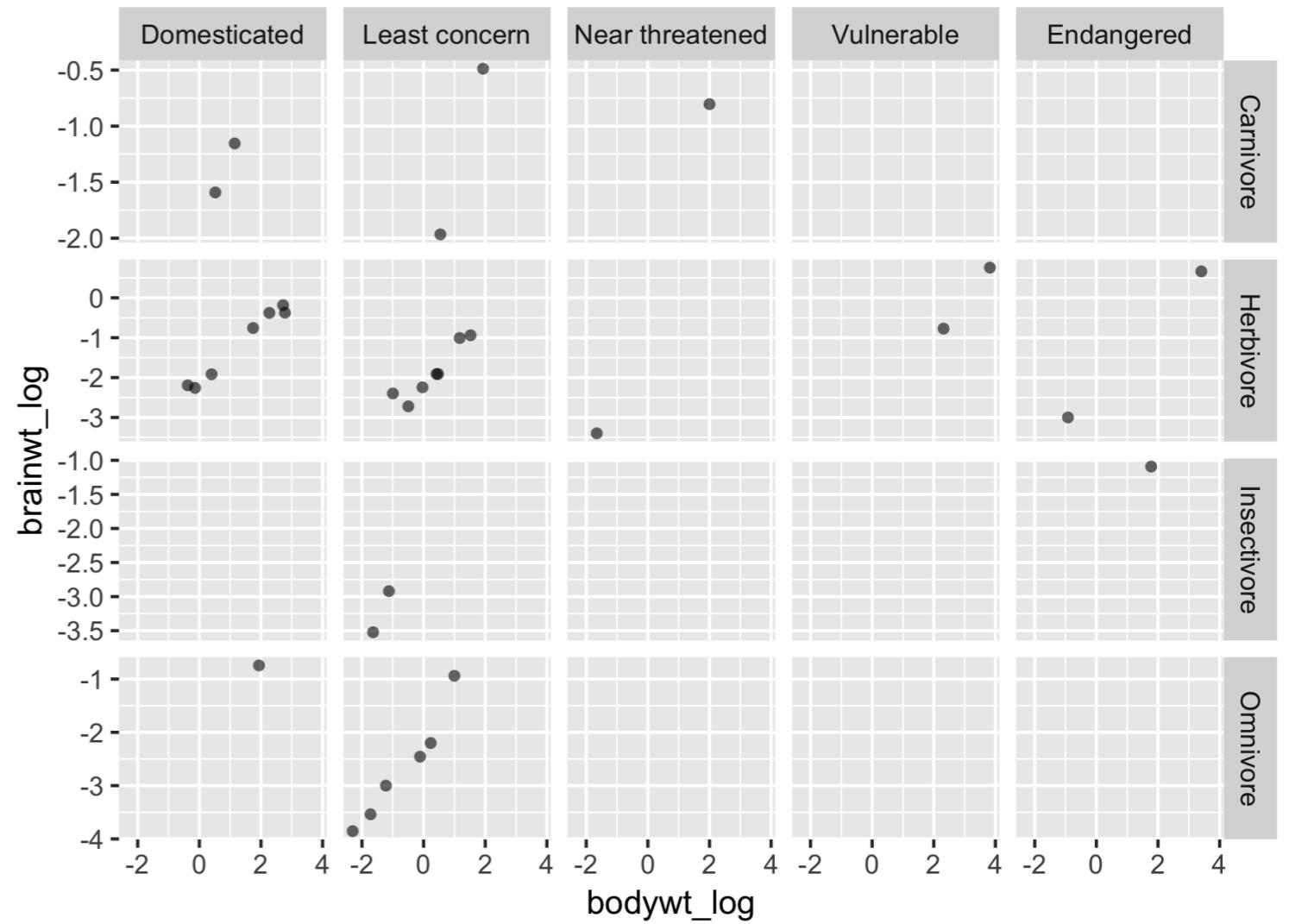
Adjusting the plotting space

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation),  
             scales = "free_x")
```



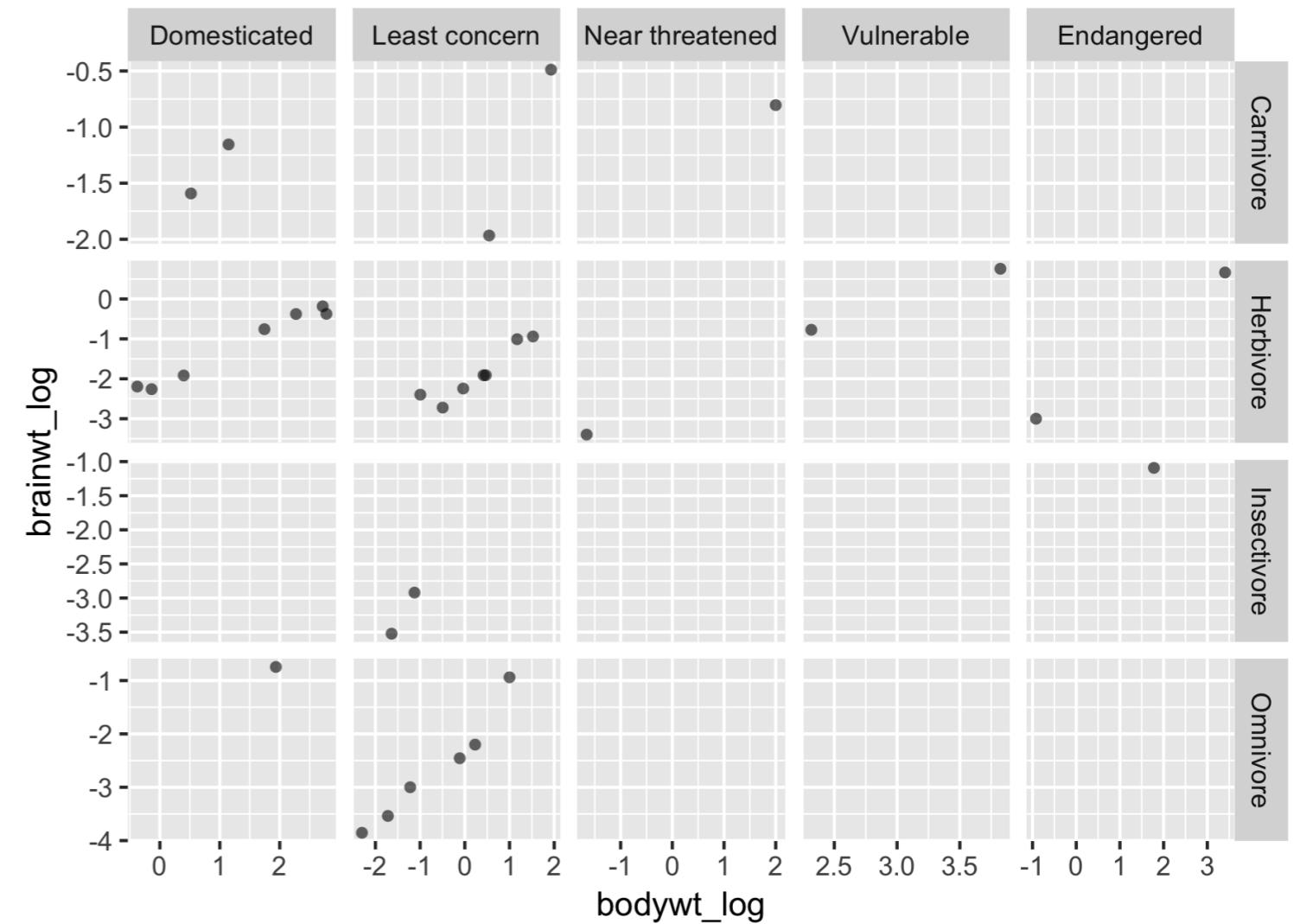
Adjusting the plotting space

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation),  
             scales = "free_y")
```



