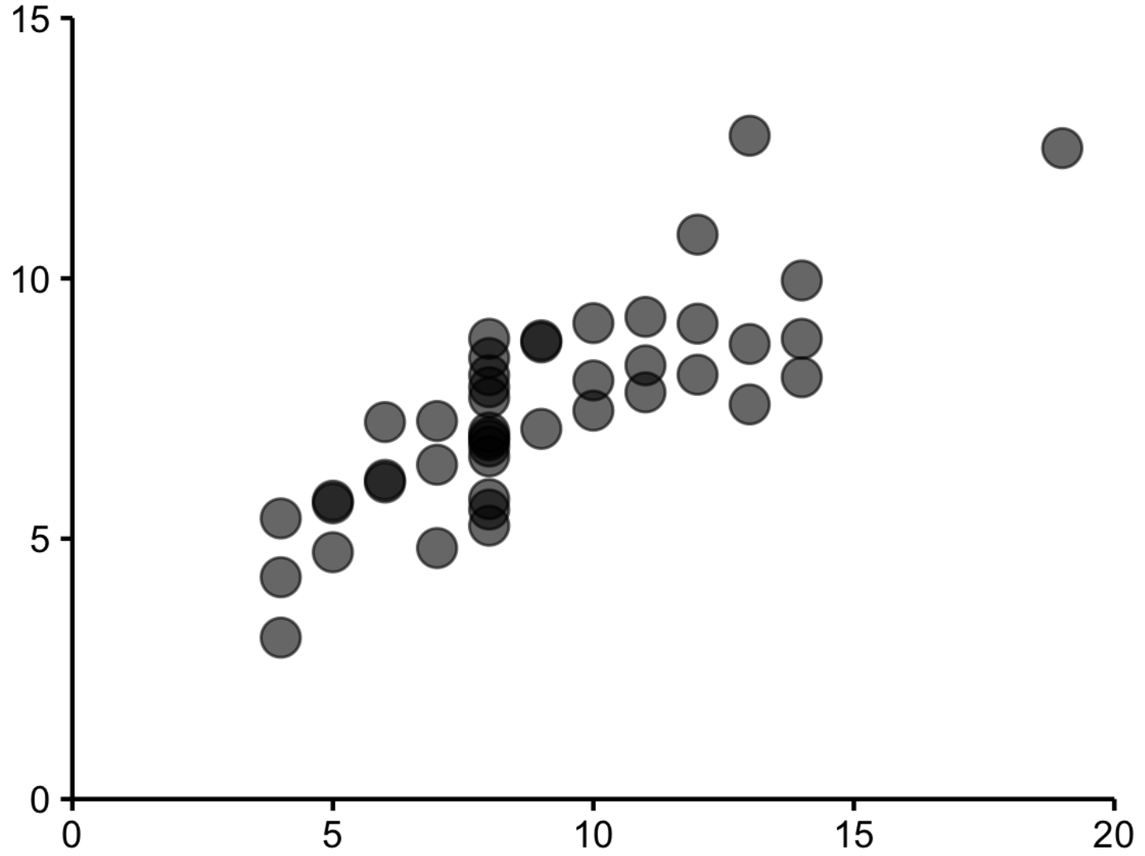
The facets layer

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


15
10
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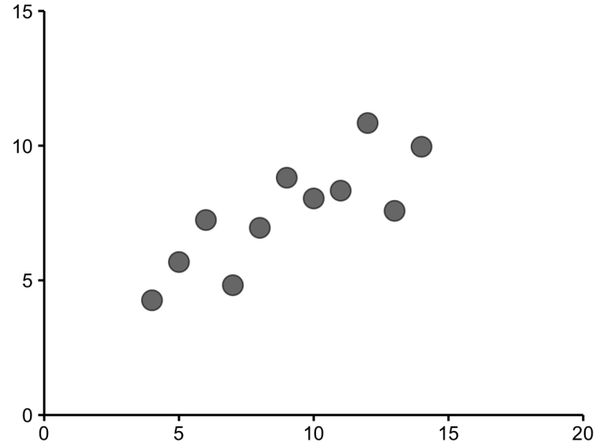
15
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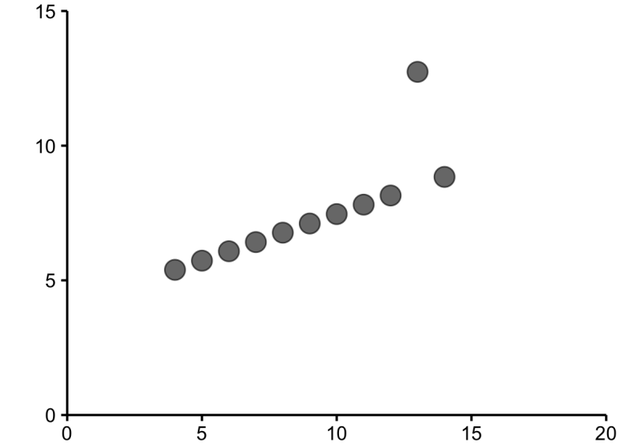
15
10
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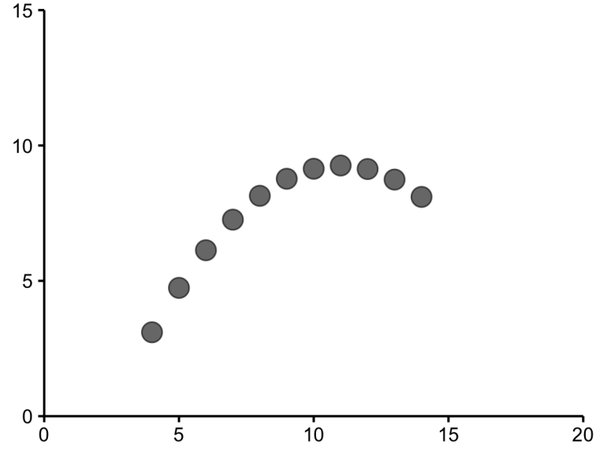
20


15
10
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10
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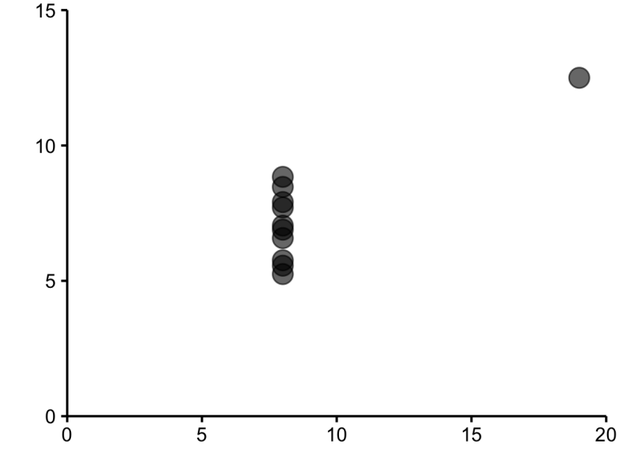
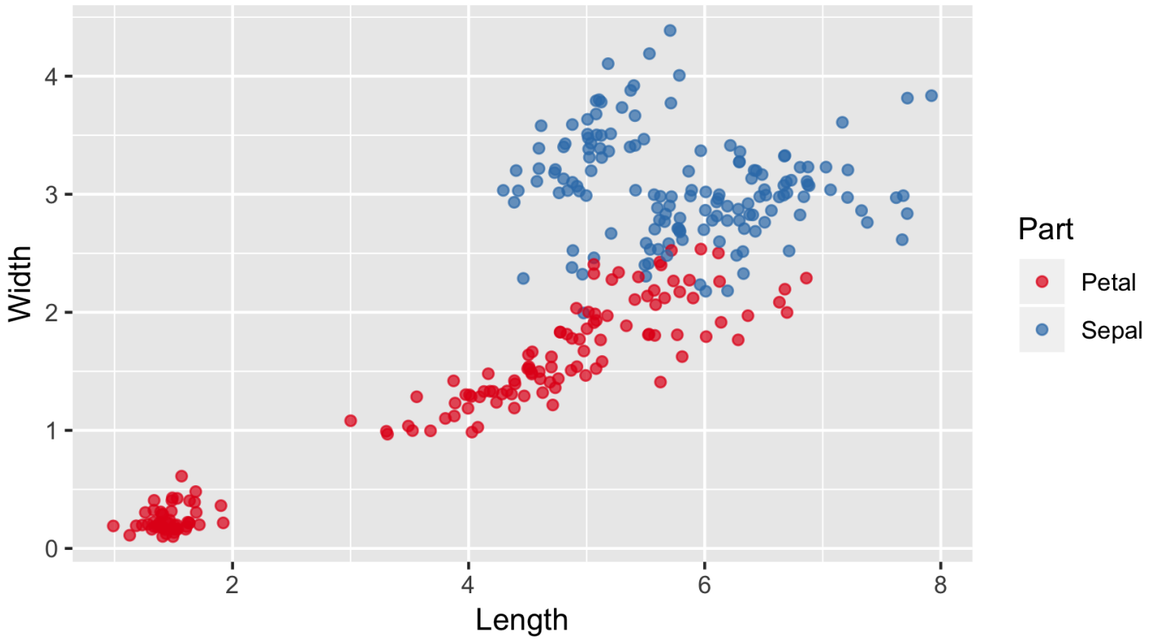
20


15
10
5
0
0
5
10
15
20

iris.wide

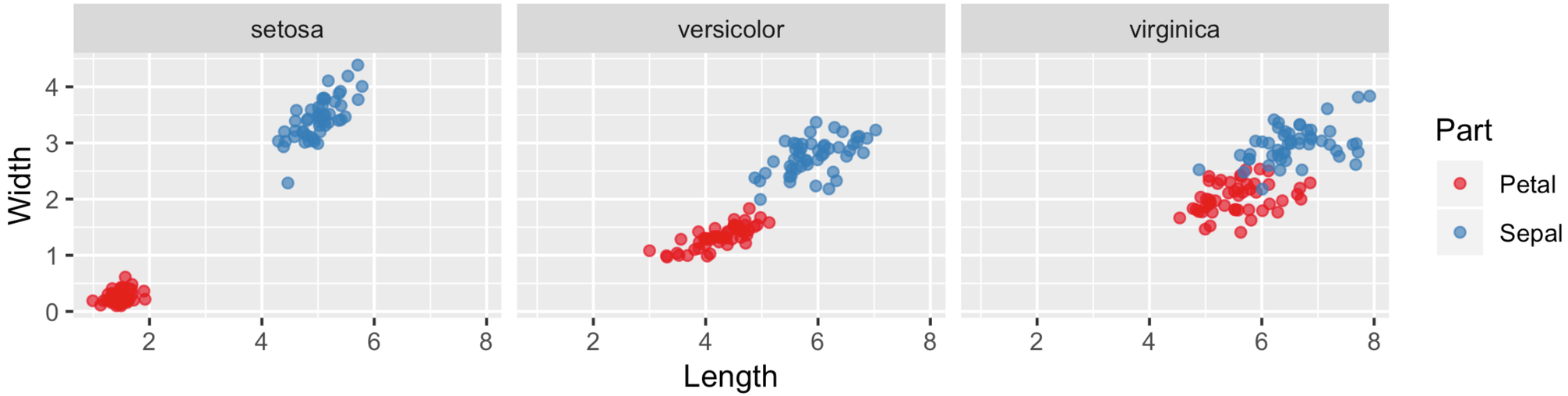
```
p <- ggplot(iris.wide, aes(x = Length,
                           y = Width,
                           ccolorol = Part)) +
  geom_jitter(alpha = 0.7) +
  scale_color_brewer(palette = "Set1") +
  coord_fixed()

p
```



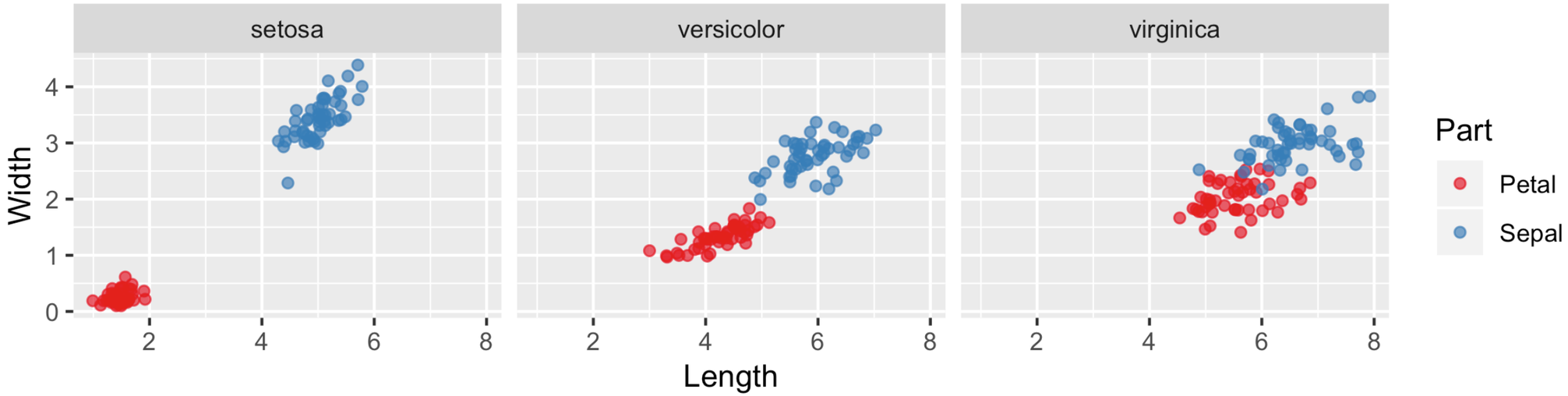
iris.wide & facet_grid()

```
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))
```



