Hoops Longwing Sample Data Visualization

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In order to start analyzing the Hoops' Longwing sample data, we will first load the `tidyverse` package suite. After loading the packages we need, we can use `readr::read_csv()` to load in the data. But, notice the imported data frame has a useless column at the beginning, which we can easily remove manually.

```
library(tidyverse)

butterfly <- read_csv("hoops_longwing_study.csv")
butterfly <- butterfly[ , -1]
```

Now that we have the data imported, we can go ahead and take a quick look at the summary and structure.

```
summary(butterfly)
```

```
##   wing_length      wing_width          age         num_offspring
##  Min.   : 7.46   Min.   : 2.730   Min.   : 2.00   Min.   : 8.00
##  1st Qu.:14.19   1st Qu.: 6.670   1st Qu.:12.00   1st Qu.:24.00
##  Median :16.78   Median : 8.135   Median :19.00   Median :28.00
##  Mean   :20.24   Mean   : 8.748   Mean   :22.68   Mean   :27.84
##  3rd Qu.:26.74   3rd Qu.:10.910   3rd Qu.:31.00   3rd Qu.:32.00
##  Max.   :42.18   Max.   :17.390   Max.   :61.00   Max.   :39.00
##  feeding_range      color_peak      num_mates      avg_scale_size
##  Min.   :-0.250   Min.   :357.9   Min.   :-2.000   Min.   :18.27
##  1st Qu.: 2.640   1st Qu.:385.9   1st Qu.: 3.000   1st Qu.:28.02
##  Median : 3.510   Median :392.0   Median : 5.000   Median :32.39
##  Mean   : 5.997   Mean   :392.0   Mean   : 6.212   Mean   :38.43
##  3rd Qu.: 5.990   3rd Qu.:398.1   3rd Qu.: 9.000   3rd Qu.:48.60
##  Max.   :69.880   Max.   :428.3   Max.   :21.000   Max.   :89.43
##  antenna_length    num_spots       population        dispersal_distance
##  Min.   :0.350   Min.   : 2.000   Length:10000       Min.   :21.84
##  1st Qu.:3.140   1st Qu.: 4.000   Class :character   1st Qu.:24.15
##  Median :3.850   Median : 6.000   Mode  :character   Median :24.67
##  Mean   :4.375   Mean   : 5.755                      Mean   :24.67
##  3rd Qu.:5.800   3rd Qu.: 7.000                      3rd Qu.:25.19
##  Max.   :7.670   Max.   :18.000                      Max.   :27.79
##   body_length      sample_id
##  Min.   : 1.000   Length:10000
##  1st Qu.: 5.100   Class :character
##  Median : 6.450   Mode  :character
##  Mean   : 6.773
##  3rd Qu.: 8.480
##  Max.   :14.590
```

```
str(butterfly)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame':    10000 obs. of  14 variables:
##  $ wing_length       : num  14.1 24.5 21.3 16.2 15.5 ...
##  $ wing_width        : num  6.56 11 8.15 5.84 6.72 ...
##  $ age               : num  40 38 25 13 43 9 36 23 37 26 ...
##  $ num_offspring     : num  33 33 29 23 35 20 35 29 33 30 ...
##  $ feeding_range     : num  10.78 8.58 3.86 3.14 13.07 ...
##  $ color_peak        : num  402 387 373 407 399 ...
##  $ num_mates         : num  4 8 8 4 3 8 11 3 0 7 ...
##  $ avg_scale_size    : num  27.7 41.6 36.2 34.1 29.8 ...
##  $ antenna_length    : num  3.05 5.48 4.85 3.68 3.57 5.76 6.29 2.05 2.49 5.54 ...
##  $ num_spots         : num  7 4 6 8 7 4 4 9 10 4 ...
##  $ population        : chr  "Ternate" "Tidore" "Kayoa" "Ternate" ...
##  $ dispersal_distance: num  25.7 24.3 23.1 25.9 25.2 ...
##  $ body_length       : num  6.91 8.16 7.03 3.56 7.12 8.42 8.19 5.02 4.36 9.86 ...
##  $ sample_id         : chr  "Ter_00001_ZW" "Tid_00002_ZW" "Kay_00003_ZB" "Ter_00004_ZW" ...
```