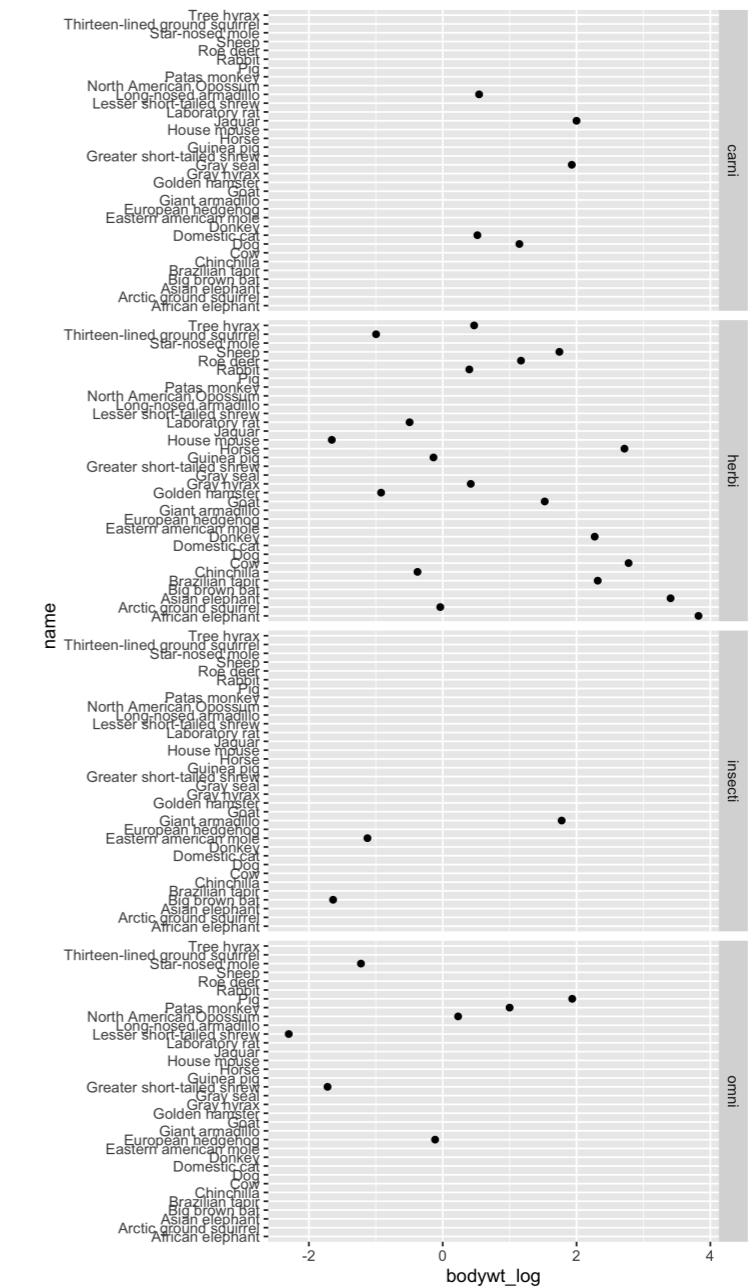
Adjusting the plotting space

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation),  
             scales = "free")
```



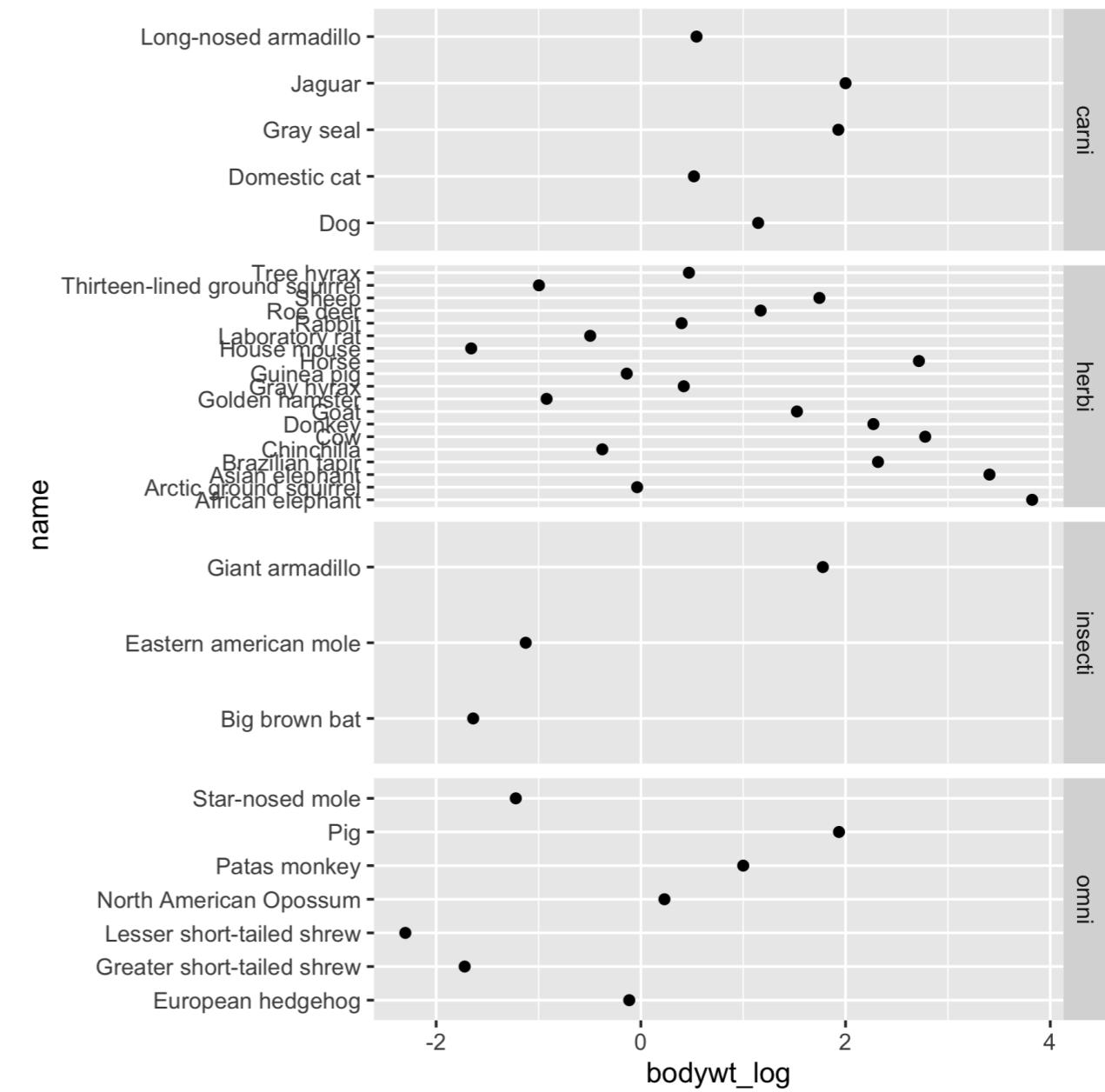