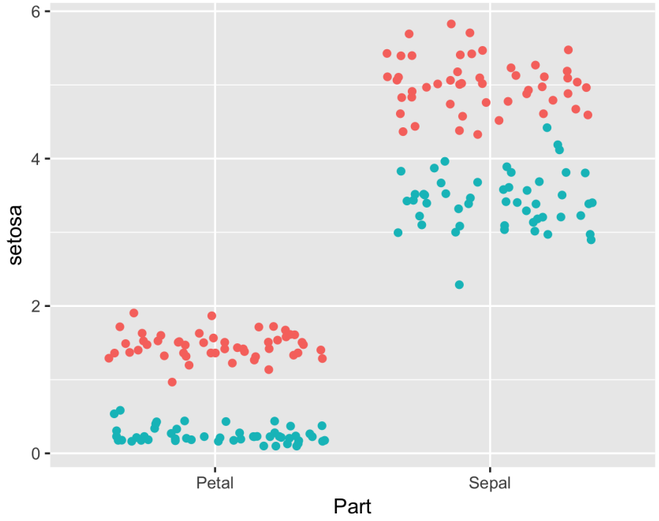
Formula notation

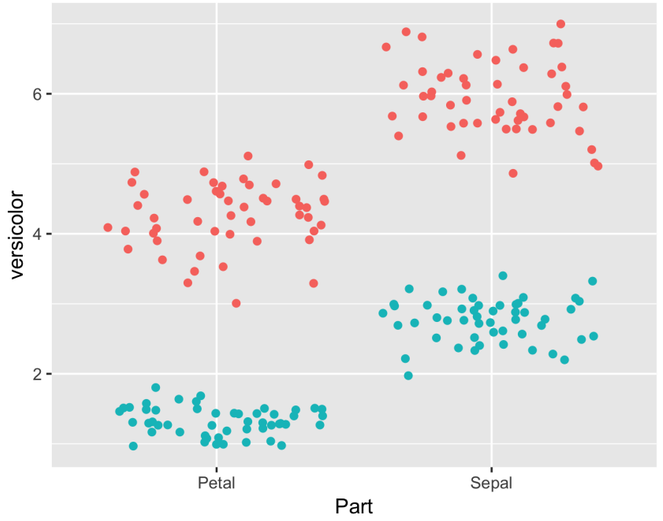
```
p <- ggplot(iris.wide, aes(x = Length, y = Width, color = Part)) +
  geom_jitter(alpha = 0.7) +
  scale_color_brewer(palette = "Set1") +
  coord_fixed()
p + facet_grid(. ~ Species)
```

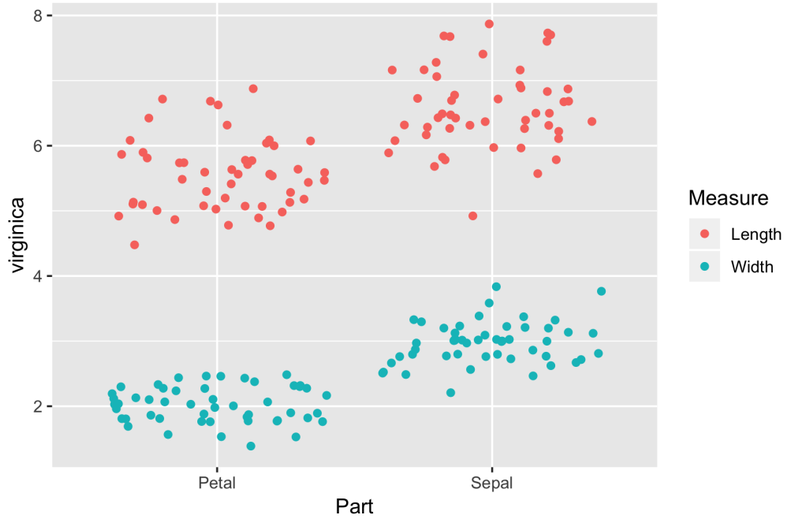


iris.wide2

```
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()
```

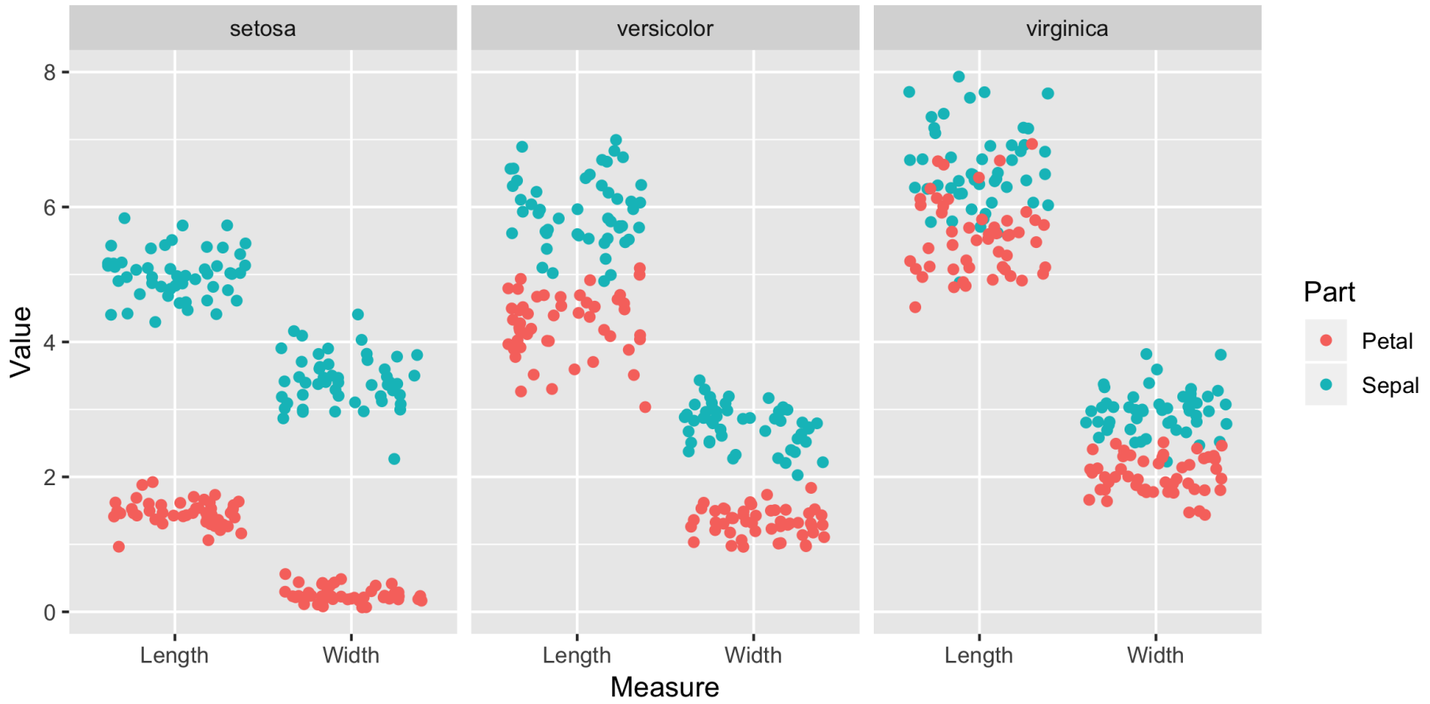






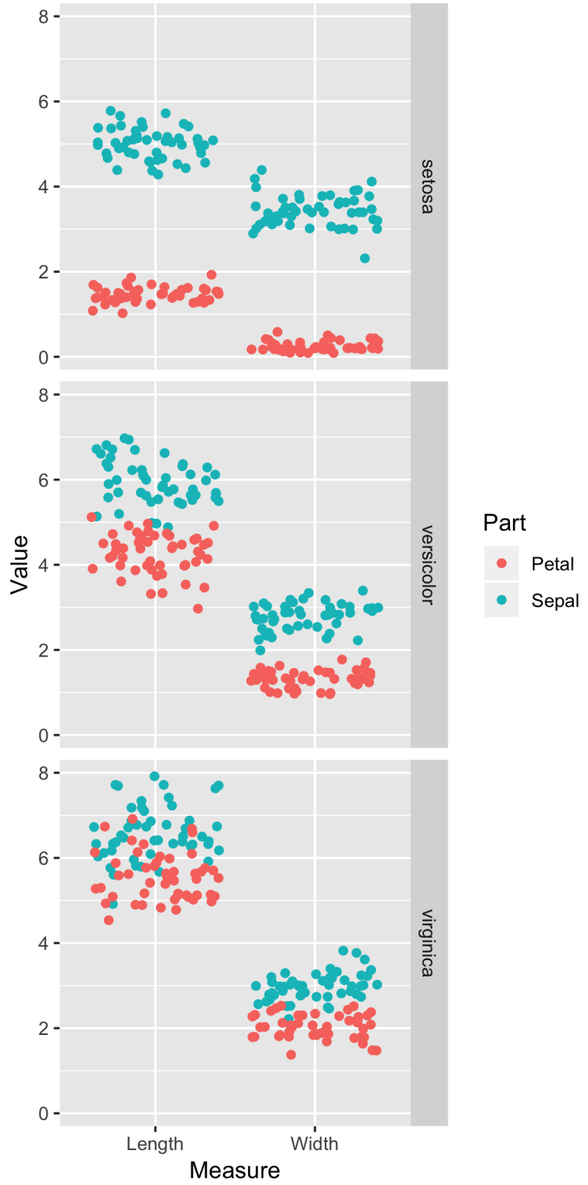
iris.tidy

```
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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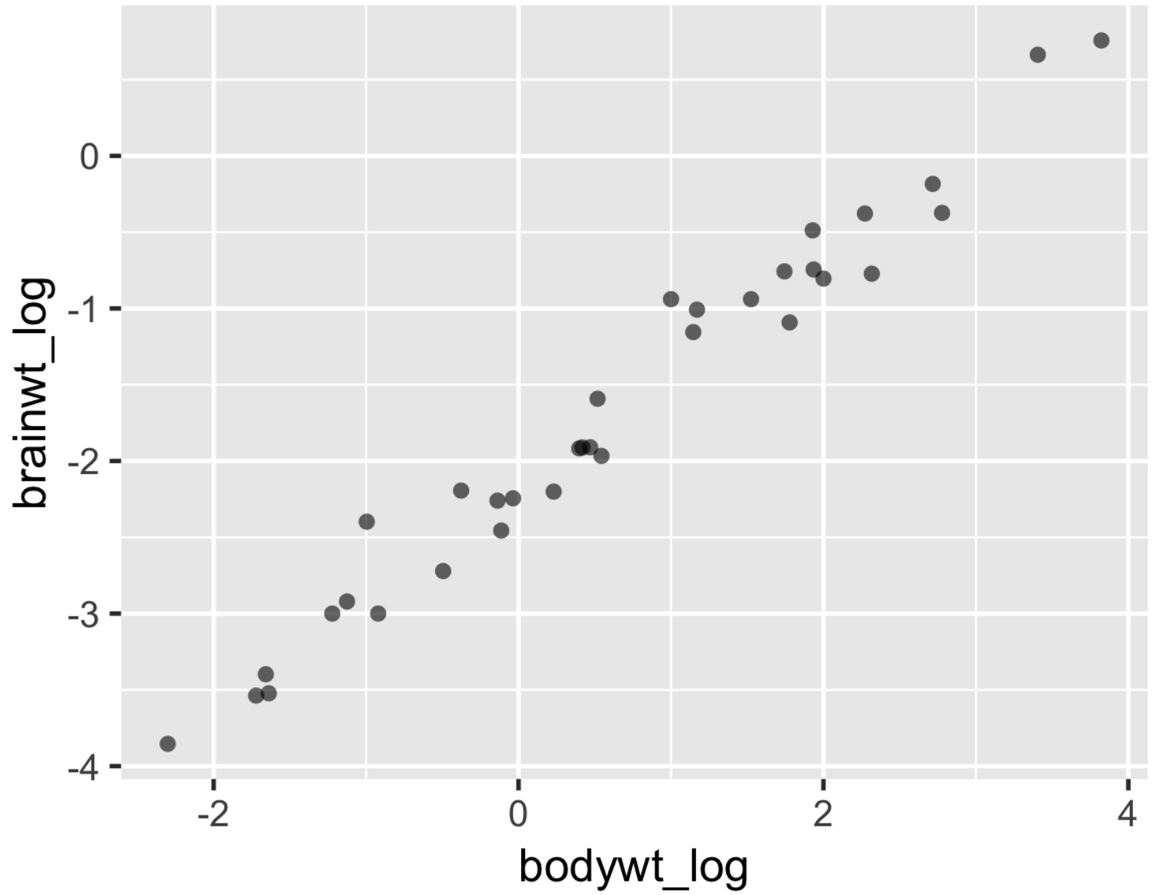
Founder, Scavetta Academy

A new dataframe

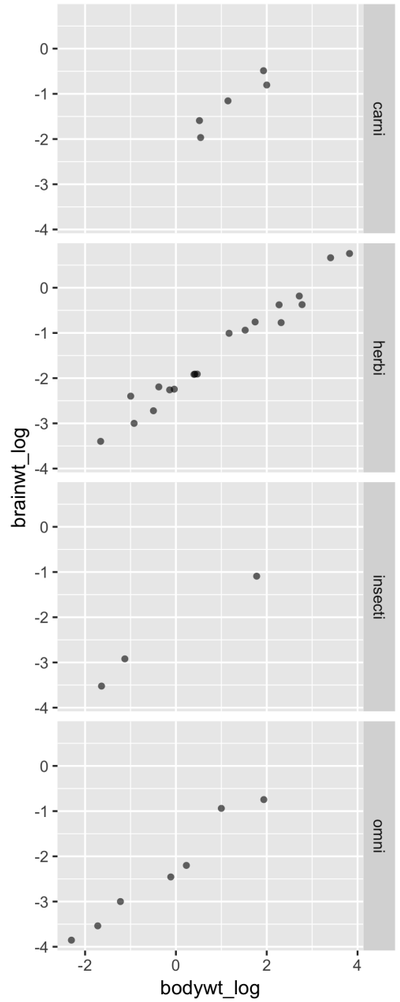
```
# Plot
p <- ggplot(msleep2, aes(bodywt_log,
                         brainwt_log)) +
  geom_point(alpha = 0.6, shape = 16) +
  coord_fixed()