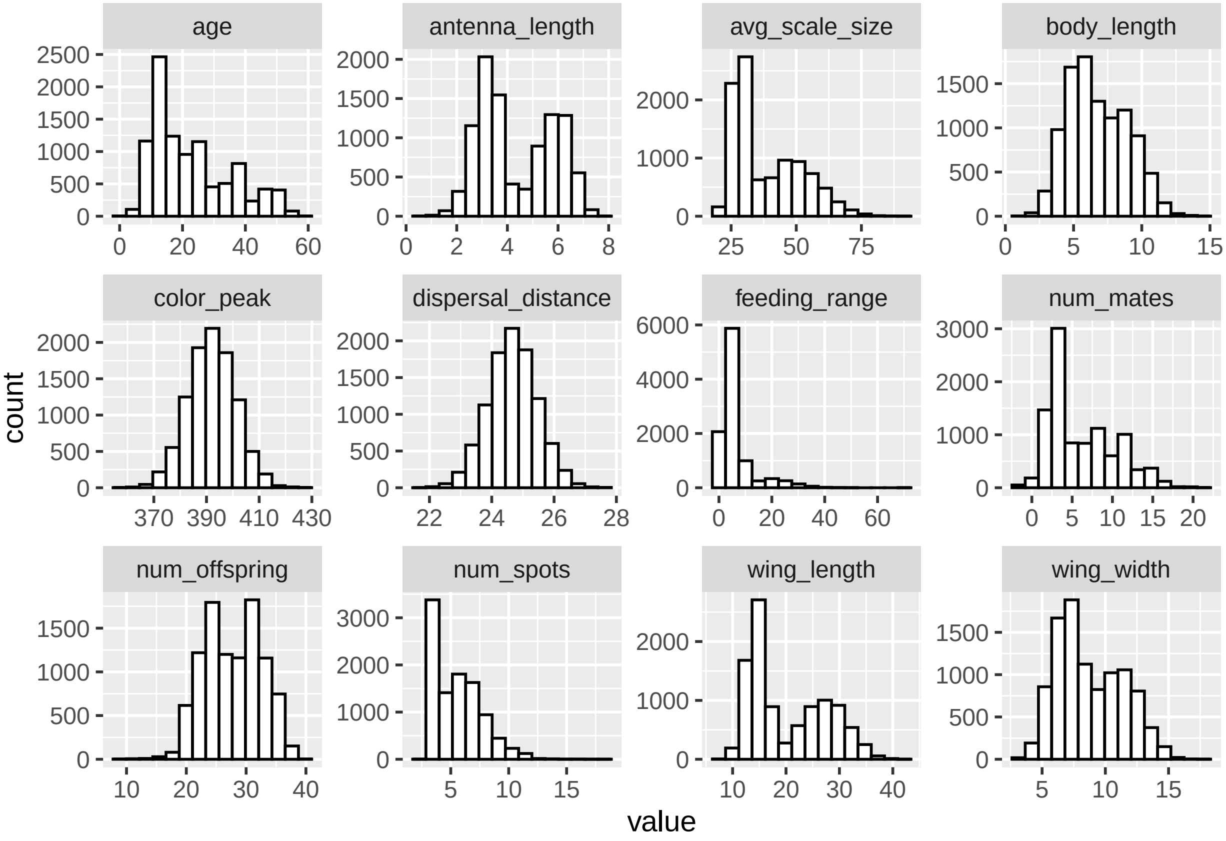
The only real change we need to make is to convert the `population` variable into a factor, since the functions provided in `readr` do not coerce strings to factors by default.

```
butterfly$population <- as.factor(butterfly$population)
summary(butterfly$population)
```

```
##   Kayoa Ternate  Tidore
##    1322    5486    3192
```