Adjusting the plotting space

```
ggplot(msleep2, aes(x = bodywt_log,  
                    y = name)) +  
  
  geom_point() +  
  
  facet_grid(rows = vars(vore))
```



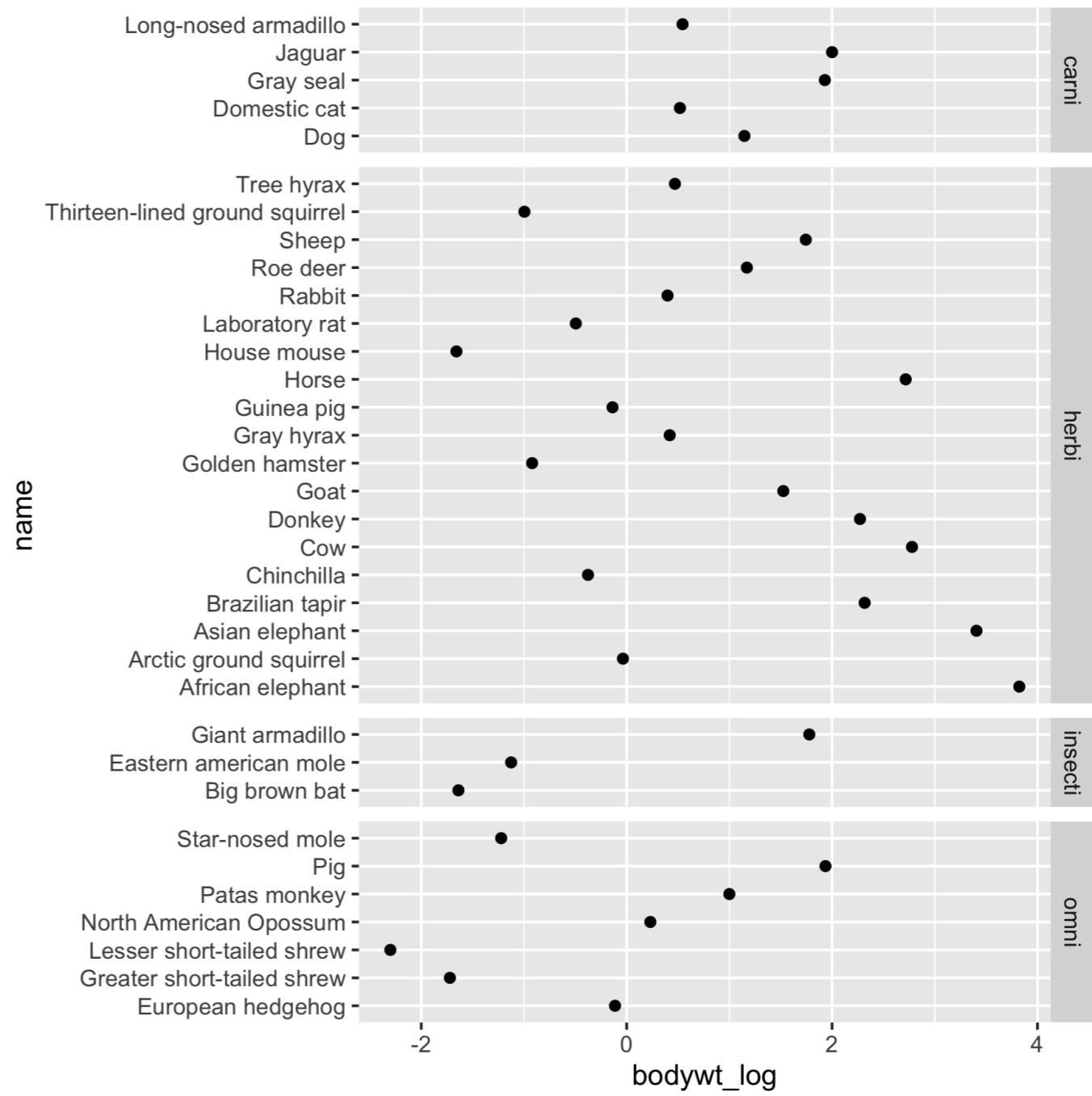
Adjusting the plotting space