p
```



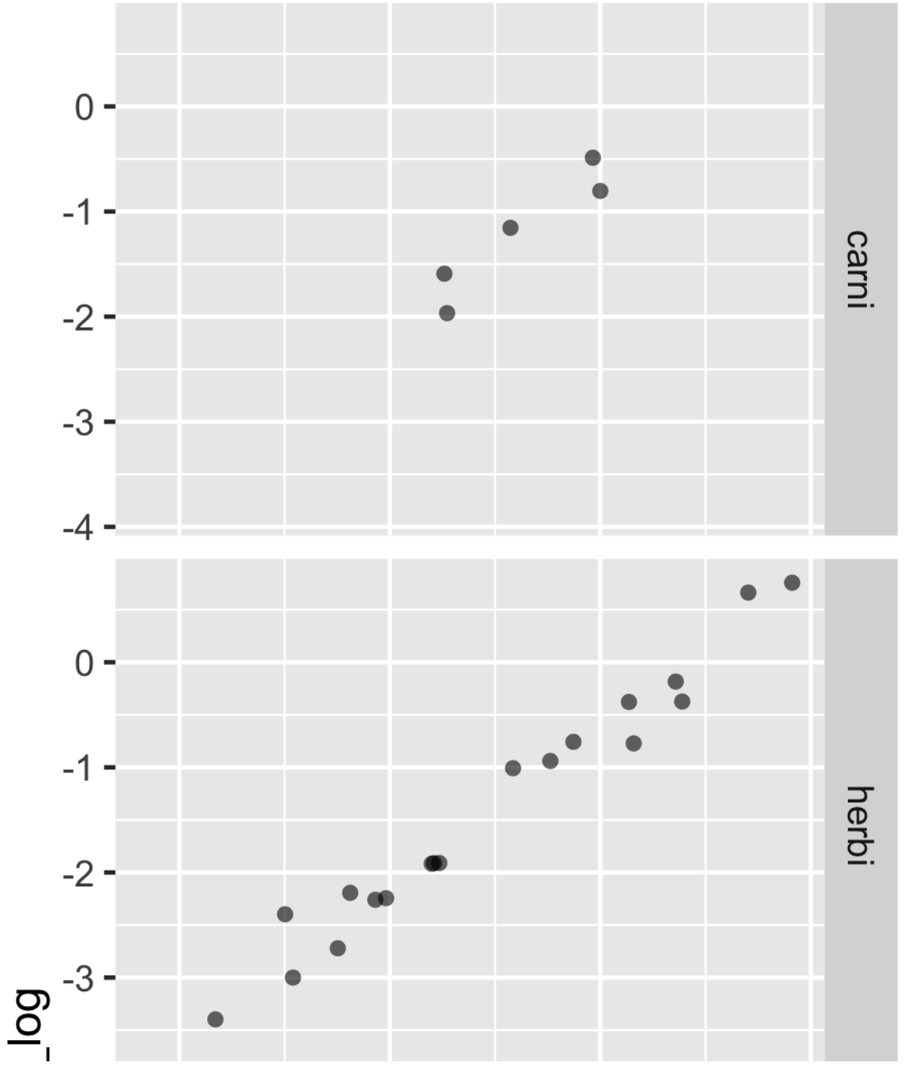
A new dataframe, with facets

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



A new dataframe, with facets

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

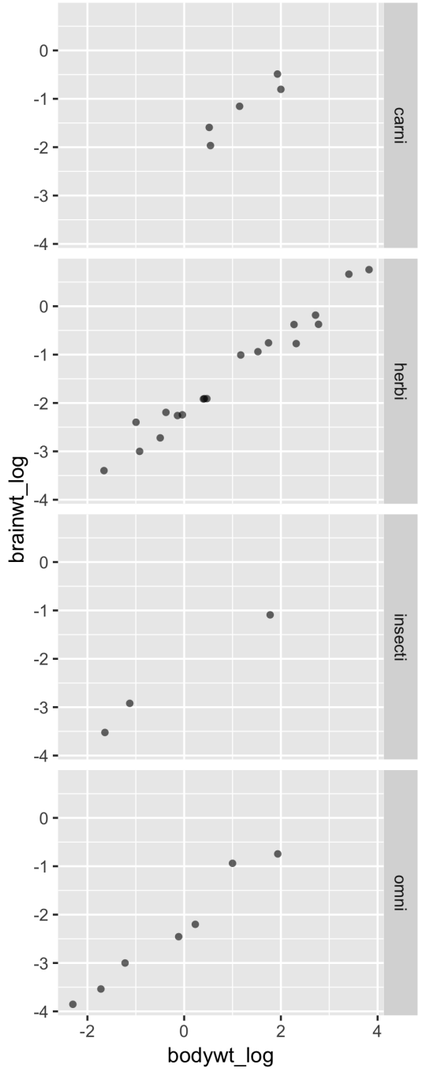


Poor labels and order

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

Two typical problems with facets:

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

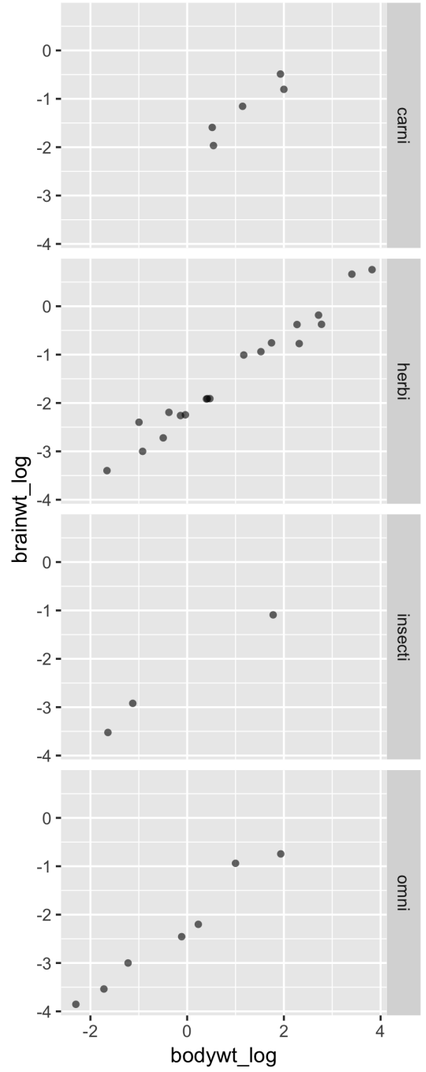


Poor labels and order

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

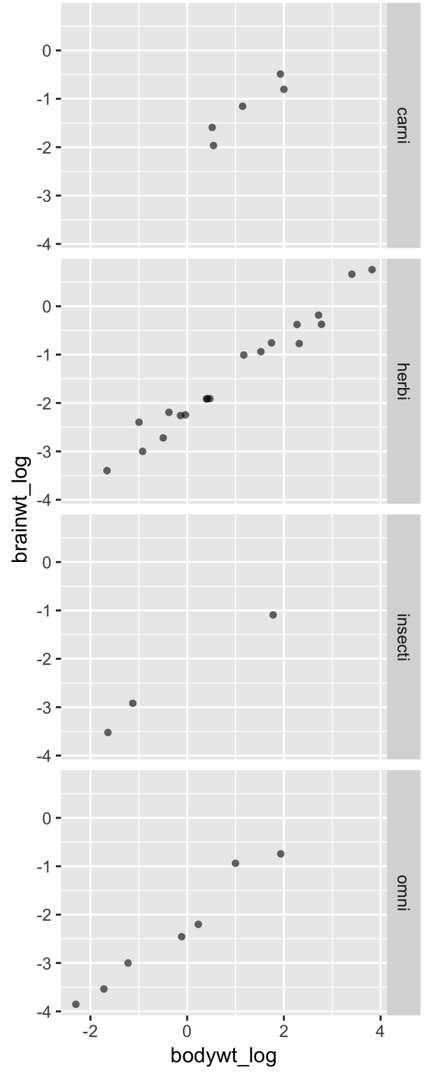
Solutions:

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



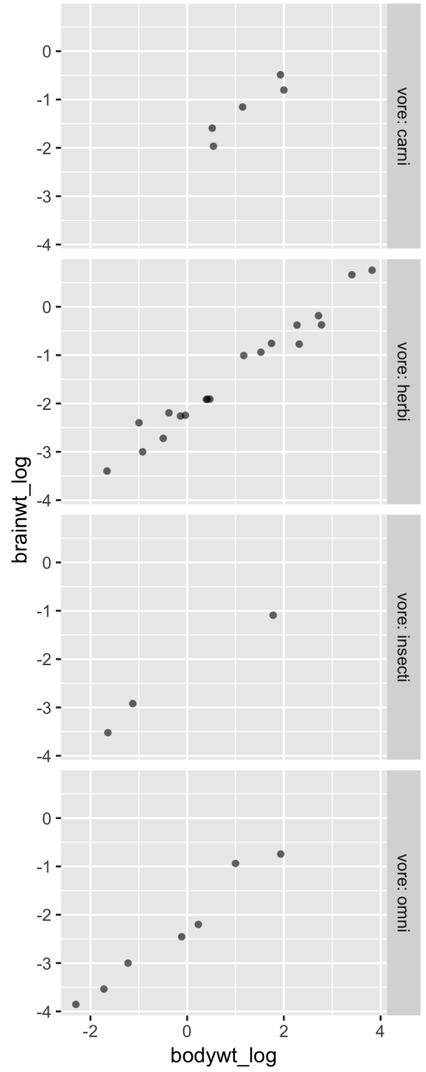
The labeller argument

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



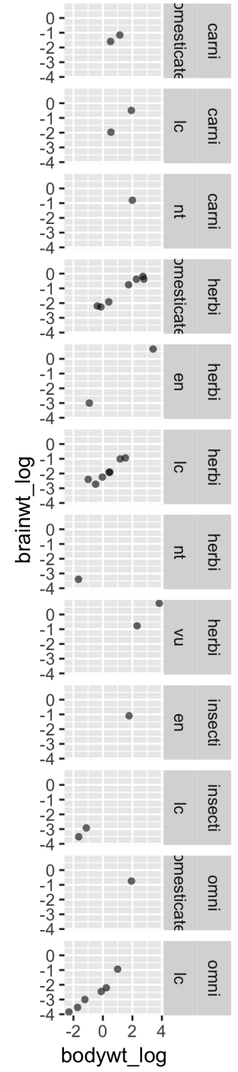
Using label_both adds the variable name

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



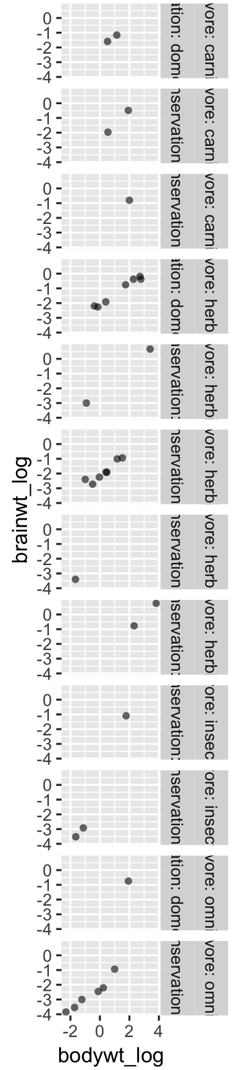
Two variables on one side

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



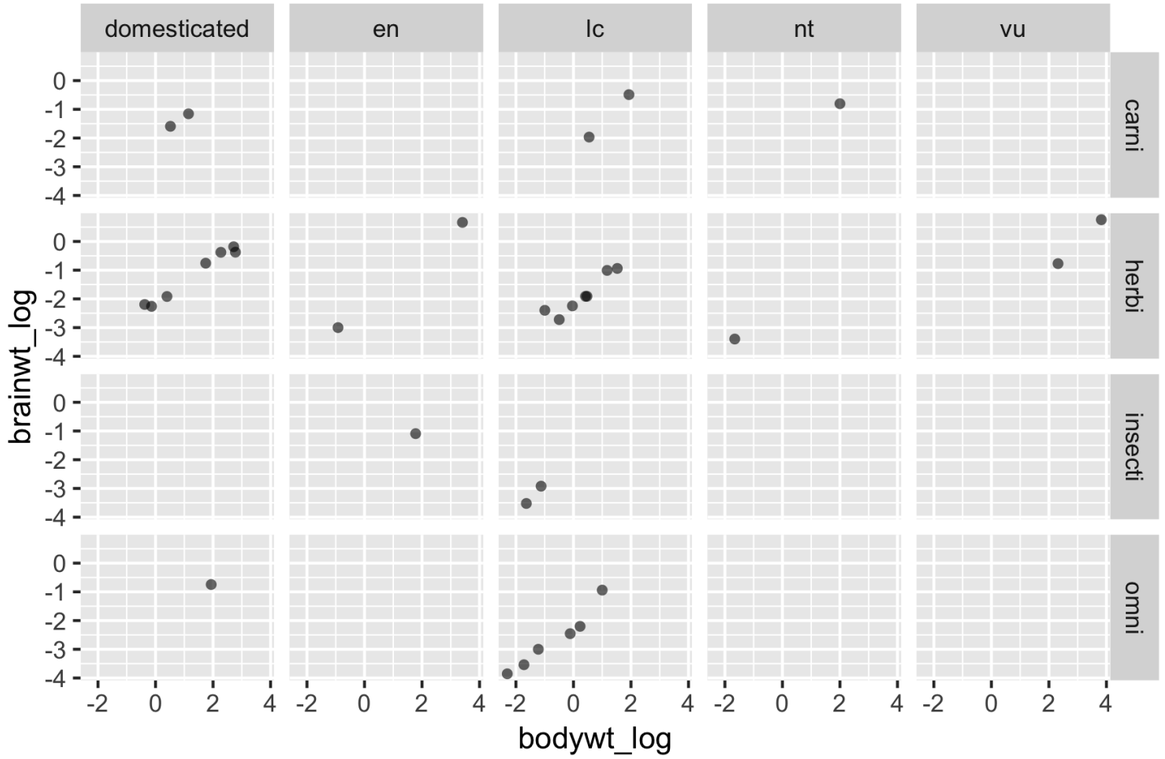
Using label_context avoids ambiguity

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



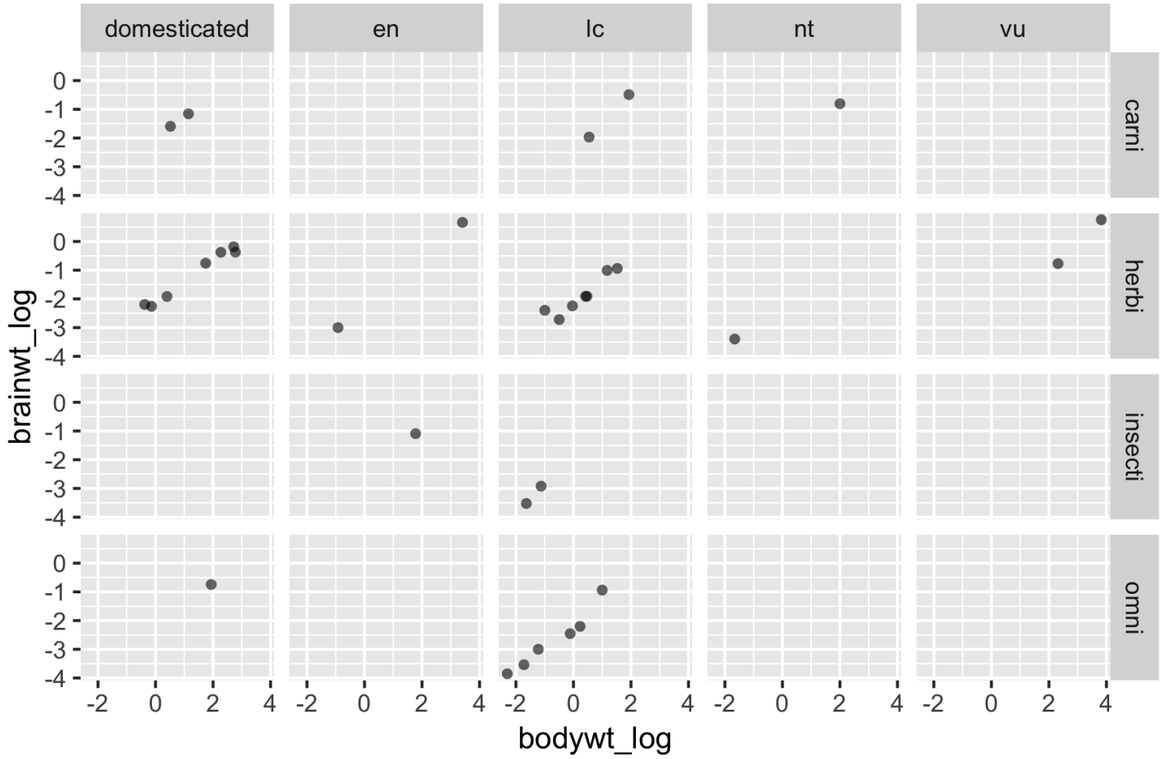
Use rows and columns when appropriate

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

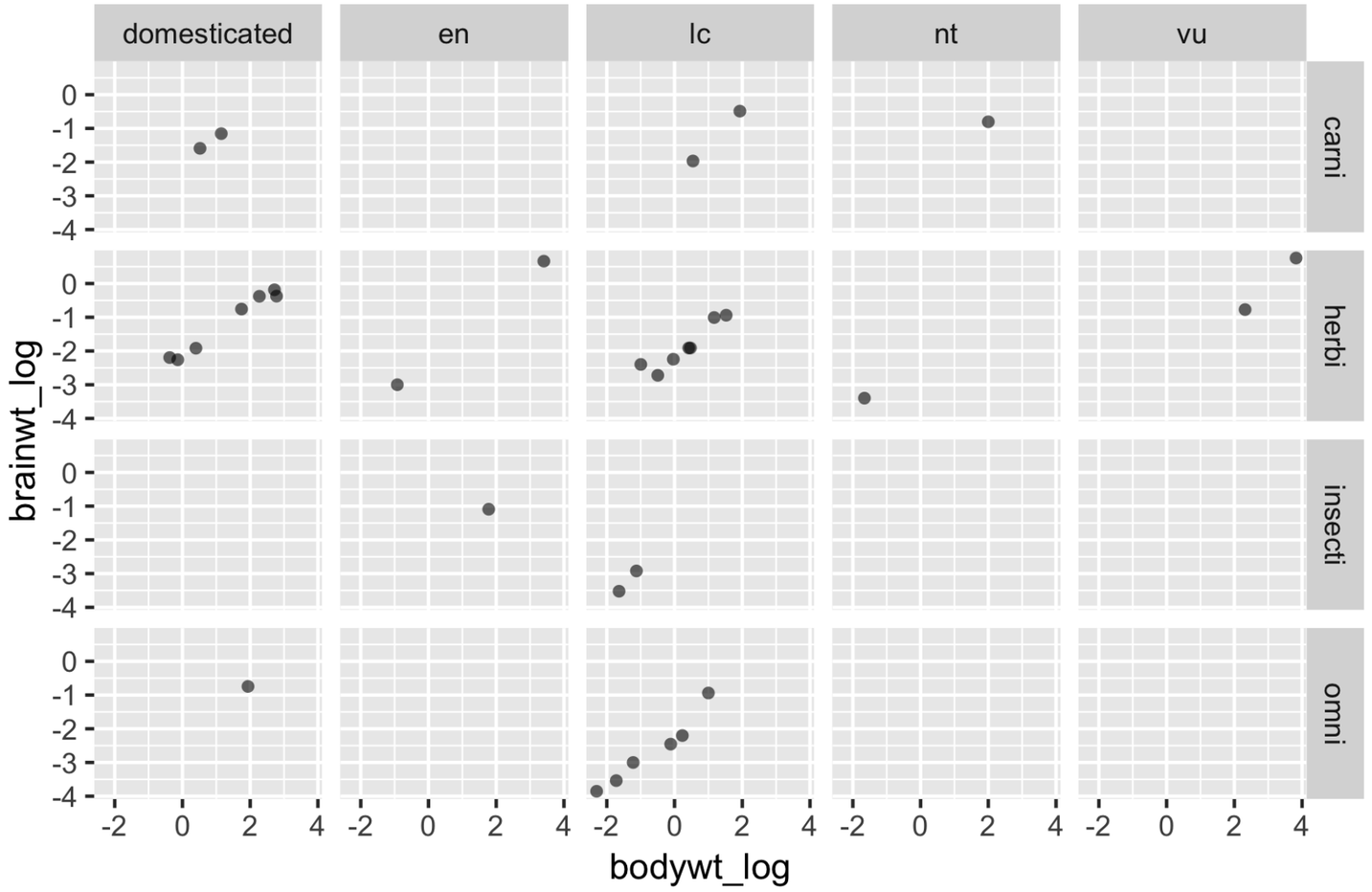


Use rows and columns when appropriate

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



Use rows and columns when appropriate



Relabeling and reordering factors

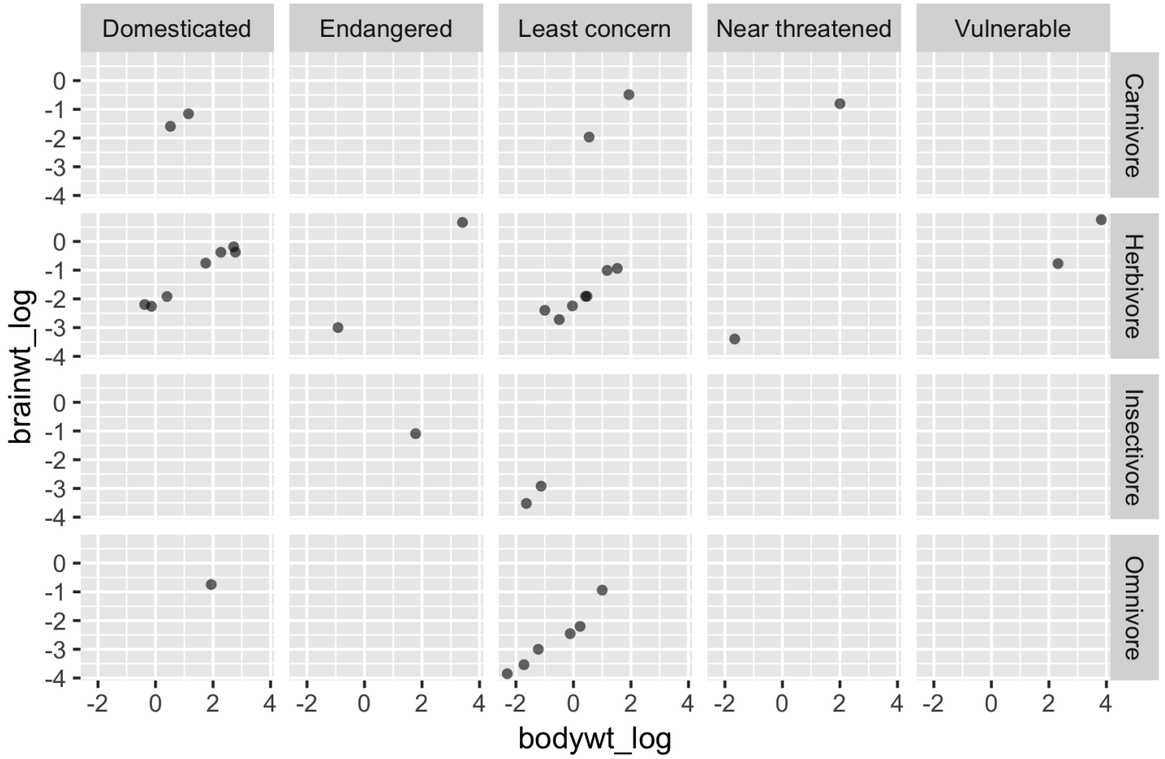
```
msleep2$conservation <- fct_recode(msleep2$conservation,
                                   Domesticated = "domesticated",
                                   `Least concern` = "lc",
                                   `Near threatened` = "nt",
                                   Vulnerable = "vu",
                                   Endangered = "en")

