Information design and data visualization
Week 3, Lecture 05

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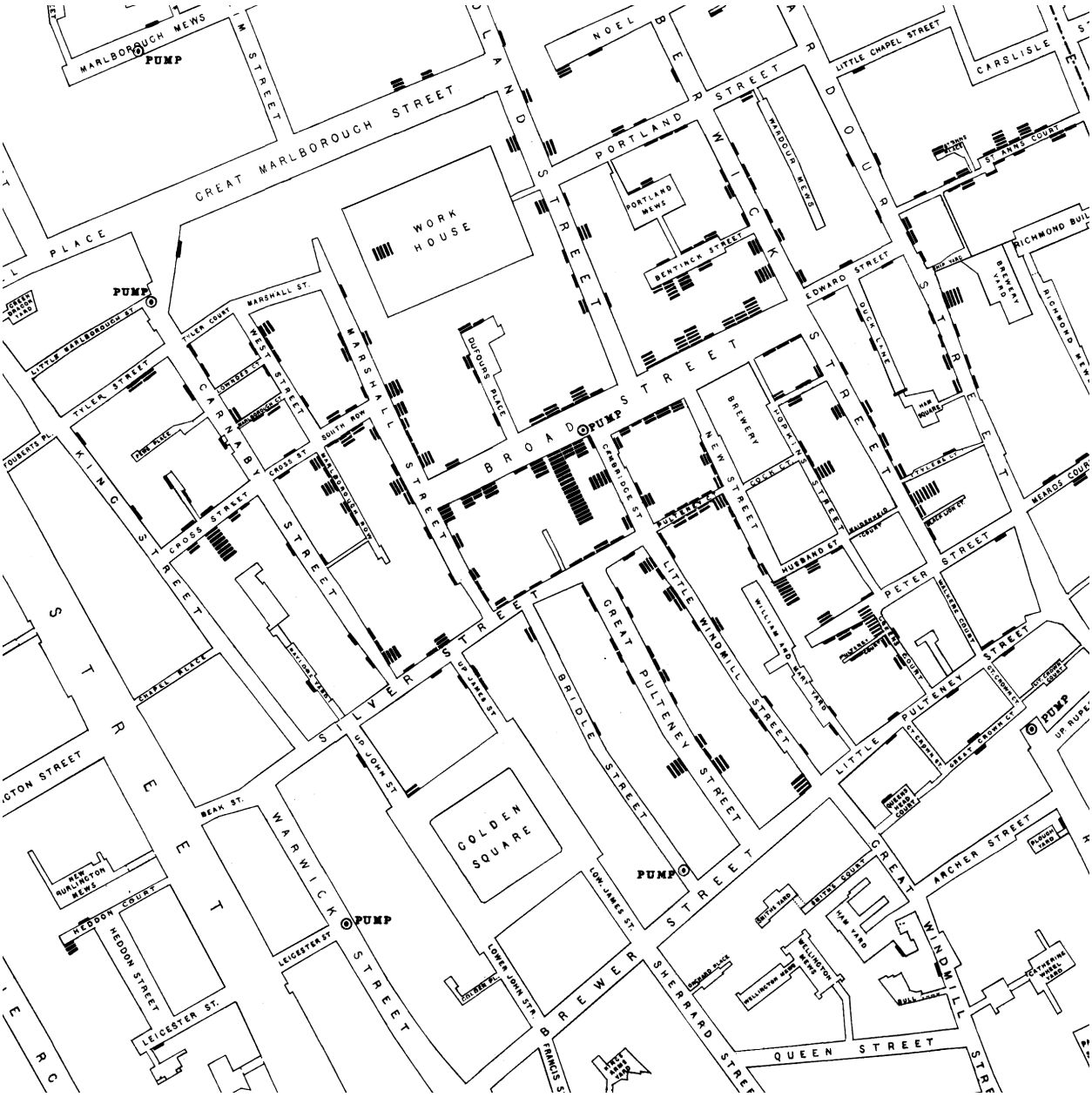
Information design