```
ggplot(msleep2, aes(x = bodywt_log,  
                    y = name)) +  
  
  geom_point() +  
  
  # Free the y scales and space  
  facet_grid(rows = vars(vore),  
             scales = "free_y")
```



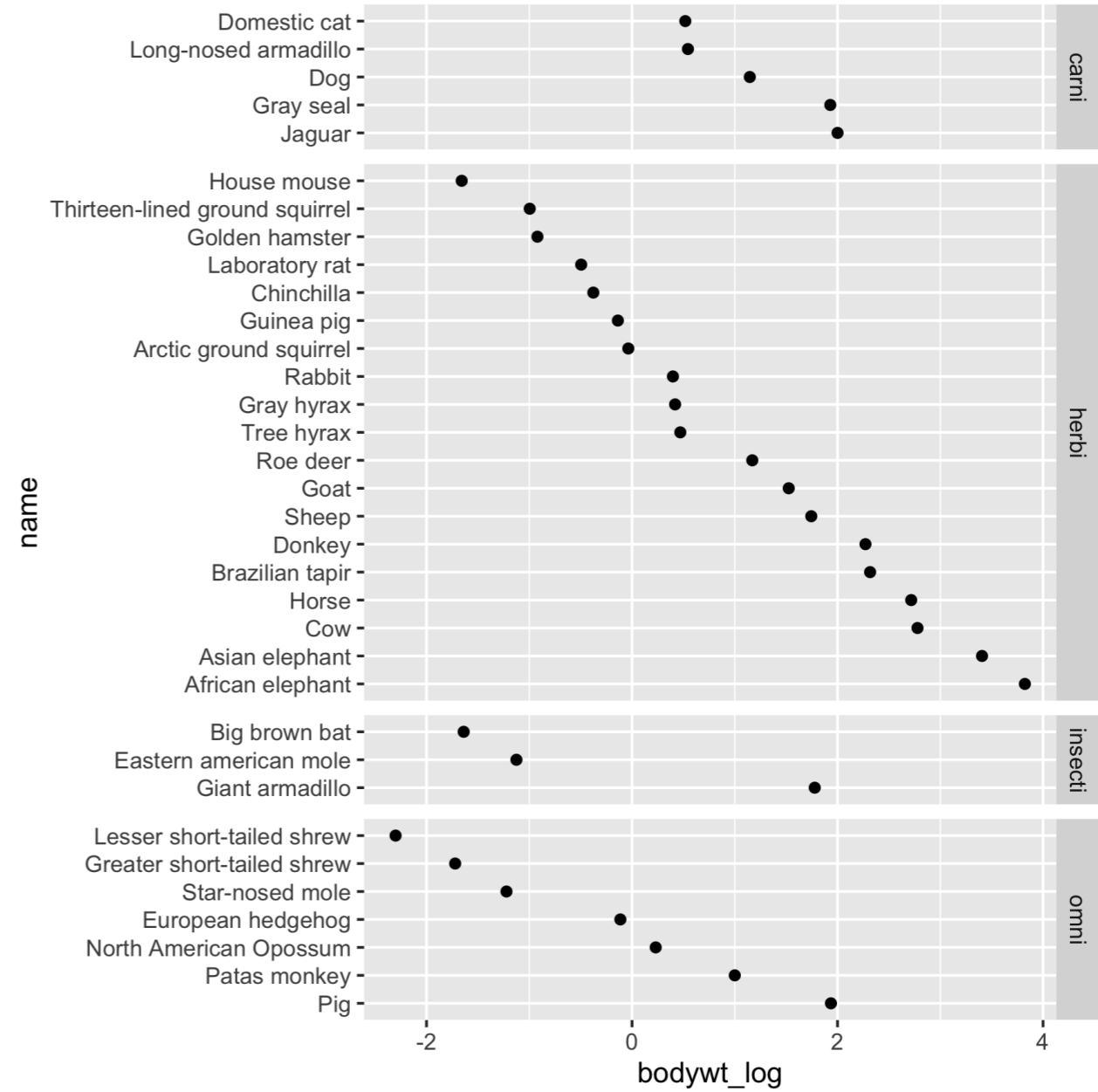
Adjusting the plotting space

```
ggplot(msleep2, aes(x = bodywt_log,  
                    y = name)) +  
  
  geom_point() +  
  
  # Free the y scales and space  
  facet_grid(rows = vars(vore),  
             scales = "free_y",  
             space = "free_y")
```



Final adjustments

```
msleep2 <- msleep2 %>%  
  # Arrange from lo to hi weight  
  arrange(-bodywt_log) %>%  
  # Redefine factor levels in order  
  mutate(name = as_factor(name))  
  