msleep2$vore = fct_recode(msleep2$vore,
                          Carnivore = "carni",
                          Herbivore = "herbi",
                          Insectivore = "insecti",
                          Omnivore = "omni")
```

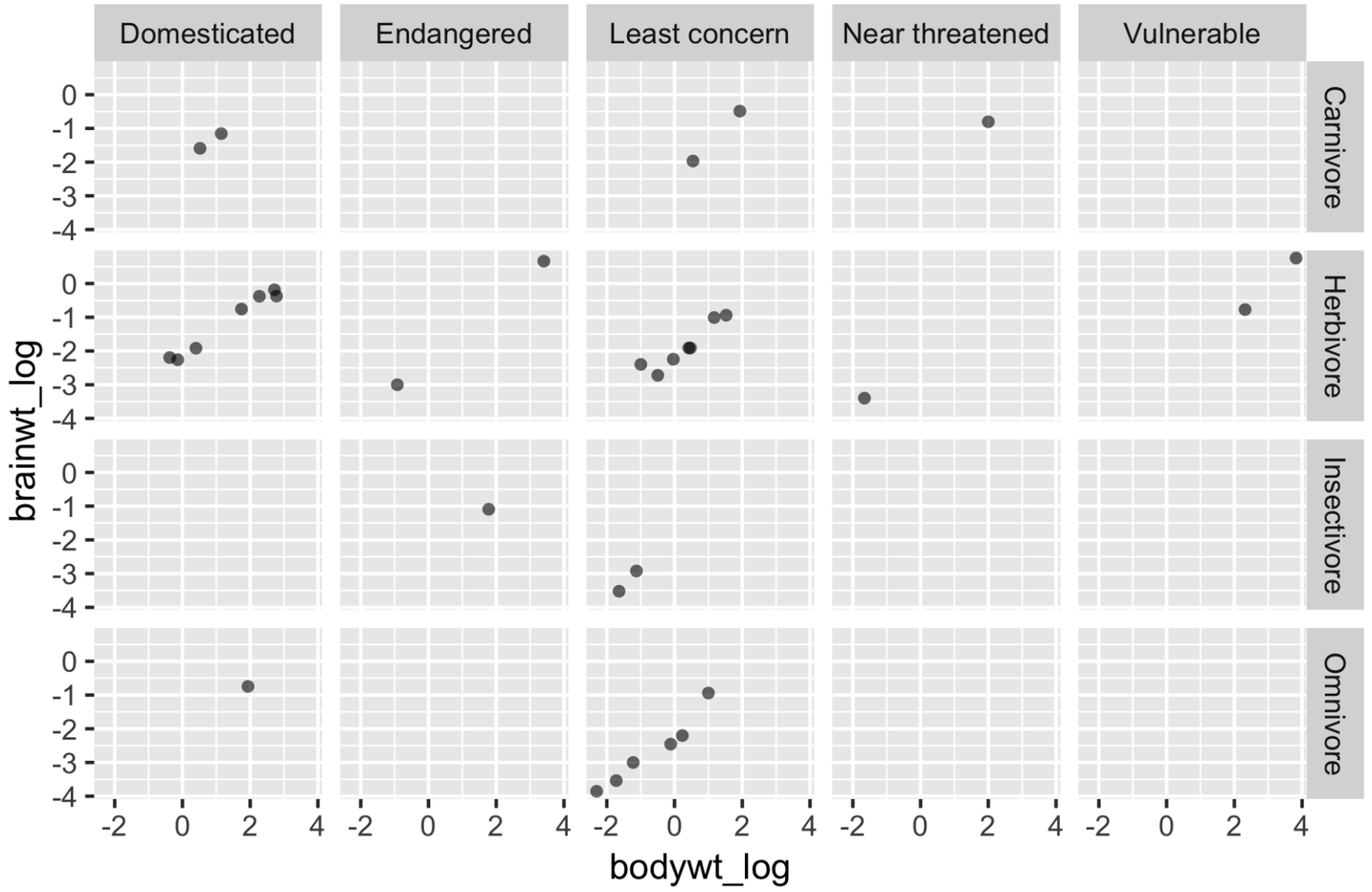
Reinitialize plot with new labels