John Snow did know something... about cholera

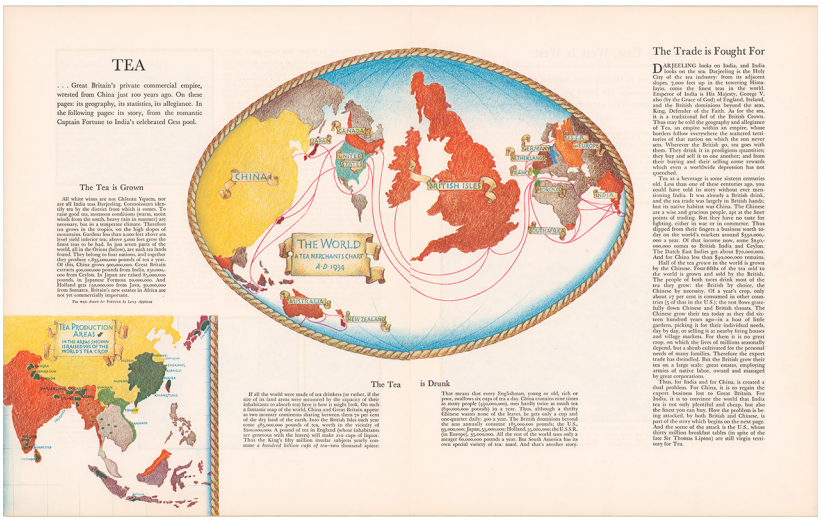
September 1854 cholera outbreak, Soho district, London



Source: John Snow, courtesy of John Mackenzie, University of Delaware

Bad figures are bad...