# New order is reflected in y axis  
ggplot(msleep2, aes(x = bodywt_log,  
                     y = name)) +  
  geom_point() +  
  # Free the y scales and space  
  facet_grid(rows = vars(vore),  
             scales = "free_y",  
             space = "free_y")
```



Let's practice!

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2

Facet wrap & margins

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2

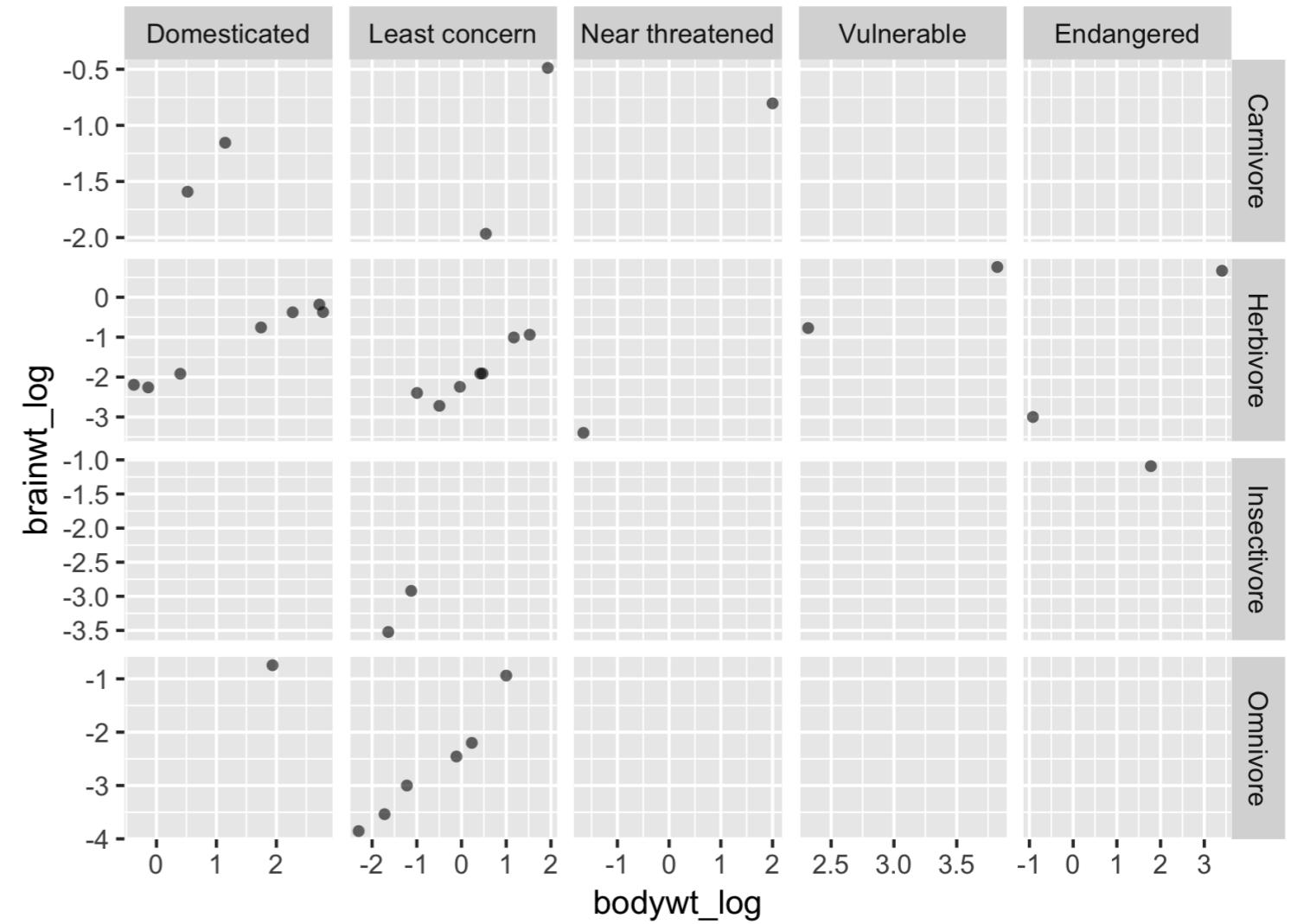


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Adjusting the plotting space

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation),  
             scales = "free")
```



