

# GGally Notes

*Federico Lopez*

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## ggcorr to plot correlation matrices

Correlation matrices show correlation coefficients between many continuous variables. These matrices are created using the `cor` function. The `ggcorr` function from the `ggally` package to plot correlation matrices.

Usage

```
ggcorr(data, method = "pairwise", palette = "RdYlGn", ...)
```

`data` data matrix

`method` character string giving a method for computing covariances. Defaults to “pairwise”.

`palette` ColorBrewer palette to be used for correlation coefficients. Defaults to “RdYlGn”.

`geom` geom object to use. Accepts either `tile` (the default) or `circle`, to plot proportionally scaled circles.

```
#install.packages("GGally")
library(GGally)
library(ggplot2)
library(dplyr)
library(tidyr)

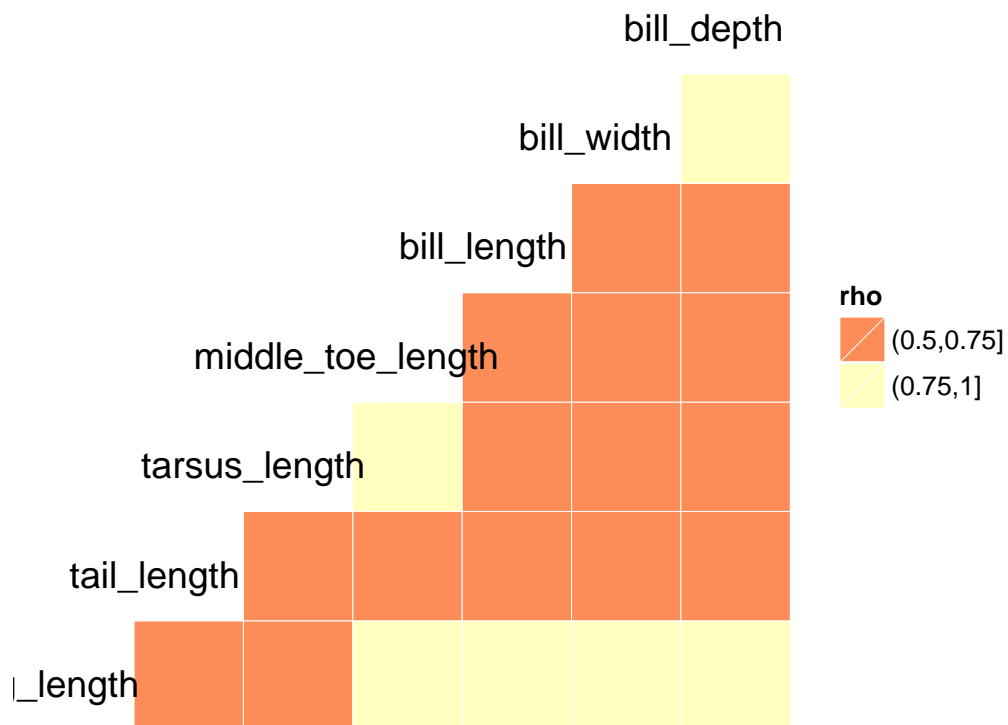
# library(rdryad)
# retrieve Anolis trait data from Kolbe et al. 2011, Evolution 65(12): 3608-3624.
# http://datadryad.org/handle/10255/dryad.34389?show=full
# anolis.data <- download_url("10255/dryad.34389")
# anolis.traits <- dryad_getfile(anolis.data)
# anolis.traits <- tbl_df(anolis.traits)
# glimpse(anolis.traits)

library(RCurl)
# http://datadryad.org/resource/doi:10.5061/dryad.qk461
# Jönsson et al. 2015, Evolution 69(4): 879-889
bird.data.url <- getURL("https://raw.githubusercontent.com/flopezo/notes/master/Jonsson_et_al_2015_data.csv")
bird.data <- read.csv(text=bird.data.url)
bird.data <- tbl_df(bird.data)
glimpse(bird.data)

## Observations: 1,579
## Variables: 9
## $ Species      (fctr) Acanthiza chrysorrhoa, Acanthiza lineata, A...
```

```
## $ Cladename      (fctr) basal_oscine, basal_oscine, basal_oscine, b...
## $ wing_length    (dbl) 59.0, 51.0, 52.0, 52.0, 65.0, 131.4, 156.3, ...
## $ tail_length     (dbl) 40.0, 37.0, 43.0, 38.0, 60.0, 85.3, 110.0, 1...
## $ tarsus_length   (dbl) 18.0, 17.0, 20.1, 17.6, 17.4, 37.3, 45.7, 48...
## $ middle_toe_length (dbl) 11.2, 10.8, 11.0, 10.9, 13.0, 25.2, 30.4, 33...
## $ bill_length     (dbl) 10.7, 6.7, 8.2, 8.3, 22.8, 29.7, 32.1, 39.0,...
## $ bill_width      (dbl) 3.9, 2.7, 3.0, 2.9, 3.8, 14.1, 16.6, 18.5, 1...
## $ bill_depth      (dbl) 2.9, 2.5, 2.2, 2.2, 3.5, 13.9, 16.6, 19.5, 1...
```

```
select(bird.data, -(Species:Cladename)) %>%
  ggcorr(hjust=0.7, vjust=0.8, size=5, layout.exp=1)
```



```
#ggcorr(bird.data[, -c(1, 2)])
#ggcorr(bird.data[, 3:9])

# ggcorr accepts a correlation matrix through the cor_matrix argument
# first argument must be set to NULL
```