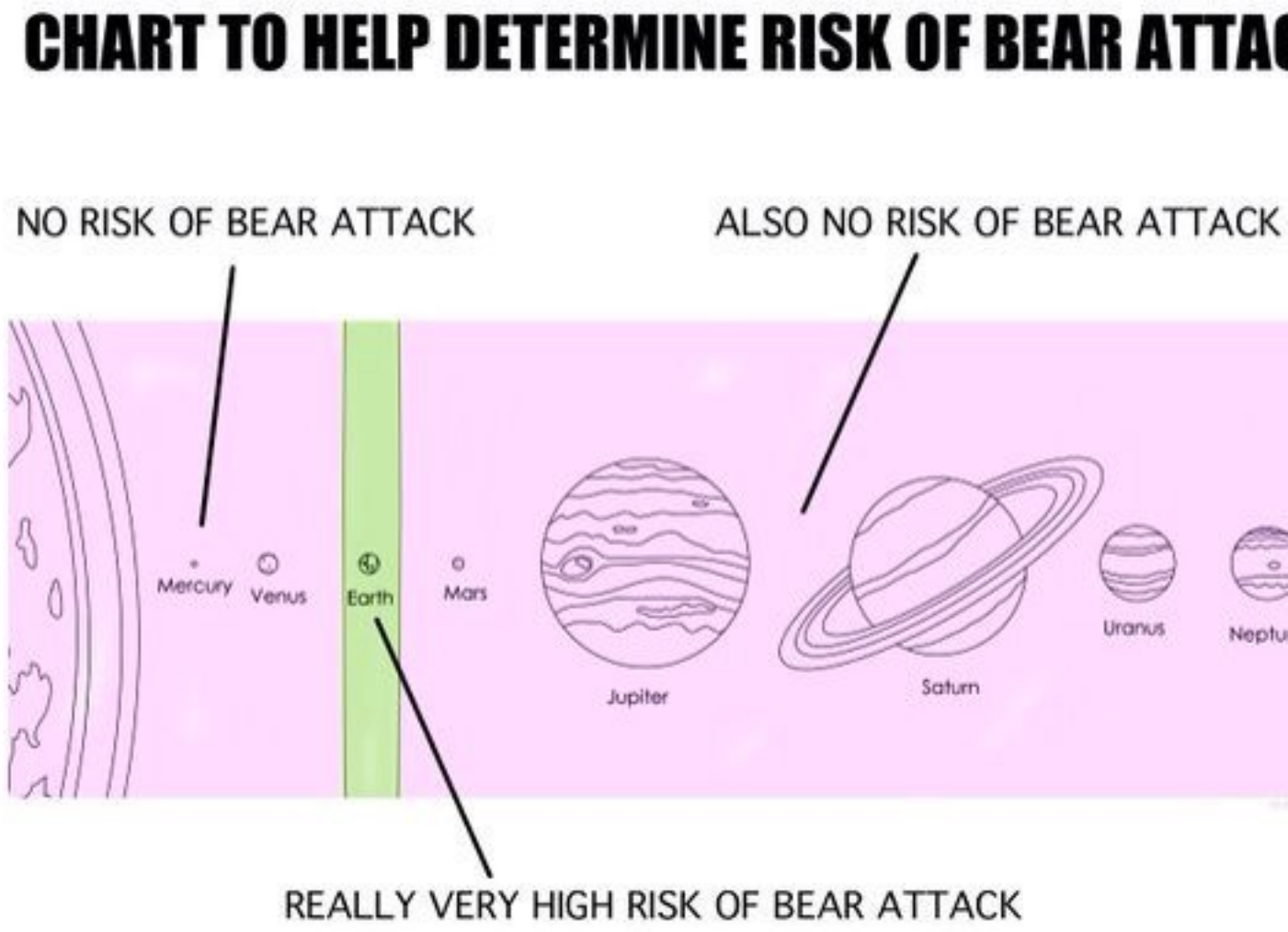
Because of bad taste



Source: "The Tea is Drunk," Fortune Magazine, June 1934, courtesy of Cornell University Library Digital Collections

- "Data-to-ink" ratio
- Aesthetics

Because of bad data



Source: @TerribleMaps

- Data quality
- Incorrect analyses
- Misleading or deceptive presentation

Because of bad perception

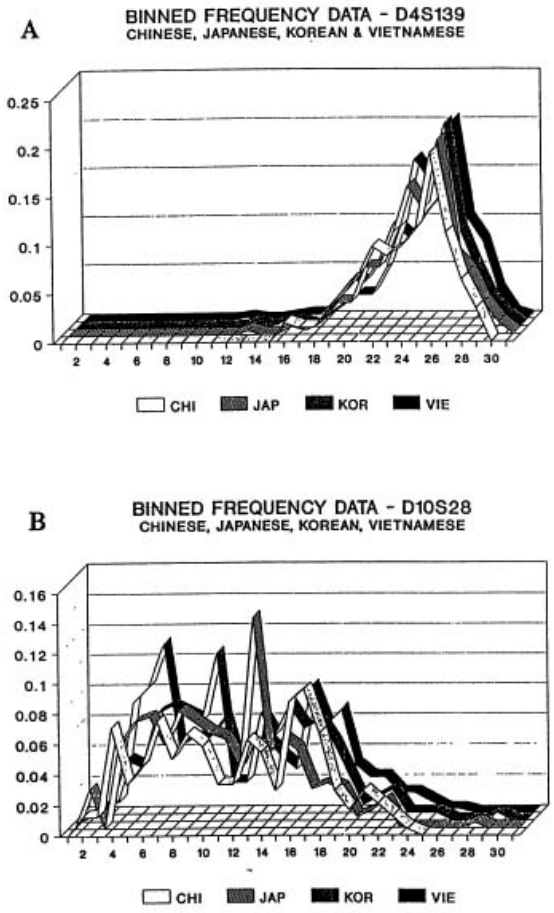
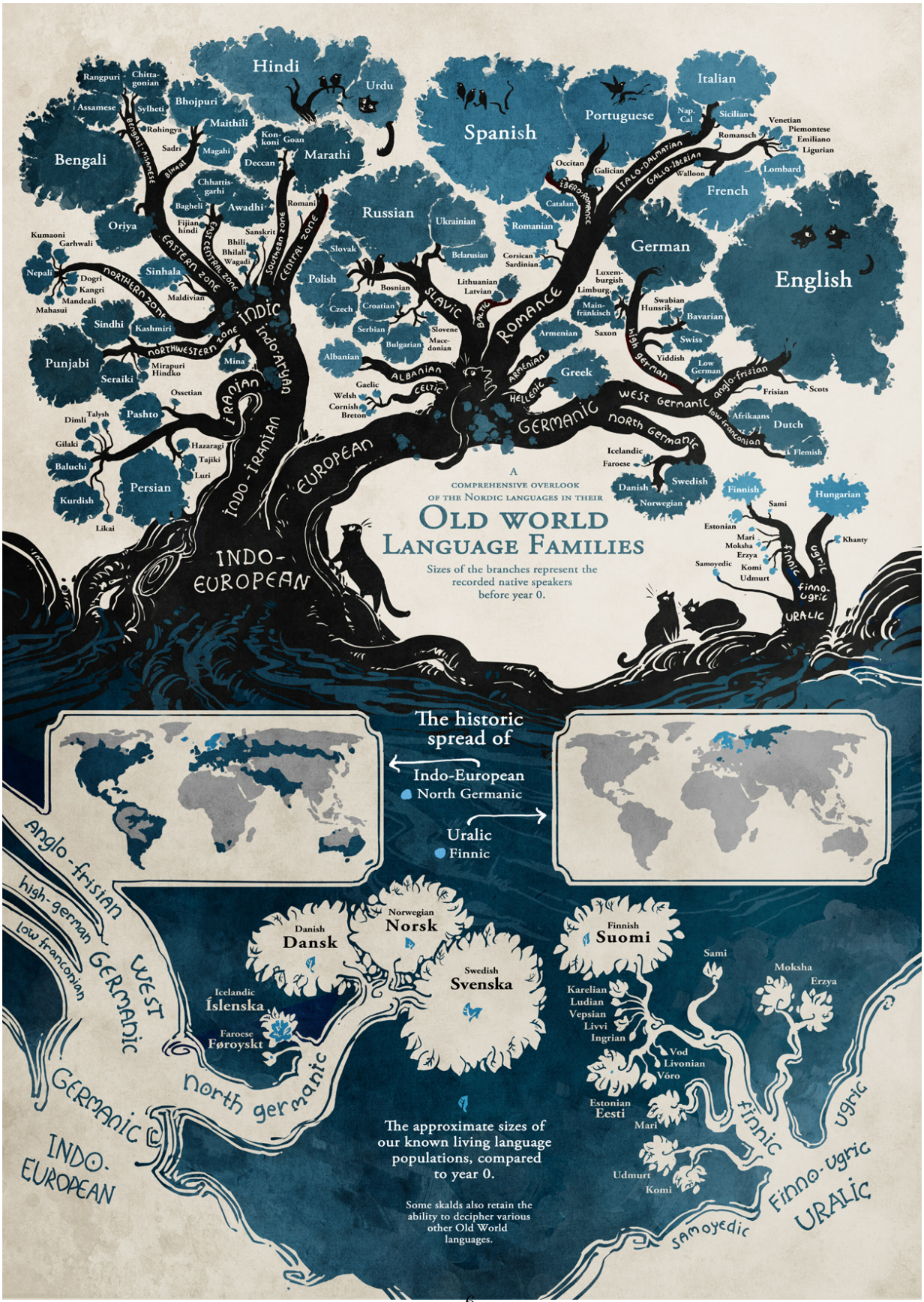