```
# 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))
```



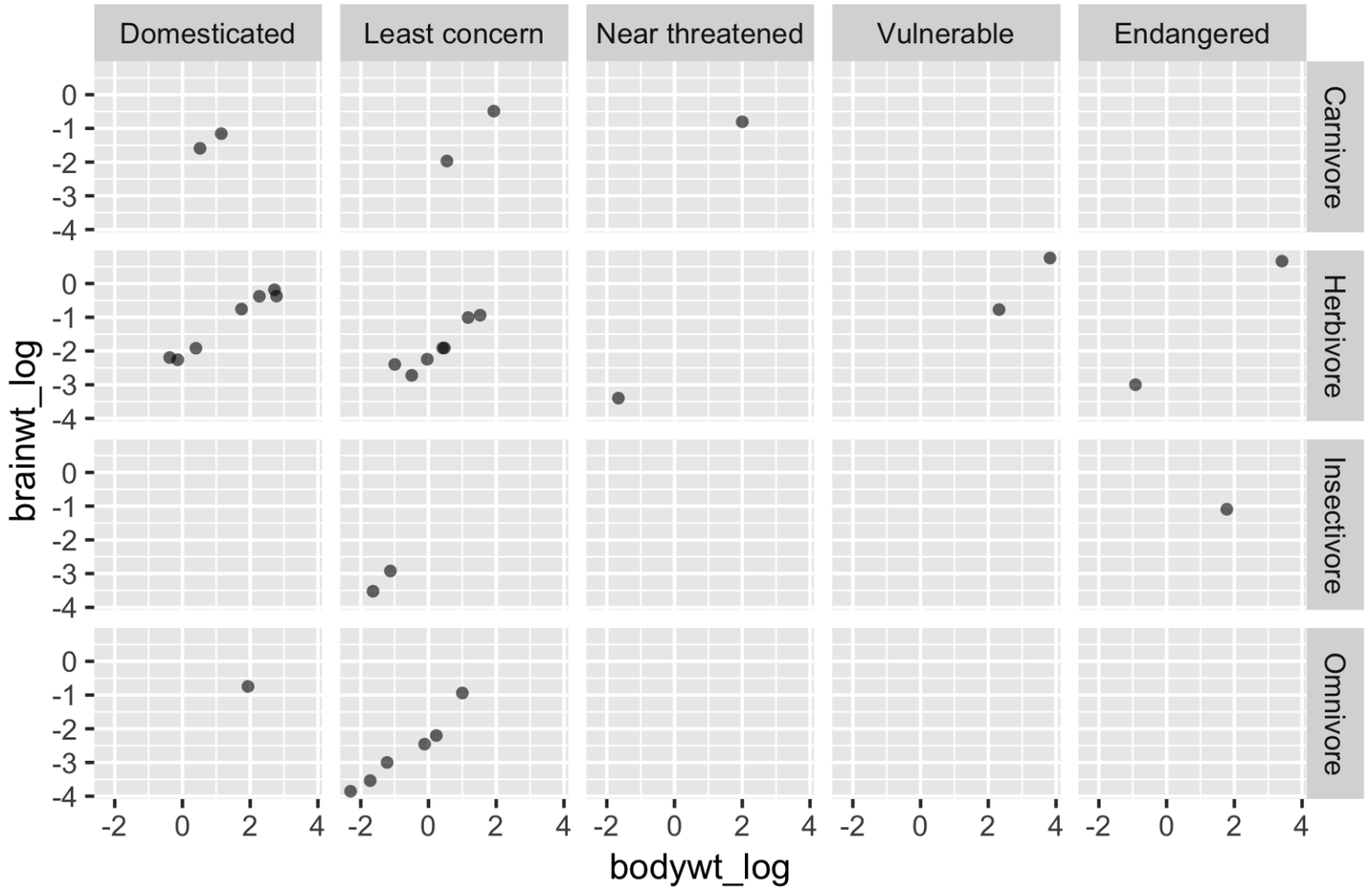
Reinitialize plot with new labels



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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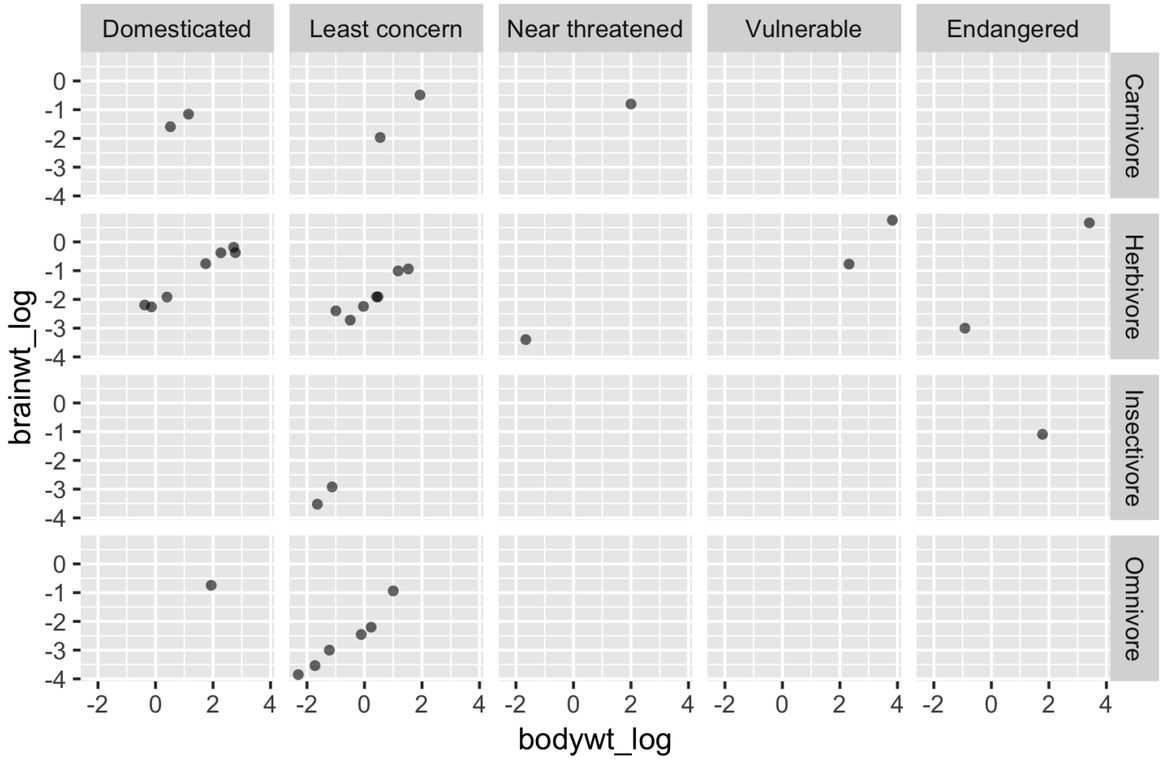
Facets and variable plotting spaces

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))
```



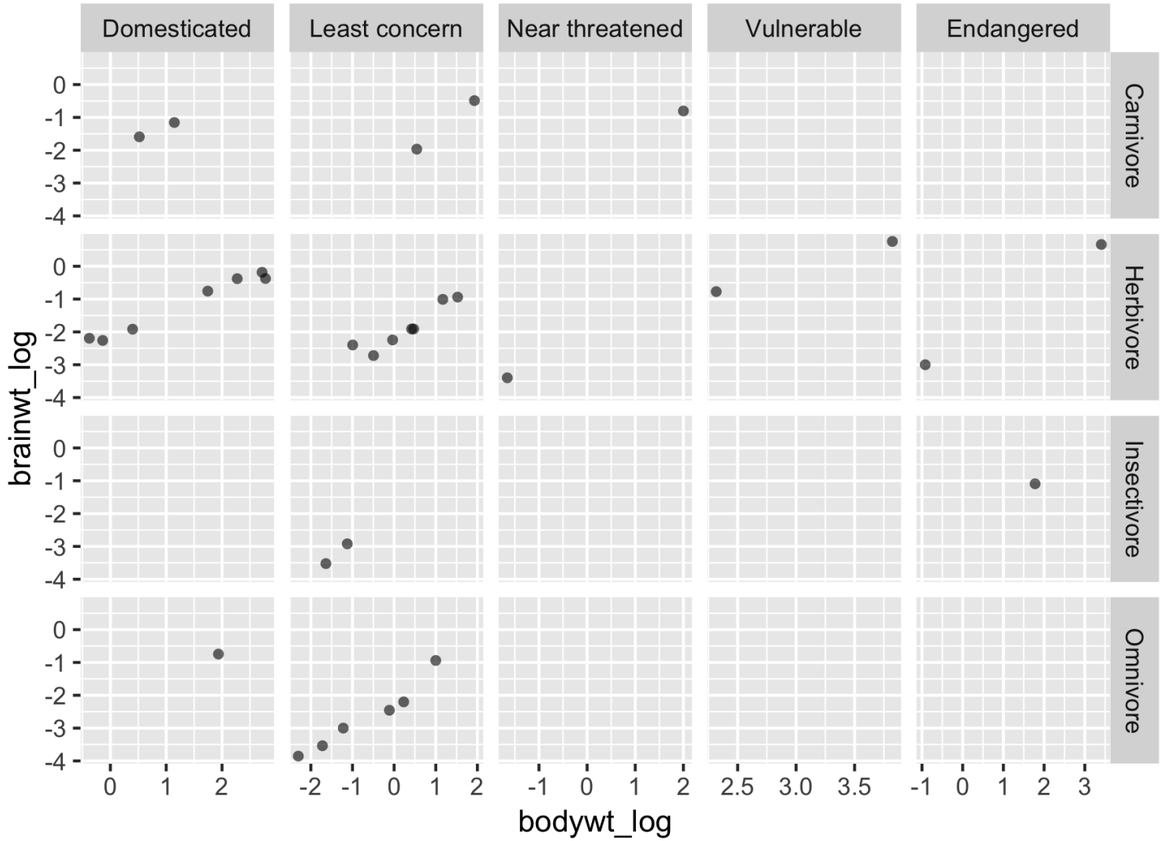
... but not with fixed scales

```
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
```