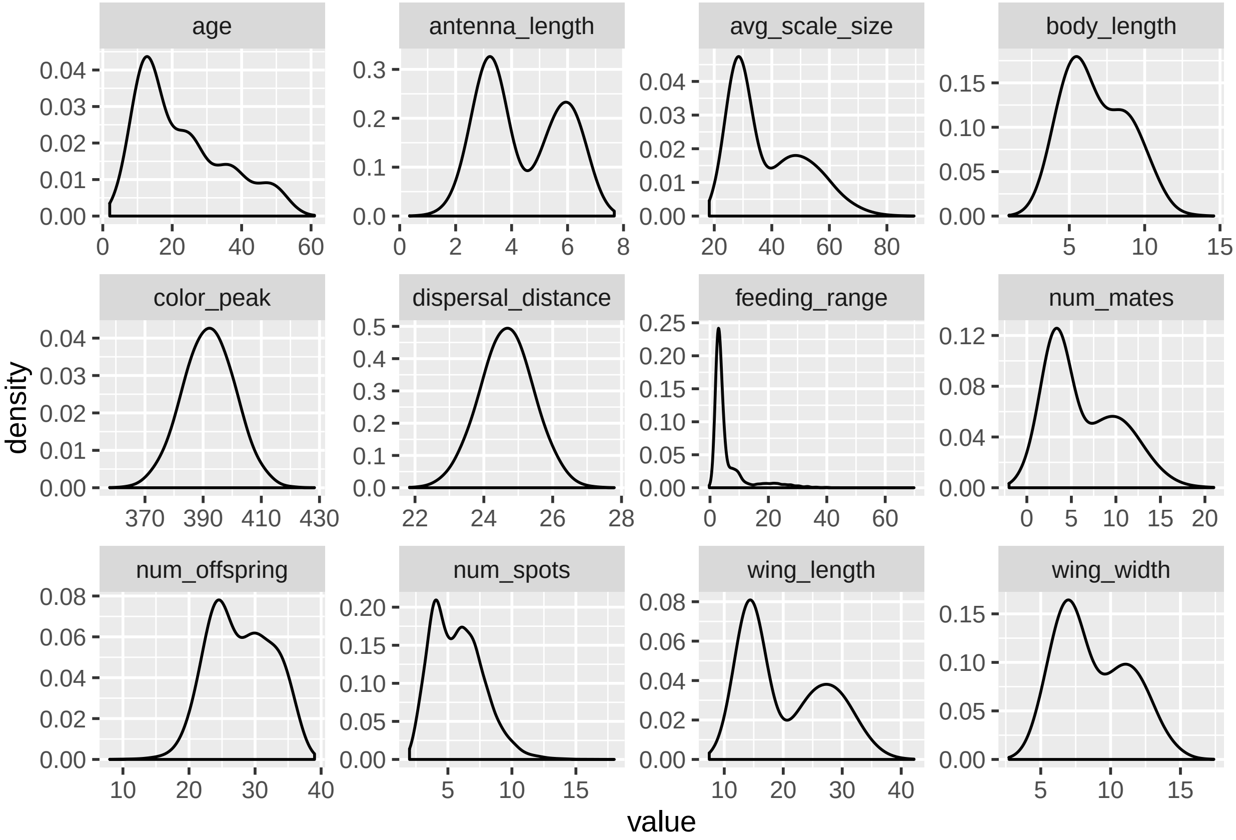
So, now we can start exploring our data. Let's start by making histograms of all the numeric data.

```
num_bins <- ceiling(log2(nrow(butterfly))) + 1
butterfly %>%
  select(-population) %>%
  gather(key = "field", value = "value", -"sample_id") %>%
  ggplot(aes(x = value)) +
  geom_histogram(col = "black",
                 fill = "white",
                 position = "identity",
                 bins = num_bins) +
  facet_wrap(~field, scales = "free")
```