FIG. 4. *Fixed bin distribution (histogram) for two loci and four Asian subpopulations (used with permission from John Hartmann): the boundaries of the* 30 *bins (vertical axis) are determined by the FBI; these bins are not of equal length. Sample sizes (numbers of individuals) for Chinese, Japanese, Korean and Vietnamese are* 103, 125, 93 *and* 215 *for* D4S139 *and* 120, 137, 100 *and* 193 *for* D10S28. *The horizontal axis is the bin number; bins are not of equal length.*

Source: Roeder, K. (1994). DNA fingerprinting: A review of the controversy. Statistical Science 9(2): 222-247, courtesy of Karl Broman, University of Wisconsin-Madison

- Ease of interpretation

Tell a story



Source: Minna Sundberg, Stand Still. Stay Silent #196

base

Useful for quick-and-dirty exploratory visualizations because you don't have to load any additional packages.

lattice

Many examples of potential uses available online; especially good at showing relationships for multiple variables or across multiple plots. However, my opinion is that almost anything `lattice` can do can be done better by `ggplot2` with cleaner code.

ggplot2

```
install.packages("tidyverse")
# OR
install.packages("ggplot2")
```

```
library(ggplot2)
```

A plot made using `ggplot()` has, at minimum, three elements:

- data set
- aesthetics
- geometry

Let's get some data to work with.

Go to the Supplementary Materials for Stoddard et al. (2018) at: https://science.sciencemag.org/content/suppl/2017/06/21/356.6344.1249.DC1