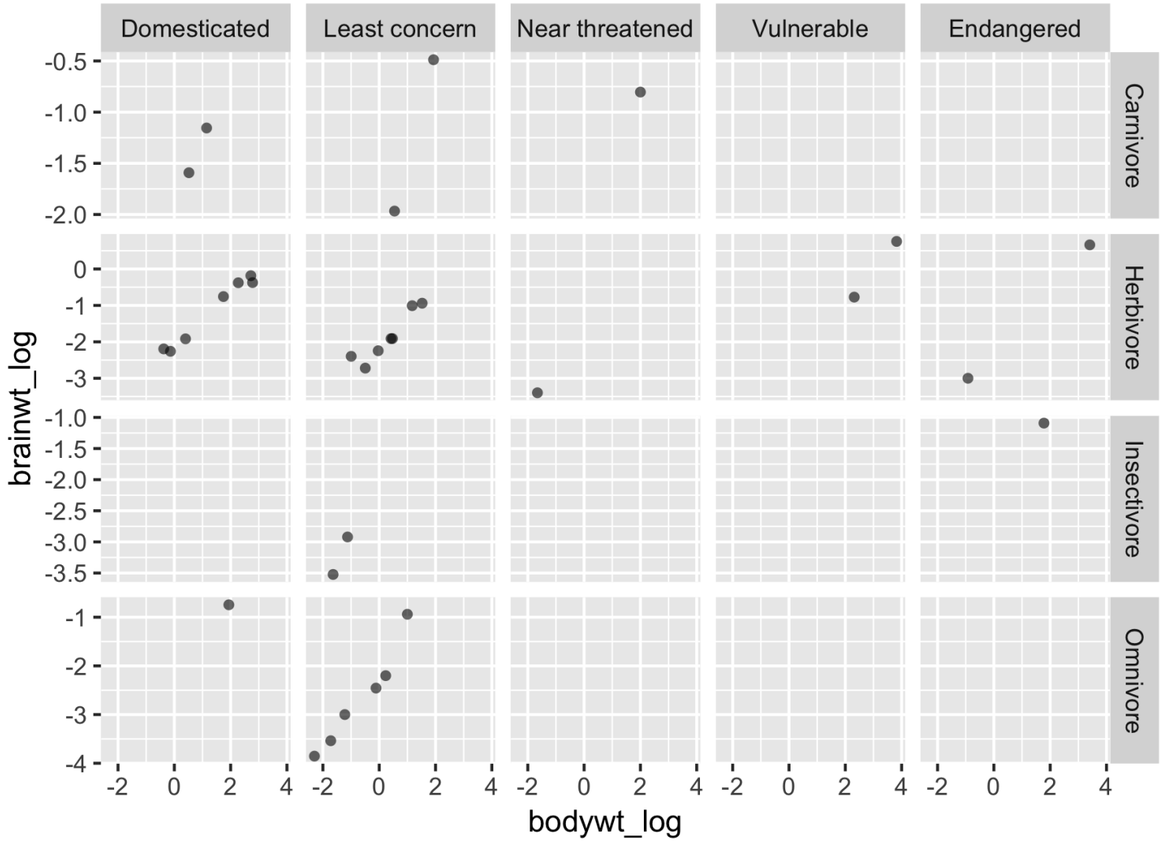
Adjusting the plotting space

```
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")
```



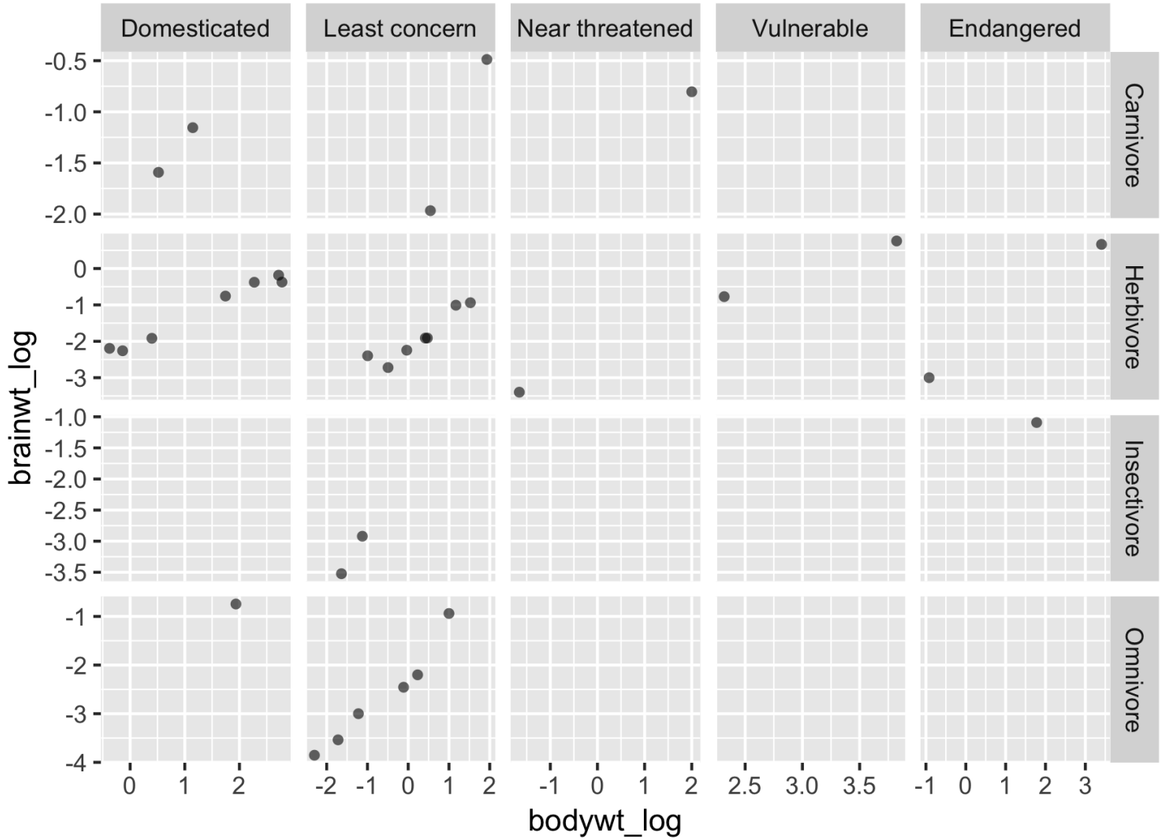
Adjusting the plotting space

```
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")
```