## Correlation methods

```
# Pearson correlation coefficients, using pairwise observations (default method)
method=c("pairwise", "pearson")
```

```

# Pearson correlation coefficients, using all observations
method=c("everything", "pearson")

# Kendall correlation coefficients, using complete observations
method=c("complete", "kendall")

# Spearman correlation coefficients, using strictly complete observations
method=c("all.obs", "spearman")

```

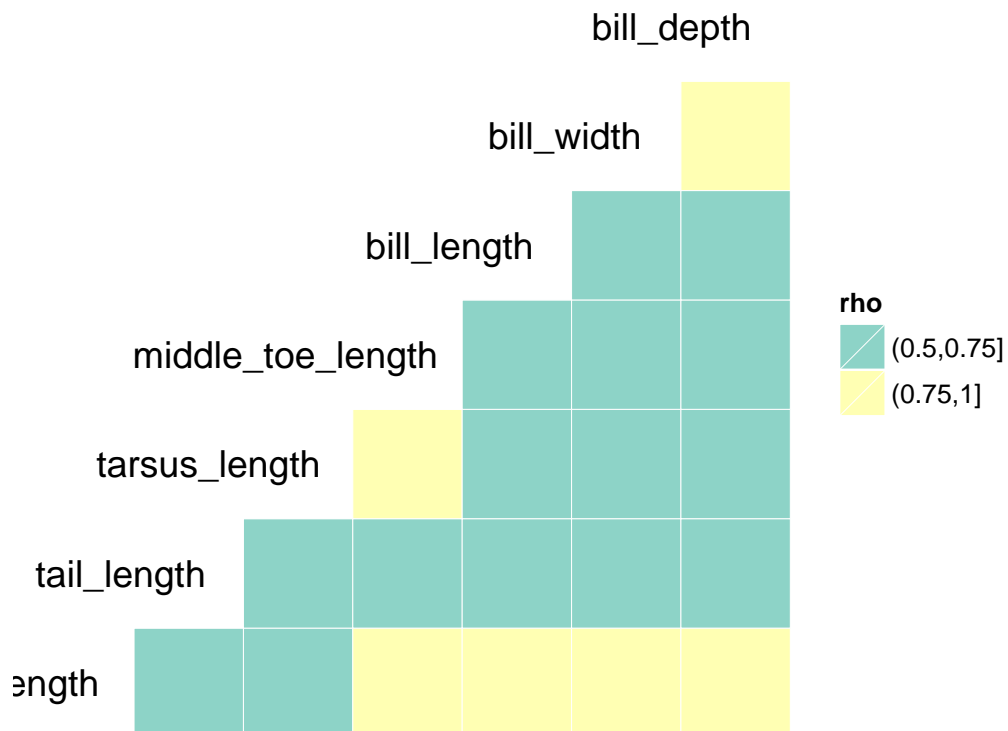
## Plotting parameters

### Change color palette and geometry

```

# nbreaks specifies how many breaks should be contained in the color scale
ggcorr(bird.data[, -c(1, 2)], nbreaks=5,
  hjust=0.9, size=5, palette="Set3", layout.exp=1)

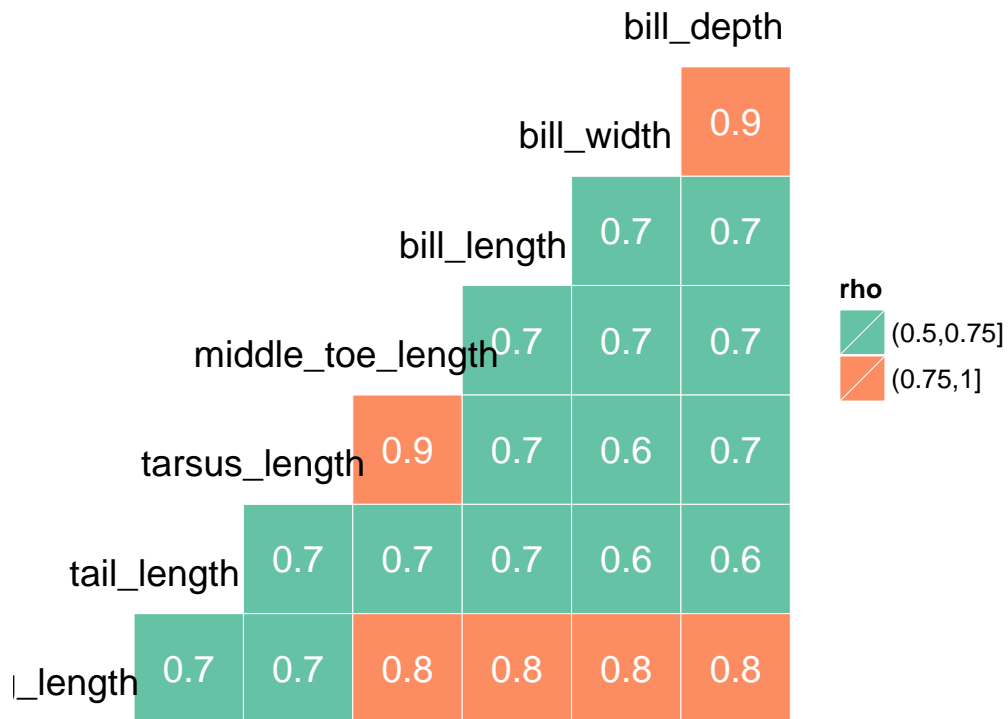
```



```

ggcorr(bird.data[, -c(1, 2)], nbreaks=5, hjust=0.7, vjust=1.0, size=5,
  palette="Set2", label=TRUE, label_size=3, label_color="white", layout.exp=1)

```



```
library(RCurl)
data.url <- getURL("https://raw.githubusercontent.com/flopezo/notes/master/Jonsson_et_al_2015_data_morphology")
bird.data <- read.csv(text=data.url)
bird.data <- tbl_df(bird.data)
glimpse(bird.data)
```

```
## Observations: 1,579
## Variables: 9
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## $ bill_length   (dbl) 10.7, 6.7, 8.2, 8.3, 22.8, 29.7, 32.1, 39.0,...
## $ bill_width    (dbl) 3.9, 2.7, 3.0, 2.9, 3.8, 14.1, 16.6, 18.5, 1...
## $ bill_depth    (dbl) 2.9, 2.5, 2.2, 2.2, 3.5, 13.9, 16.6, 19.5, 1...
```

```
ggcorr(bird.data[, -c(1, 2)], hjust=0.7, size=5,
  palette="Set2", label=TRUE, label_size=3, label_color="white", layout.exp=1)
```