Click "Data S1" to download the data, in Excel format, and put it in your `/data` folder.

```
library(readxl)
```

```
egg = read_xlsx(path="./data/aaj1945_DataS1_Egg_shape_by_species_v2.xlsx",
                      sheet=1)
egg = as.data.frame(egg)
```

```
head(egg)
```

```
##             Order       Family        MVZDatabase             Species
## 1 ACCIPITRIFORMES Accipitridae   Accipiter badius   Accipiter badius
## 2 ACCIPITRIFORMES Accipitridae Accipiter cooperii Accipiter cooperii
## 3 ACCIPITRIFORMES Accipitridae Accipiter gentilis Accipiter gentilis
## 4 ACCIPITRIFORMES Accipitridae    Accipiter nisus    Accipiter nisus
## 5 ACCIPITRIFORMES Accipitridae Accipiter striatus Accipiter striatus
## 6 ACCIPITRIFORMES Accipitridae  Aegypius monachus  Aegypius monachus
##   Asymmetry Ellipticity AvgLength (cm) Number of images Number of eggs
## 1    0.1378   0.3435262         3.8642                1              2
## 2    0.0937   0.2715367         4.9008               27            103
## 3    0.1114   0.3186002         5.9863                7             18
## 4    0.0808   0.2390652         4.0355               13             61
## 5    0.0749   0.2542802         3.8700               15             57
## 6    0.0700   0.3476181         8.9076                1              1
```

```
str(egg)
```

```
## 'data.frame':    1402 obs. of  9 variables:
##  $ Order           : chr  "ACCIPITRIFORMES" "ACCIPITRIFORMES" "ACCIPITRIFORMES" "ACCIPITRIFORMES" ..
##  $ Family          : chr  "Accipitridae" "Accipitridae" "Accipitridae" "Accipitridae" ...
##  $ MVZDatabase     : chr  "Accipiter badius" "Accipiter cooperii" "Accipiter gentilis" "Accipiter nis
##  $ Species         : chr  "Accipiter badius" "Accipiter cooperii" "Accipiter gentilis" "Accipiter nis
##  $ Asymmetry       : num  0.1378 0.0937 0.1114 0.0808 0.0749 ...
##  $ Ellipticity     : num  0.344 0.272 0.319 0.239 0.254 ...
##  $ AvgLength (cm)  : num  3.86 4.9 5.99 4.04 3.87 ...
##  $ Number of images: num  1 27 7 13 15 1 191 1 7 2 ...
##  $ Number of eggs  : num  2 103 18 61 57 1 391 2 17 4 ...
```

Those spaces in the column names may cause problems, so let's fix them.

```
colnames(egg)
```

```
## [1] "Order"            "Family"           "MVZDatabase"
## [4] "Species"          "Asymmetry"        "Ellipticity"
## [7] "AvgLength (cm)"   "Number of images" "Number of eggs"
```

```
colnames(egg)[7:9] = c("AvgLength","NumberOfImages","NumberOfEggs")
```

And check out the help page for the `ggplot()` function before we use it.