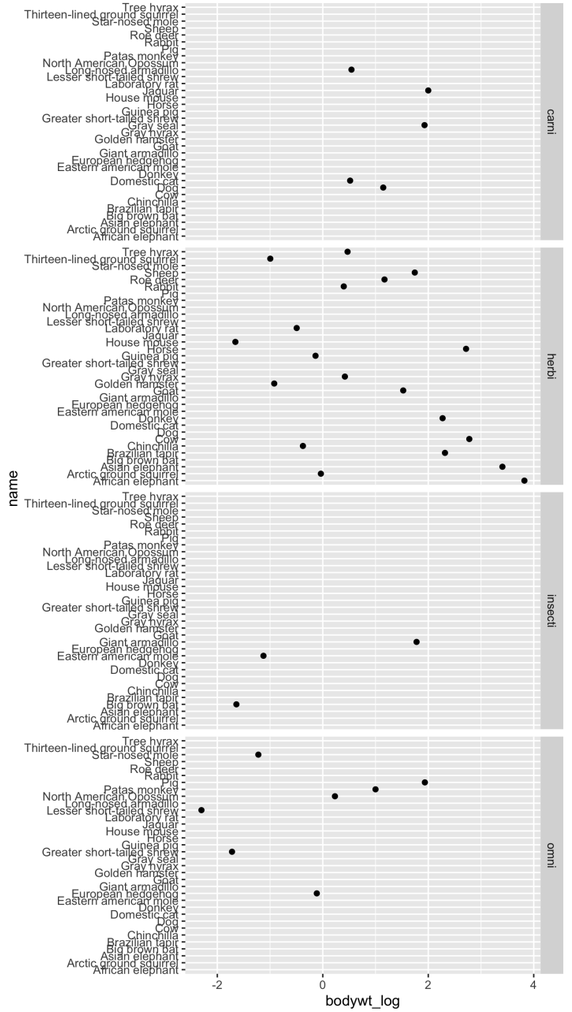
Adjusting the plotting space

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



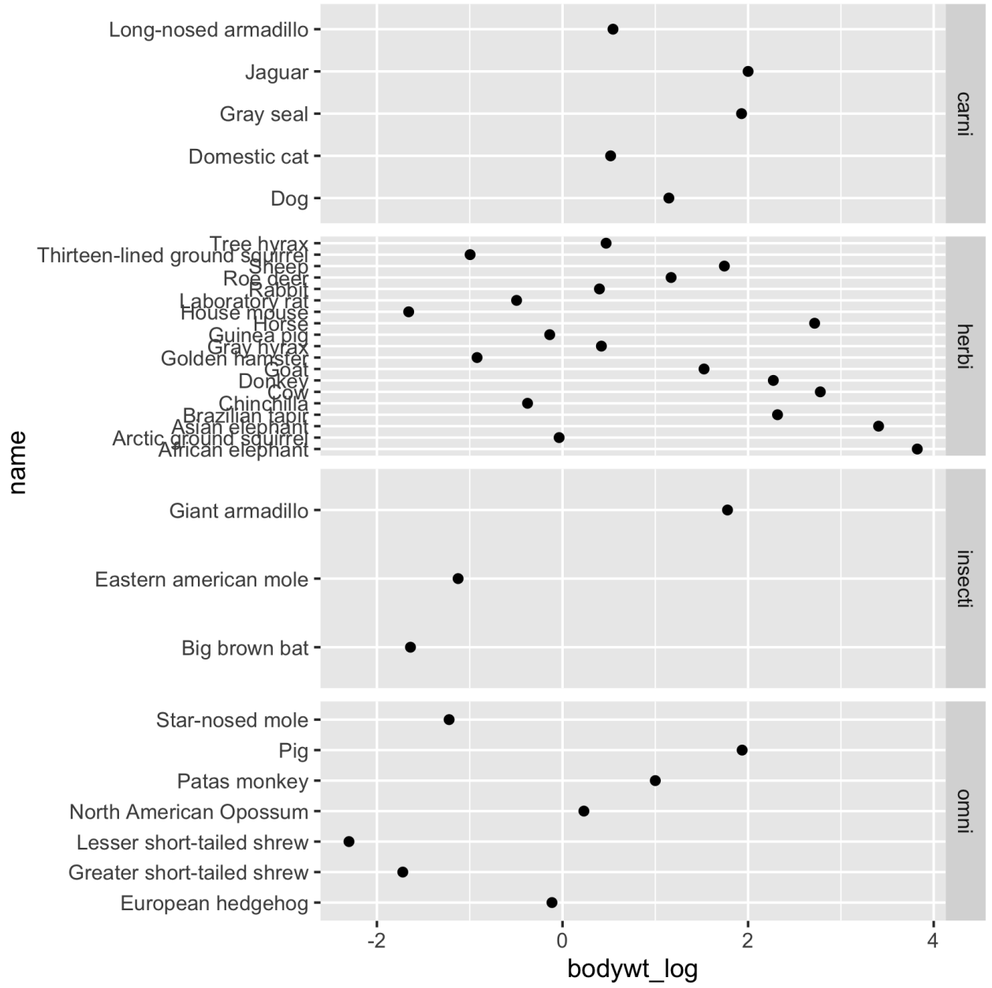
Adjusting the plotting space

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



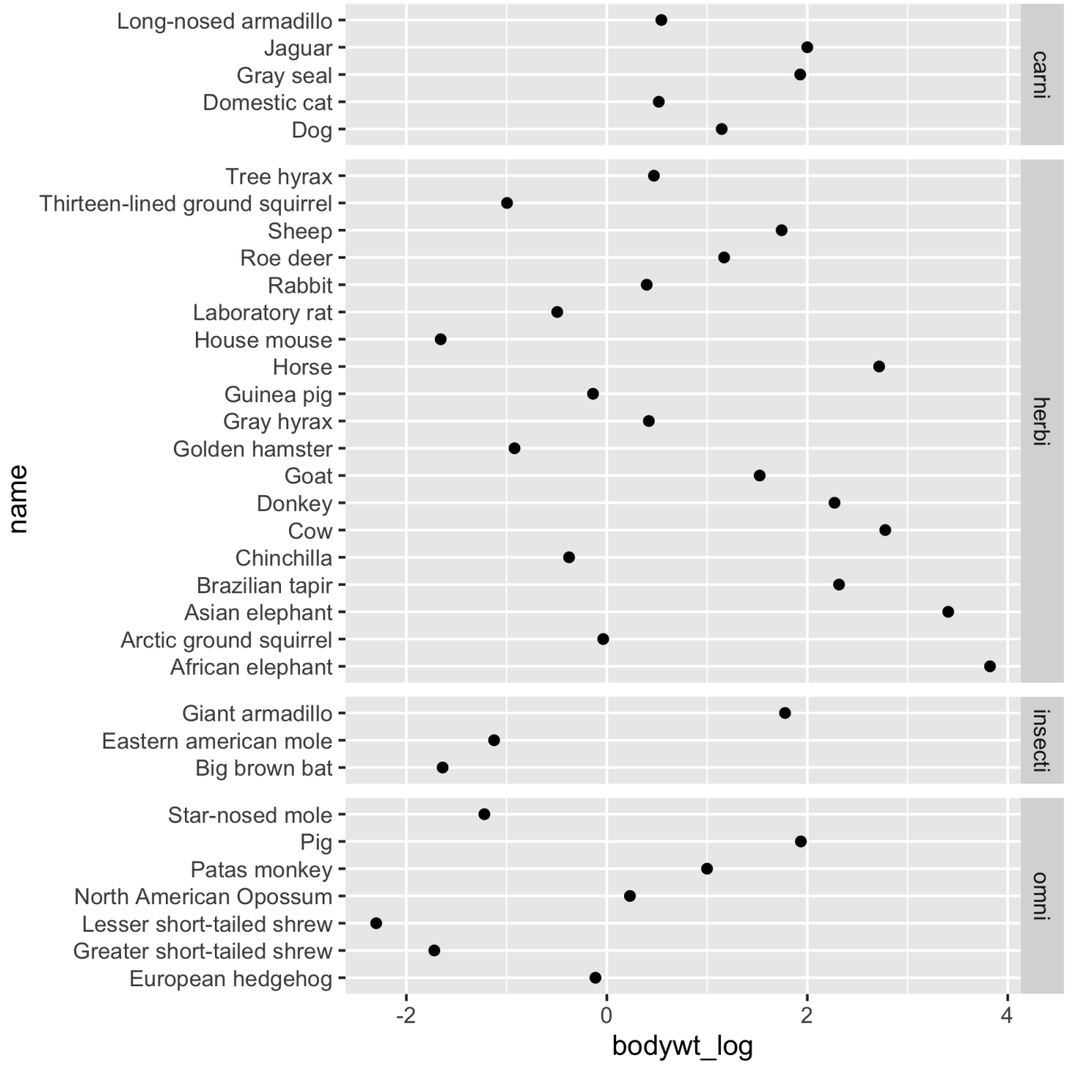
Adjusting the plotting space

```
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

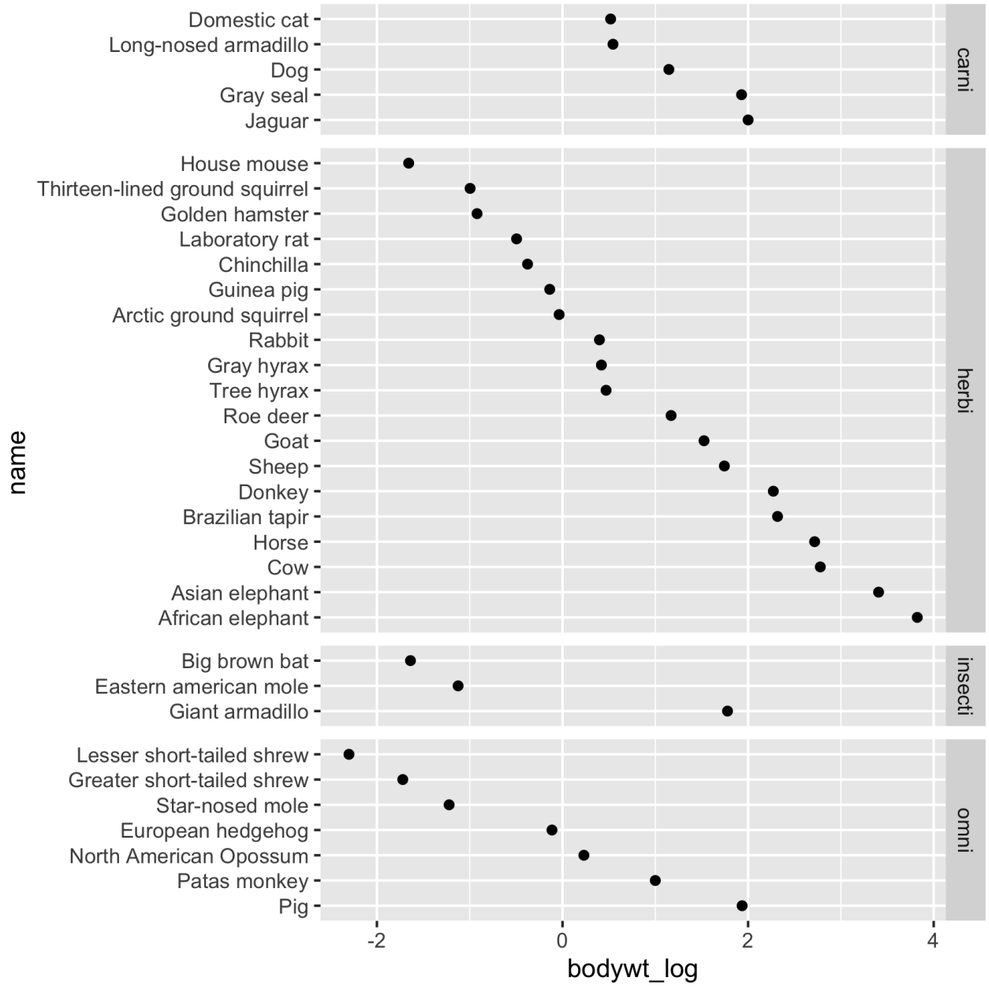
```
ggplot(msleep2, aes(x = bodywt_log,
                    y = name)) +
  geom_point() +
  # Free the y scales and space
  facet_grid(rows = vars(vore),
             scales = "free_y",
             space = "free_y")
```



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

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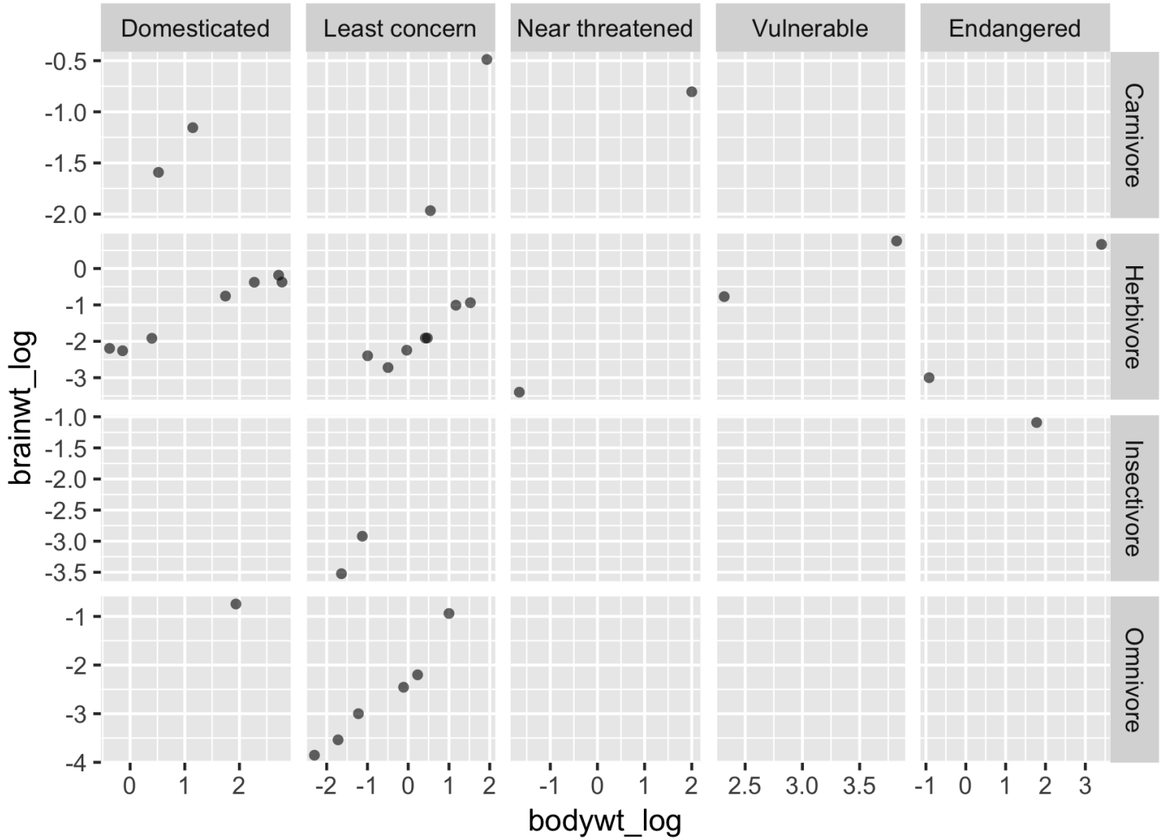
datacamp

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")
```



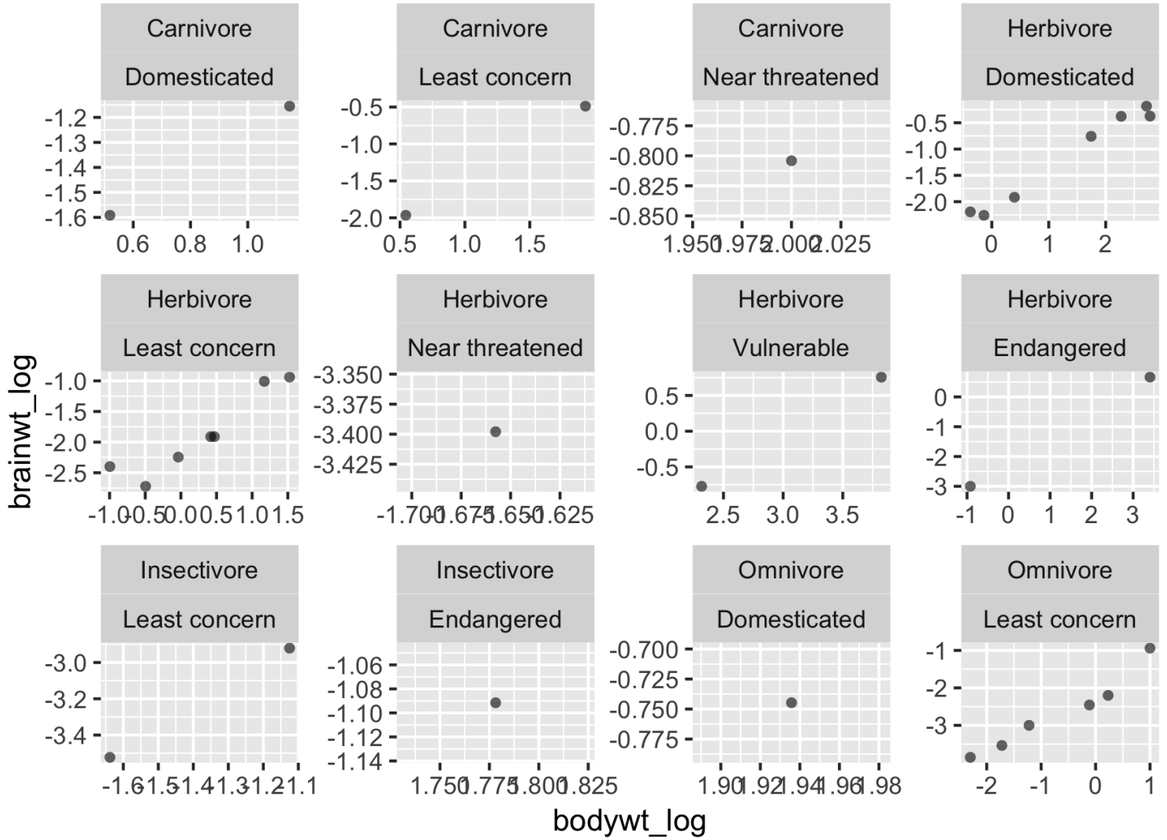
Using facet_wrap()