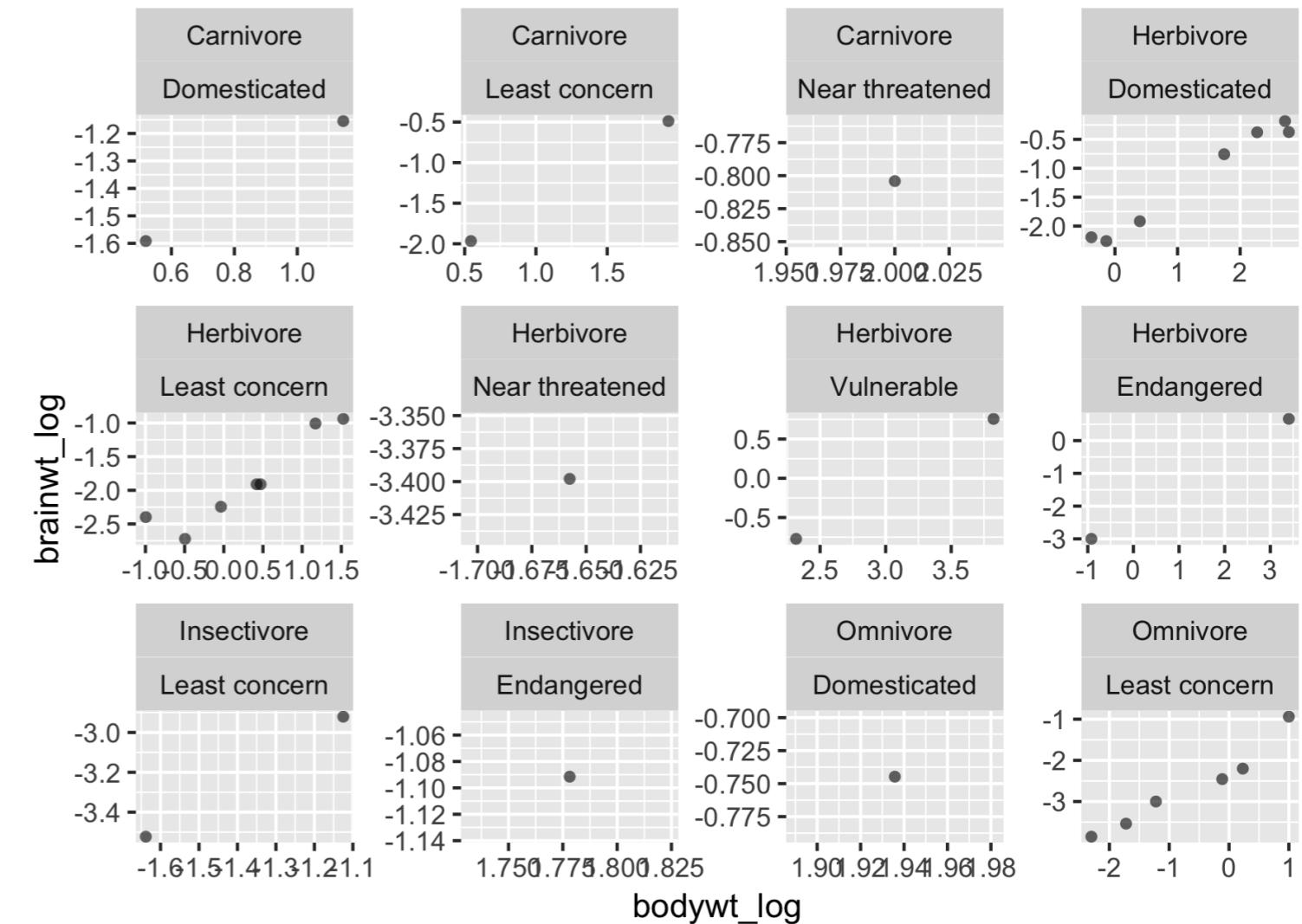
Using `facet_wrap()`

Use cases:

1. When you want both x and y axes to be free on every individual plot
 - i.e. Not just per row or column as per `facet_grid()`

Using facet_wrap() - Scenario 1

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  facet_wrap(vars(vore, conservation),  
             scales = "free")
```



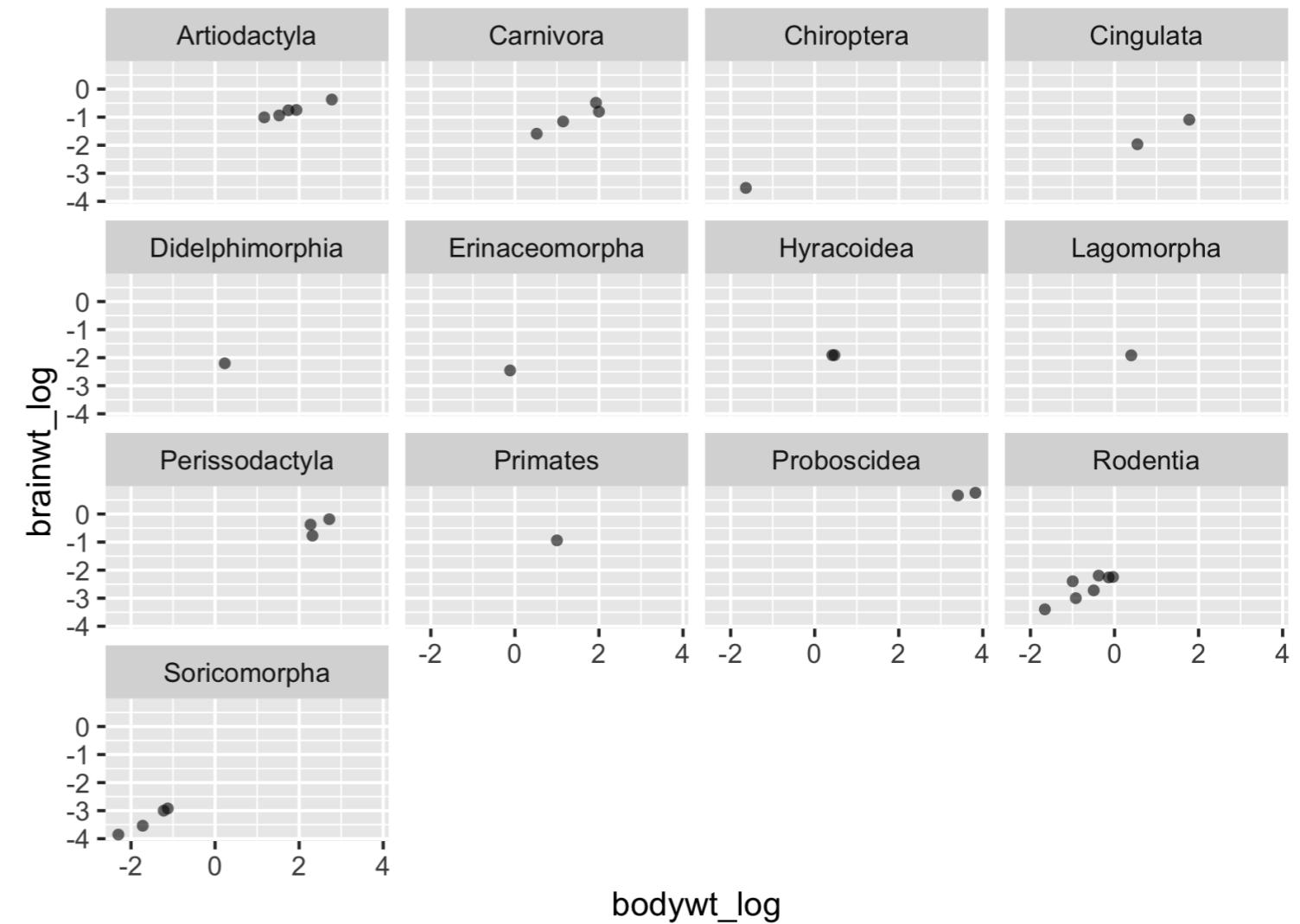
Using `facet_wrap()`

Use cases:

1. When you want both x and y axes to be free on every individual plot
 - i.e. Not just per row or column as per `facet_grid()`
2. When your categorical (factor) variable has many groups (levels)
 - i.e. too many sub plots for column or row-wise faceting
 - A more typical scenario

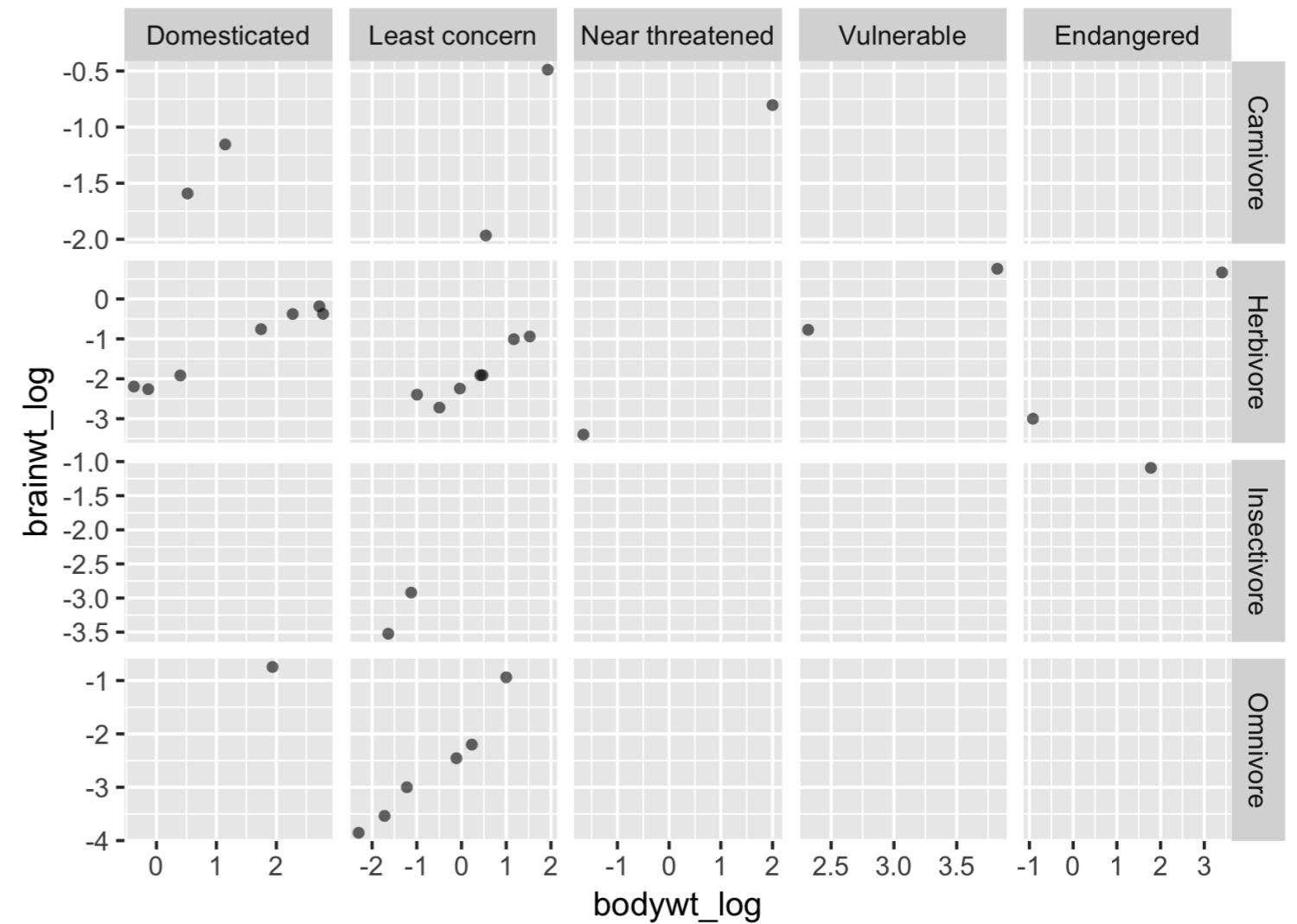
Using `facet_wrap()` - Scenario 2

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  facet_wrap(vars(order))
```