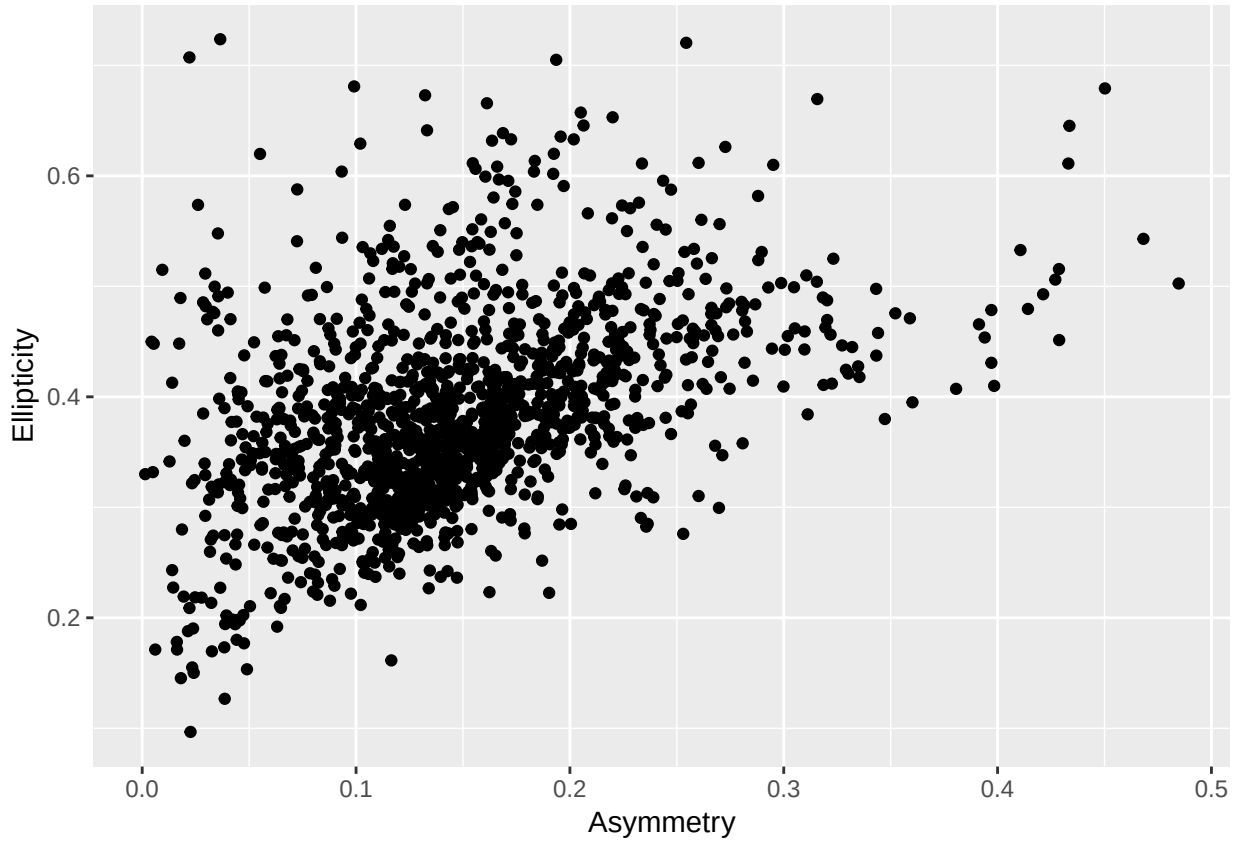
```
?ggplot
```

Not very helpful... A better resource is the tidyverse page for `ggplot2`: https://ggplot2.tidyverse.org/

Now we can make our first plot with the three elements needed: data, aesthetic mappings, and a geometry.

```
ggplot(data=egg, mapping=aes(x=Asymmetry, y=Ellipticity)) +
  geom_point()
```

```
## Warning: Removed 2 rows containing missing values (geom_point).
```



The function warns us that we have some missing values. Let's find them and remove them.

```
egg[is.na(egg$Asymmetry),]
```

```
##      Order Family MVZDatabase Species Asymmetry Ellipticity AvgLength
## 1401  <NA>   <NA>        <NA>    <NA>        NA          NA        NA
## 1402  <NA>   <NA>        <NA>    <NA>        NA          NA        NA
##      NumberOfImages NumberOfEggs
## 1401             NA           NA
## 1402             NA           NA
```

```
egg[is.na(egg$Ellipticity),]
```

```
##      Order Family MVZDatabase Species Asymmetry Ellipticity AvgLength
## 1401  <NA>   <NA>        <NA>    <NA>        NA          NA        NA
## 1402  <NA>   <NA>        <NA>    <NA>        NA          NA        NA
##      NumberOfImages NumberOfEggs
## 1401             NA           NA
## 1402             NA           NA
```

```
tail(egg)
```

```
##              Order     Family               MVZDatabase
## 1397  TINAMIFORMES  Tinamidae      Rhynchotus rufescens
## 1398 TROGONIFORMES Trogonidae       Euptilotis neoxenus
## 1399 TROGONIFORMES Trogonidae Harpactes erythrocephalus
## 1400 TROGONIFORMES Trogonidae            Trogon elegans
## 1401          <NA>       <NA>                      <NA>
## 1402          <NA>       <NA>                      <NA>
```