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")
```



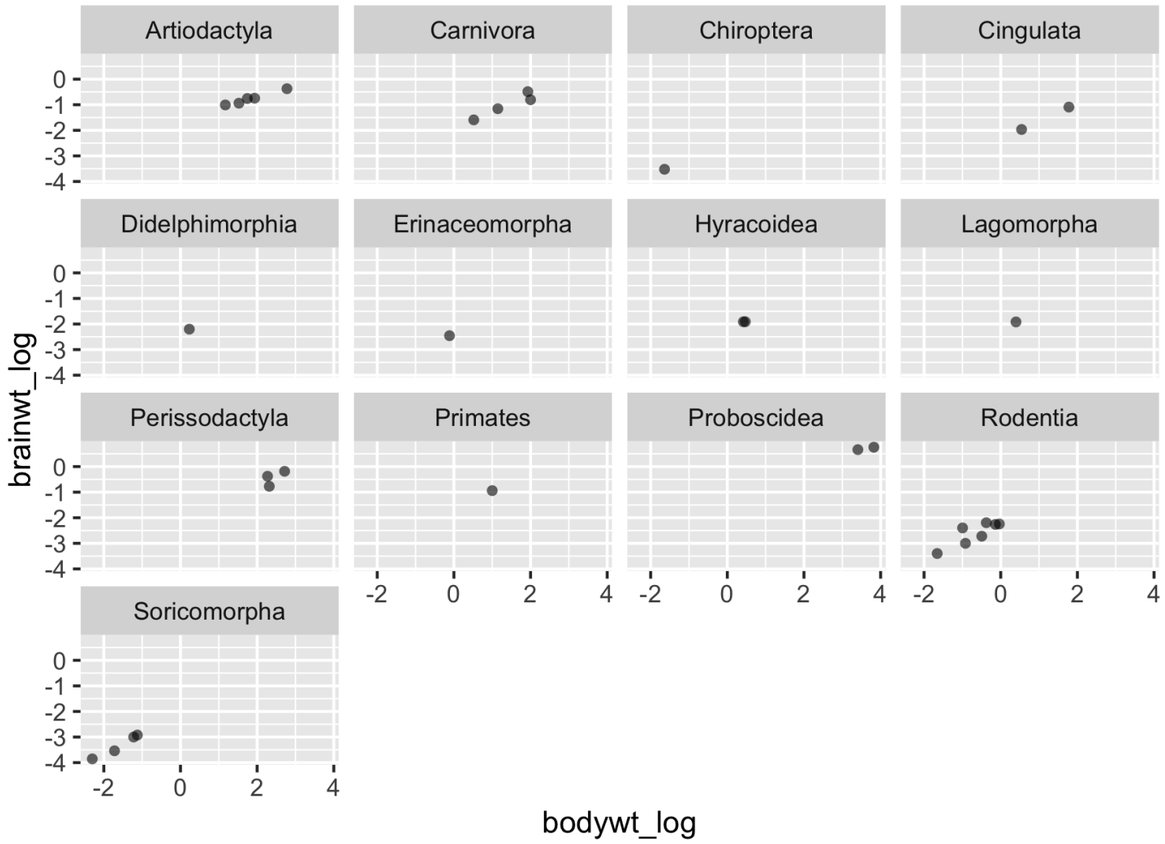
Using facet_wrap()

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

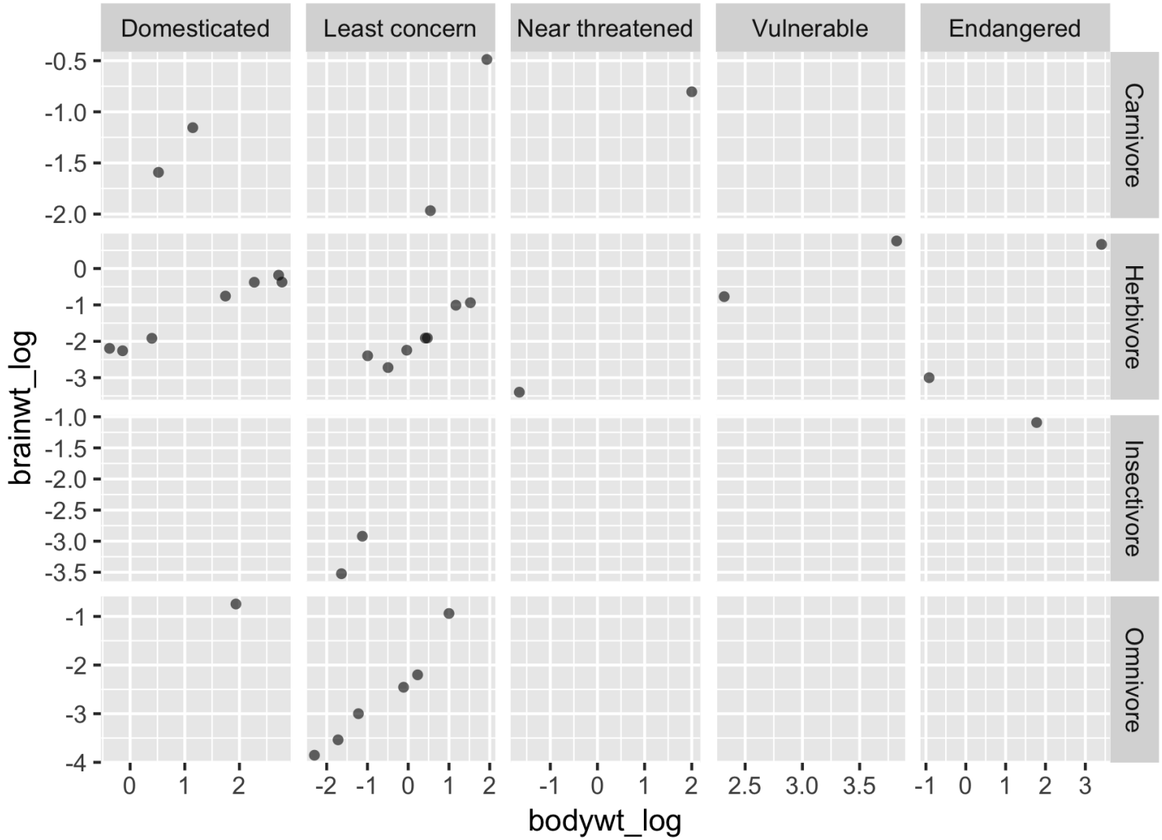
Using facet_wrap() - Scenario 2

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



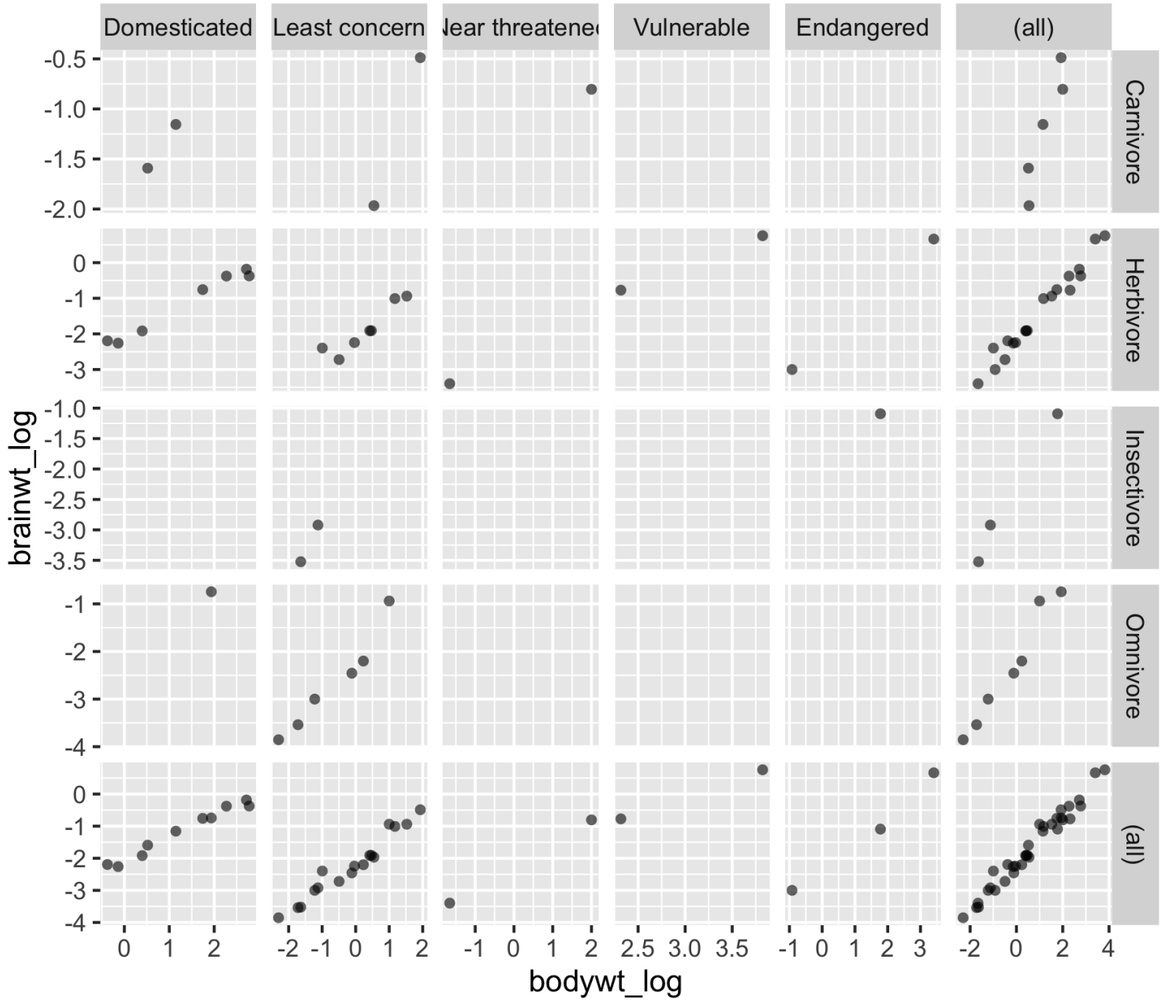
Using margin plots

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



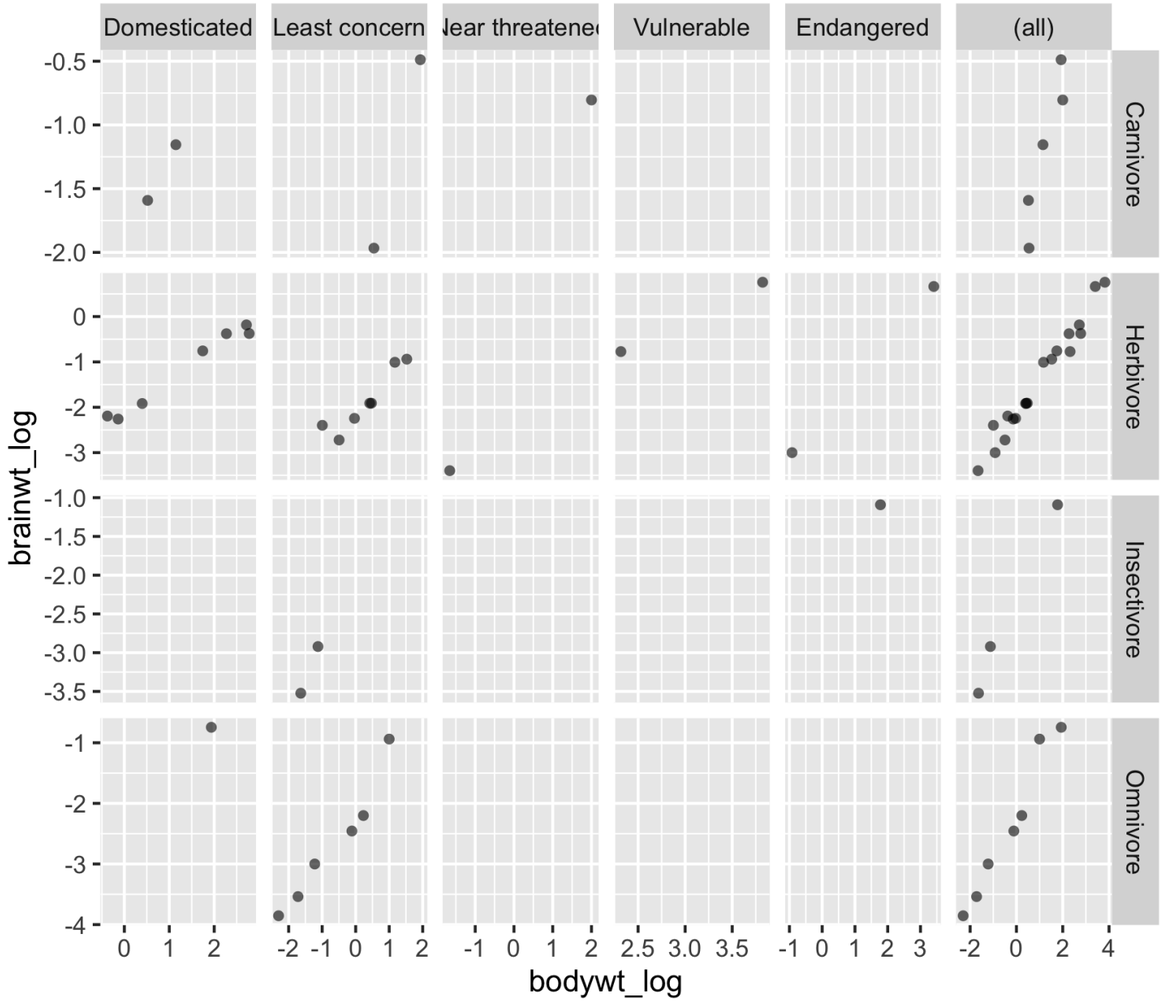
Using margin plots

```
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")
```



Let's practice!

INTERMEDIATE DATA VISUALIZATION WITH GGPLOT2