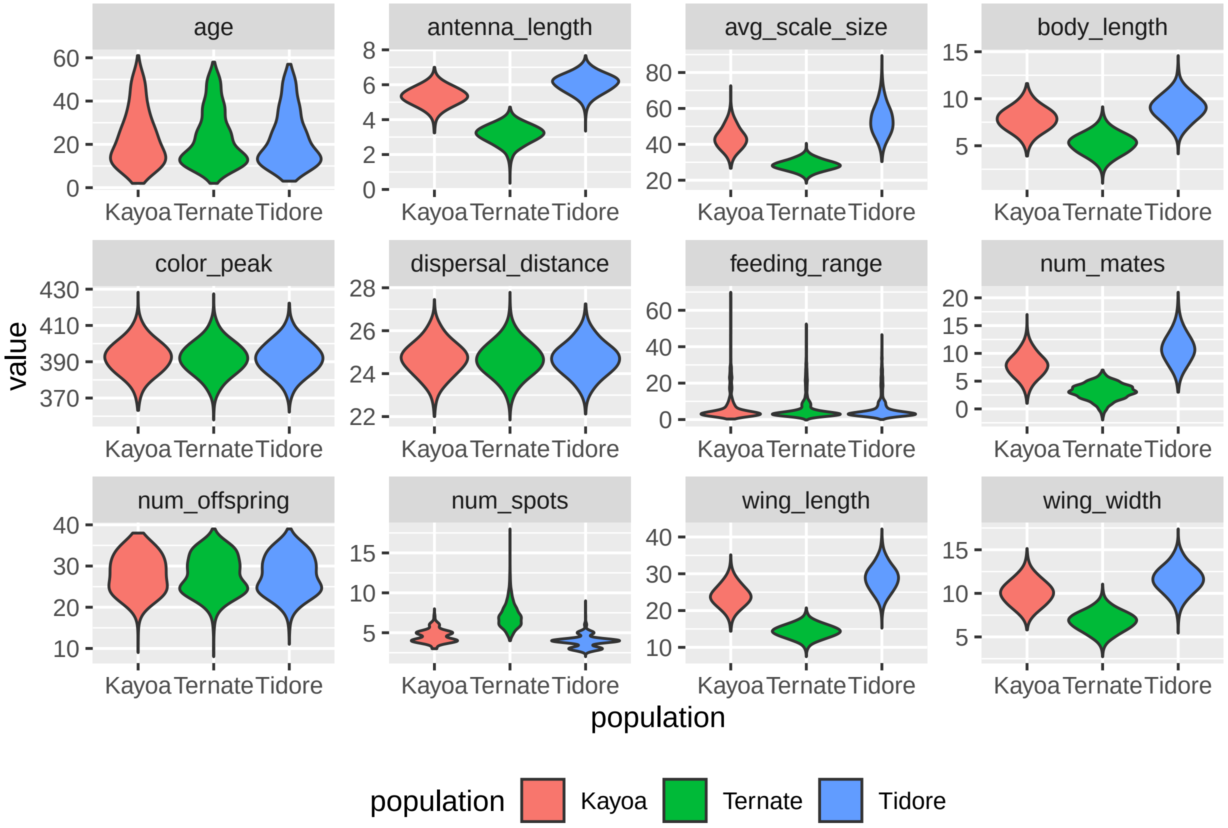
We can also visualize the distributions of the data using density curves, although we have to adjust the interpolation settings because part of our data is integers.

```
# An alternative way to view the data
butterfly %>%
  select(-population) %>%
  gather(key = "field", value = "value", -"sample_id") %>%
  ggplot(aes(x = value)) +
  geom_density(adjust = 2) +
  facet_wrap(~field, scales = "free")
```



Now we have one categorical variable, so let's look at all of our data stratified by the `population` value.