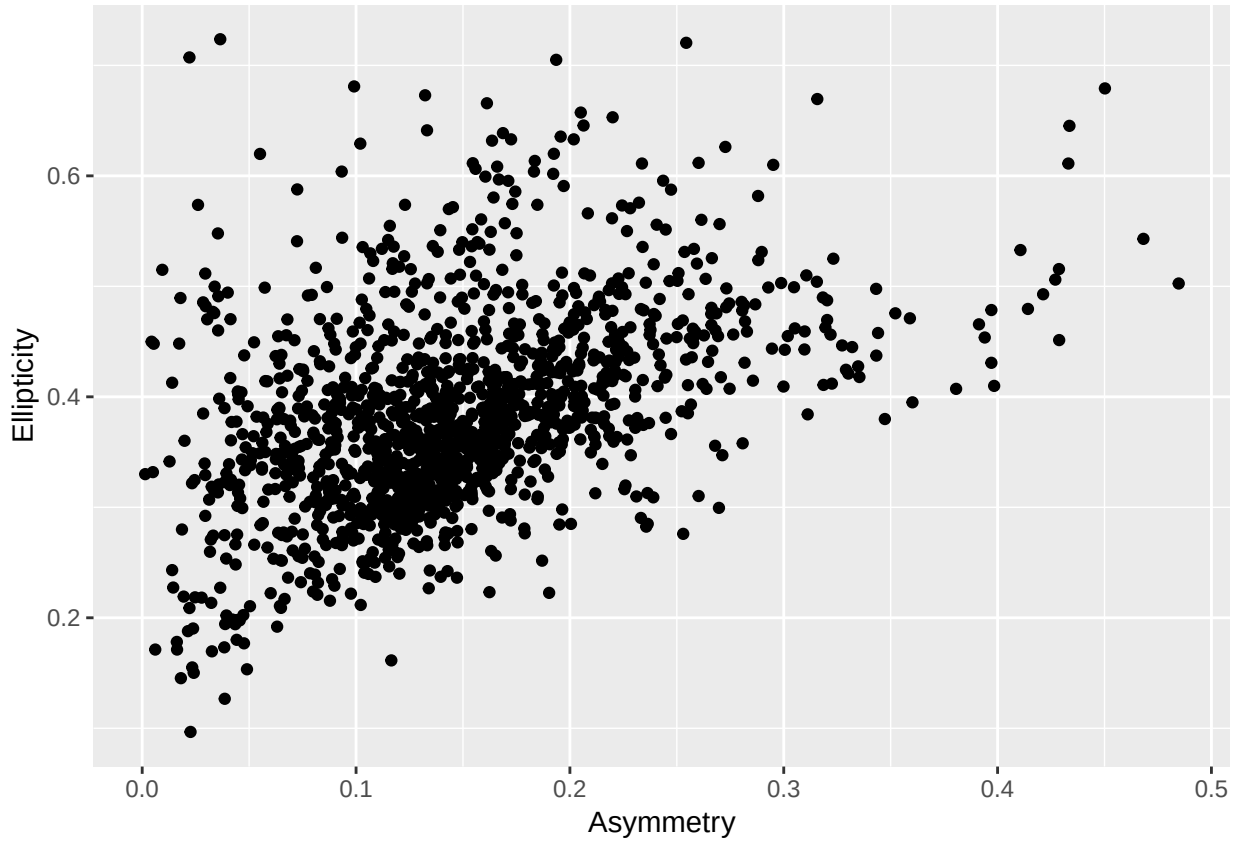
```
##                         Species Asymmetry Ellipticity AvgLength
## 1397      Rhynchotus rufescens    0.0484   0.3542979    5.5407
## 1398       Euptilotis neoxenus    0.1472   0.2362926    3.0608
## 1399 Harpactes erythrocephalus    0.0490   0.1533892    2.7930
## 1400            Trogon elegans    0.2357   0.2824952    2.8055
## 1401                      <NA>        NA          NA        NA
## 1402                      <NA>        NA          NA        NA
##      NumberOfImages NumberOfEggs
## 1397              1            1
## 1398              1            1
## 1399              1            3
## 1400              1            4
## 1401             NA           NA
## 1402             NA           NA
```

Sometimes Excel spreadsheets can have empty rows at the bottom that get interpreted as data.

```
egg = egg[-c(1401,1402),]
tail(egg)
```

```
##              Order     Family               MVZDatabase
## 1395  TINAMIFORMES  Tinamidae          Eudromia elegans
## 1396  TINAMIFORMES  Tinamidae    Nothoprocta perdicaria
## 1397  TINAMIFORMES  Tinamidae      Rhynchotus rufescens
## 1398 TROGONIFORMES Trogonidae       Euptilotis neoxenus
## 1399 TROGONIFORMES Trogonidae Harpactes erythrocephalus
## 1400 TROGONIFORMES Trogonidae            Trogon elegans
##                         Species Asymmetry Ellipticity AvgLength
## 1395          Eudromia elegans    0.0418   0.3772397    5.2926
## 1396    Nothoprocta perdicaria    0.0535   0.3820363    4.3292
## 1397      Rhynchotus rufescens    0.0484   0.3542979    5.5407
## 1398       Euptilotis neoxenus    0.1472   0.2362926    3.0608
## 1399 Harpactes erythrocephalus    0.0490   0.1533892    2.7930
## 1400            Trogon elegans    0.2357   0.2824952    2.8055
##      NumberOfImages NumberOfEggs
## 1395              3           11
## 1396              1            3
## 1397              1            1
## 1398              1            1
## 1399              1            3
## 1400              1            4
```

```
ggplot(data=egg, mapping=aes(x=Asymmetry, y=Ellipticity)) +
  geom_point()
```