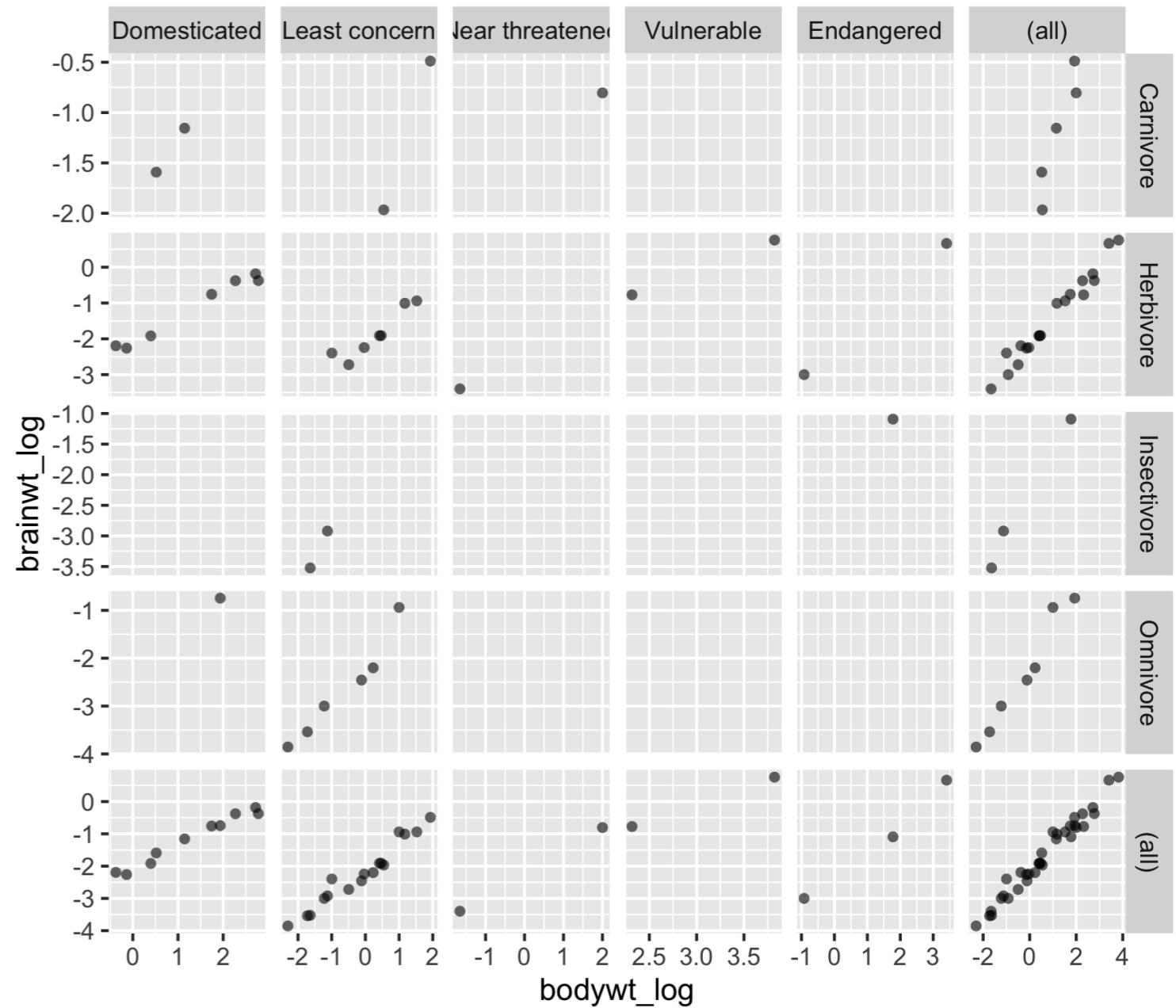
Using margin plots

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation),  
             scales = "free")
```



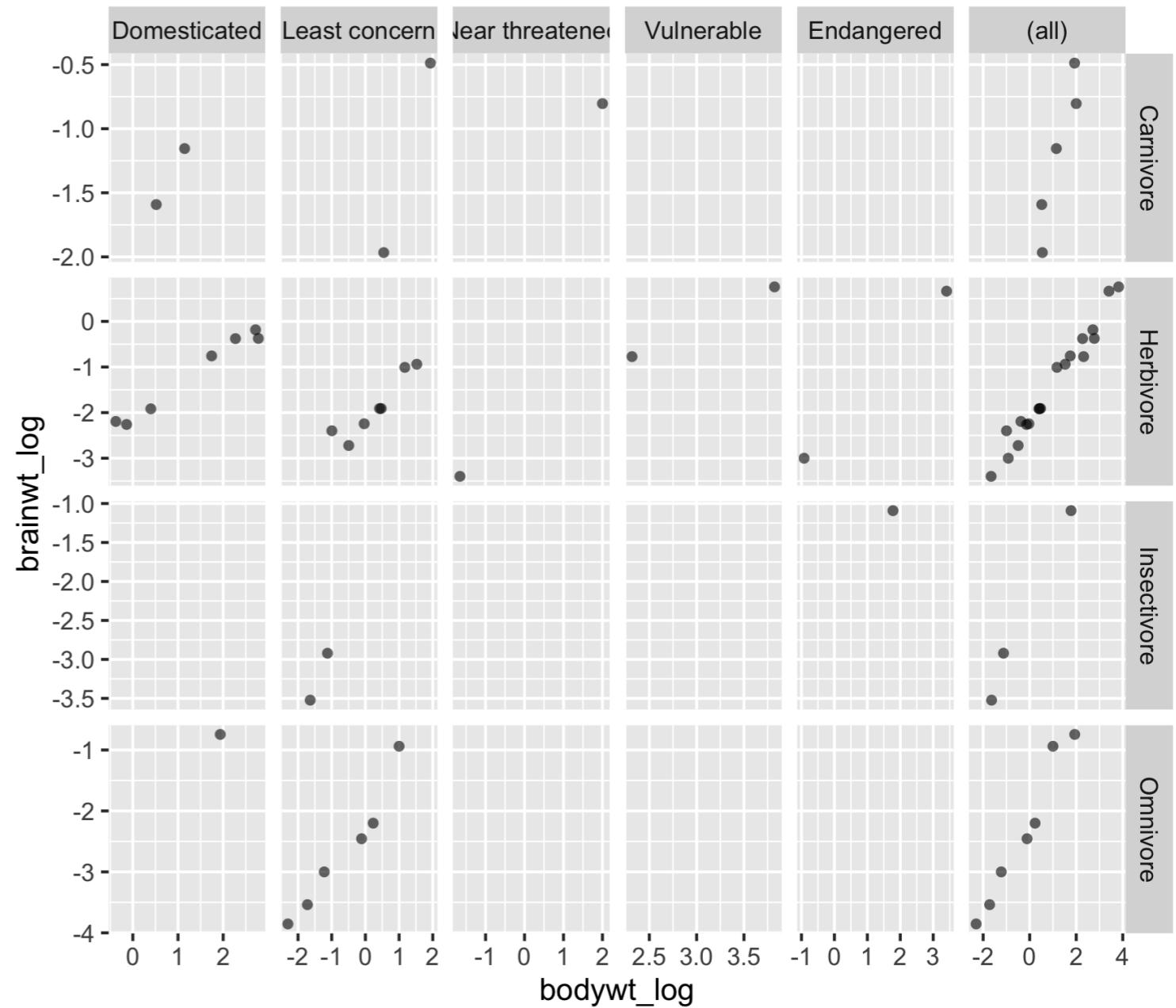
Using margin plots

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation),  
             scales = "free",  
             margins = TRUE)
```



Using margin plots

```
ggplot(msleep2, aes(bodywt_log,  
                      brainwt_log)) +  
  geom_point(alpha = 0.6, shape = 16) +  
  facet_grid(rows = vars(vore),  
             cols = vars(conservation),  
             scales = "free",  
             margins = "conservation")
```



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