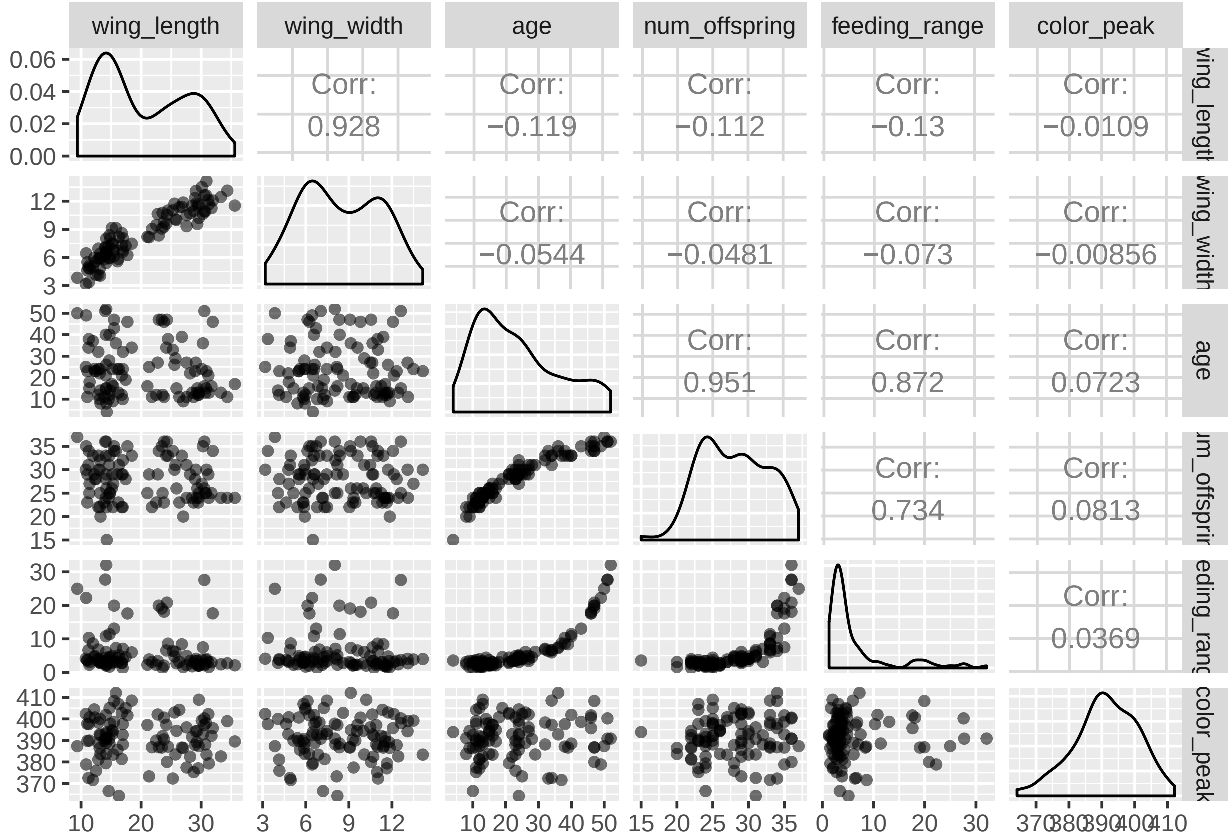
```
butterfly %>%
  gather(key = "field", value = "value", -c(sample_id, population)) %>%
  ggplot(aes(x = population, y = value, fill = population)) +
  geom_violin(adjust = 2) +
  facet_wrap(~field, scales = "free") +
  theme(legend.position = "bottom")
```



Now, using the `GGally` package, we can also make a scatterplot matrix like we did with `graphics::pairs()`. In order to get this to be visible, we'll need to split up the data.

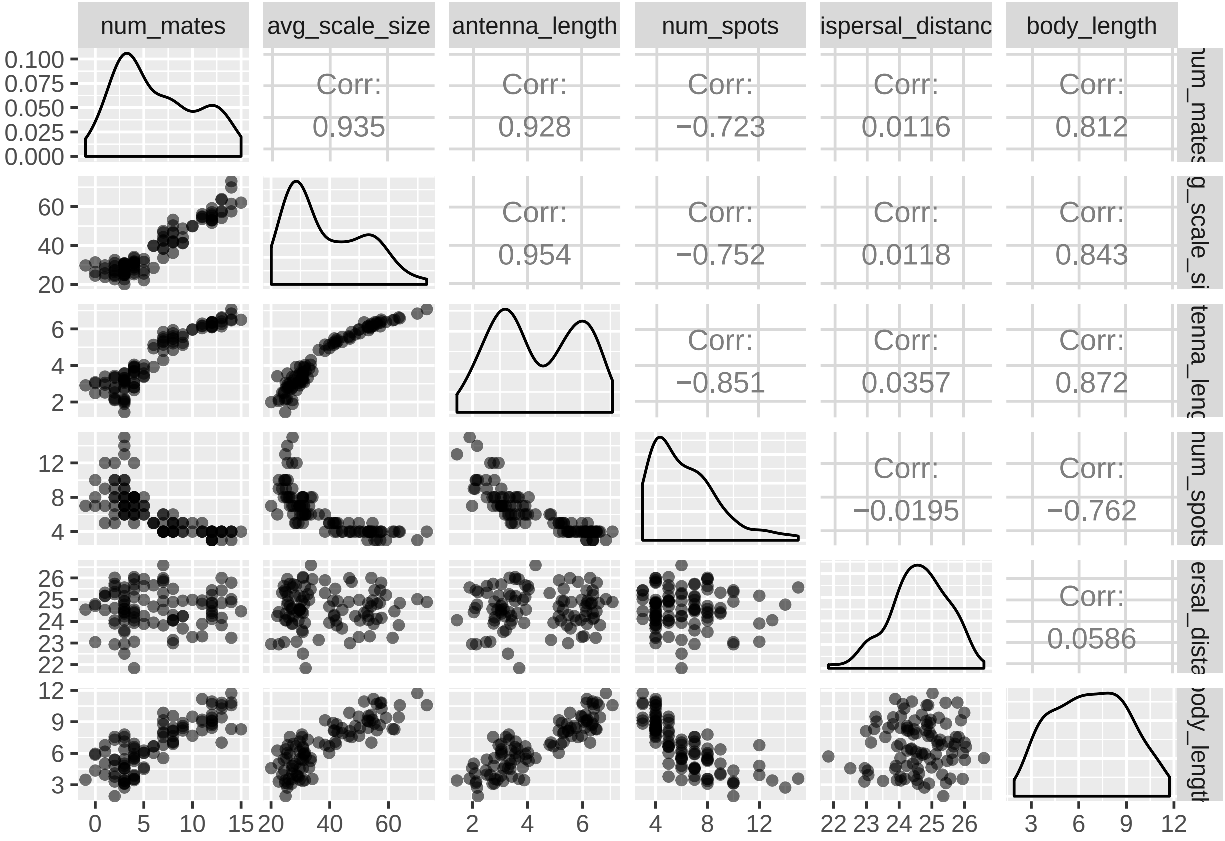
```r
library(GGally)

butterfly[1:100, 1:6] %>%
  ggpairs(aes(alpha = 0.2))
```



For the second half of the data, we also need to exclude our non-numeric variables.

```
butterfly[1:100, 7:14] %>%
  select(-c(sample_id, population)) %>%
  ggpairs(aes(alpha = 0.2))
```



As you can probably see, this visualization is not ideal when we have a lot of data.

Let's try a correlation table as well. However, note that while a correlation table can give us a good sense of linaer relationships, we lose any information we had about nonlinear relationships, which we have to examine visually if we don't have a hypothesis about their existence.

```r
library(pander)
butterfly %>%
  select(-c(sample_id, population)) %>%
  cor() %>%
  pander()
```

Table 1: Table continues below

	wing_length	wing_width	age	num_offspring
wing_length	1	0.9226	-0.001907	-0.002996
wing_width	0.9226	1	0.001328	-0.001489
age	-0.001907	0.001328	1	0.9413
num_offspring	-0.002996	-0.001489	0.9413	1
feeding_range	-0.004469	-0.00217	0.8559	0.7075
color_peak	0.01542	0.02052	0.00448	0.0009257
num_mates	0.9495	0.8747	-0.002376	-0.003543
avg_scale_size	0.9799	0.903	0.000683	-0.0002265
antenna_length	0.9906	0.9143	-0.002996	-0.00398
num_spots	-0.8294	-0.9372	0.00375	0.005168
dispersal_distance	0.01612	0.02096	0.0007418	-0.003065
body_length	0.8823	0.8511	-0.0002991	-0.002555

Table 2: Table continues below

	feeding_range	color_peak	num_mates
wing_length	-0.004469	0.01542	0.9495
wing_width	-0.00217	0.02052	0.8747
age	0.8559	0.00448	-0.002376
num_offspring	0.7075	0.0009257	-0.003543
feeding_range	1	0.01034	-0.004402
color_peak	0.01034	1	0.009925
num_mates	-0.004402	0.009925	1
avg_scale_size	-0.001537	0.01469	0.942
antenna_length	-0.005578	0.01548	0.9281
num_spots	0.005558	-0.01968	-0.769
dispersal_distance	0.006433	0.9468	0.01057
body_length	-0.0007702	0.01103	0.837

Table 3: Table continues below

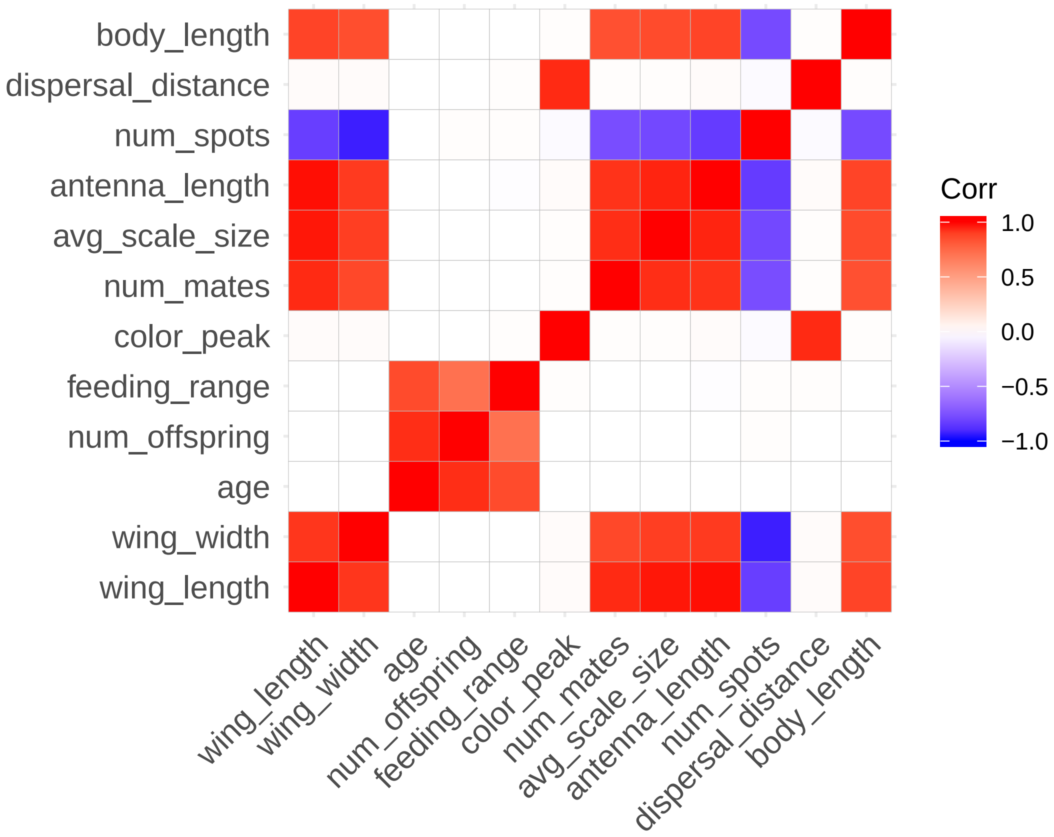
	avg_scale_size	antenna_length	num_spots
wing_length	0.9799	0.9906	-0.8294
wing_width	0.903	0.9143	-0.9372
age	0.000683	-0.002996	0.00375
num_offspring	-0.0002265	-0.00398	0.005168
feeding_range	-0.001537	-0.005578	0.005558

	avg_scale_size	antenna_length	num_spots
color_peak	0.01469	0.01548	-0.01968
num_mates	0.942	0.9281	-0.769
avg_scale_size	1	0.9554	-0.7921
antenna_length	0.9554	1	-0.8447
num_spots	-0.7921	-0.8447	1
dispersal_distance	0.01492	0.01626	-0.02037
body_length	0.8639	0.875	-0.7775

	dispersal_distance	body_length
wing_length	0.01612	0.8823
wing_width	0.02096	0.8511
age	0.0007418	-0.0002991
num_offspring	-0.003065	-0.002555
feeding_range	0.006433	-0.0007702
color_peak	0.9468	0.01103
num_mates	0.01057	0.837
avg_scale_size	0.01492	0.8639
antenna_length	0.01626	0.875
num_spots	-0.02037	-0.7775
dispersal_distance	1	0.01044
body_length	0.01044	1

Or, we can use a function from the `ggcorrplot` library to make a visual representation of the same data.

```
library(ggcorrplot)
butterfly %>%
  select(-c(sample_id, population)) %>%
  cor() %>%
  ggcorrplot()
```


body_length
dispersal_distance
num_spots
antenna_length
avg_scale_size
num_mates
color_peak
feeding_range
num_offspring
age
wing_width
wing_length
wing_length
wing_width
age
num_offspring
feeding_range
color_peak
num_mates
avg_scale_size
antenna_length
num_spots
dispersal_distance
body_length
Corr