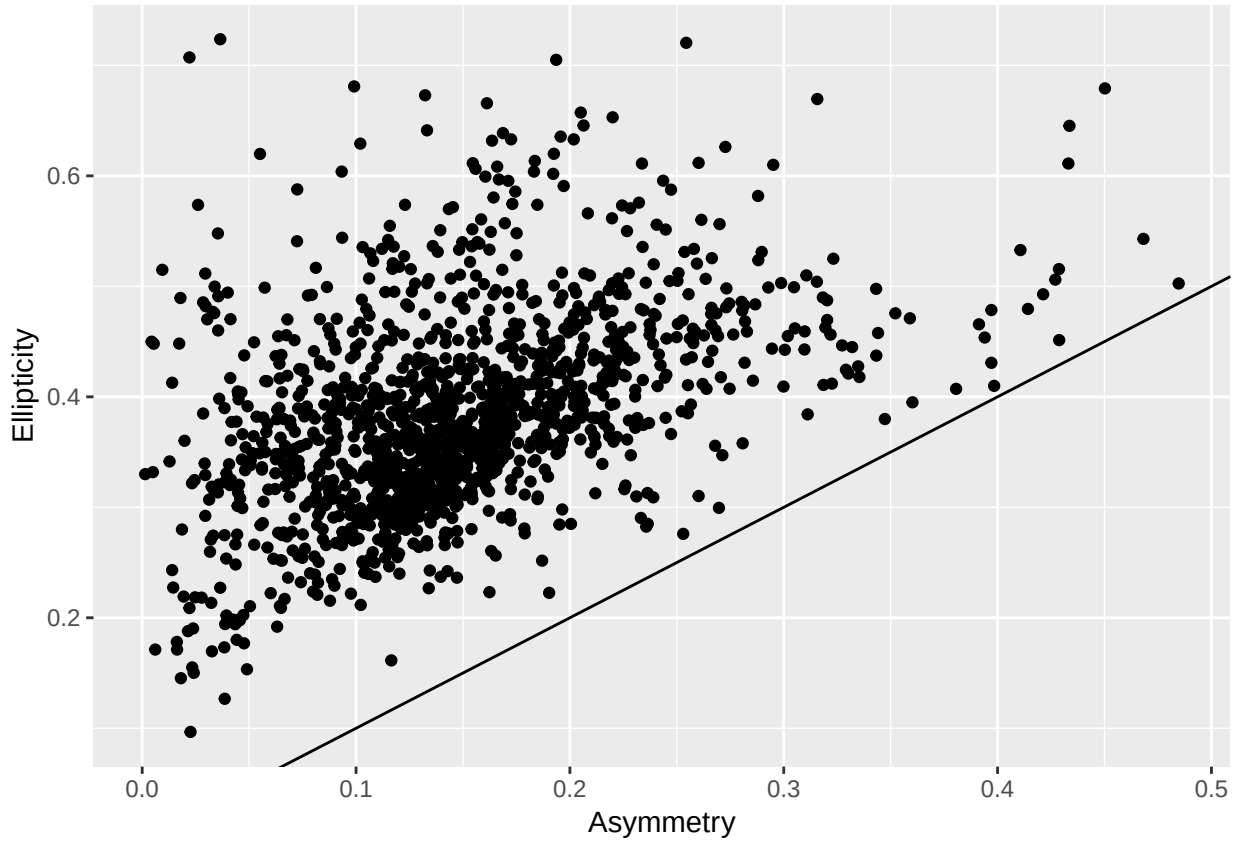


The `ggplot2` reference page on the tidyverse website has a list of `geom`s and other layers you can apply: https://ggplot2.tidyverse.org/reference/

One of the first ones is `geom_abline()`, which is one way to add a reference line to our plot.

```
?geom_abline
```

```
ggplot(data=egg, mapping=aes(x=Asymmetry, y=Ellipticity)) +
  geom_point() +
  geom_abline(slope=1, intercept=0)
```



We see that every point is above the 1:1 line; that is, an egg's ellipticity is always greater than its asymmetry.

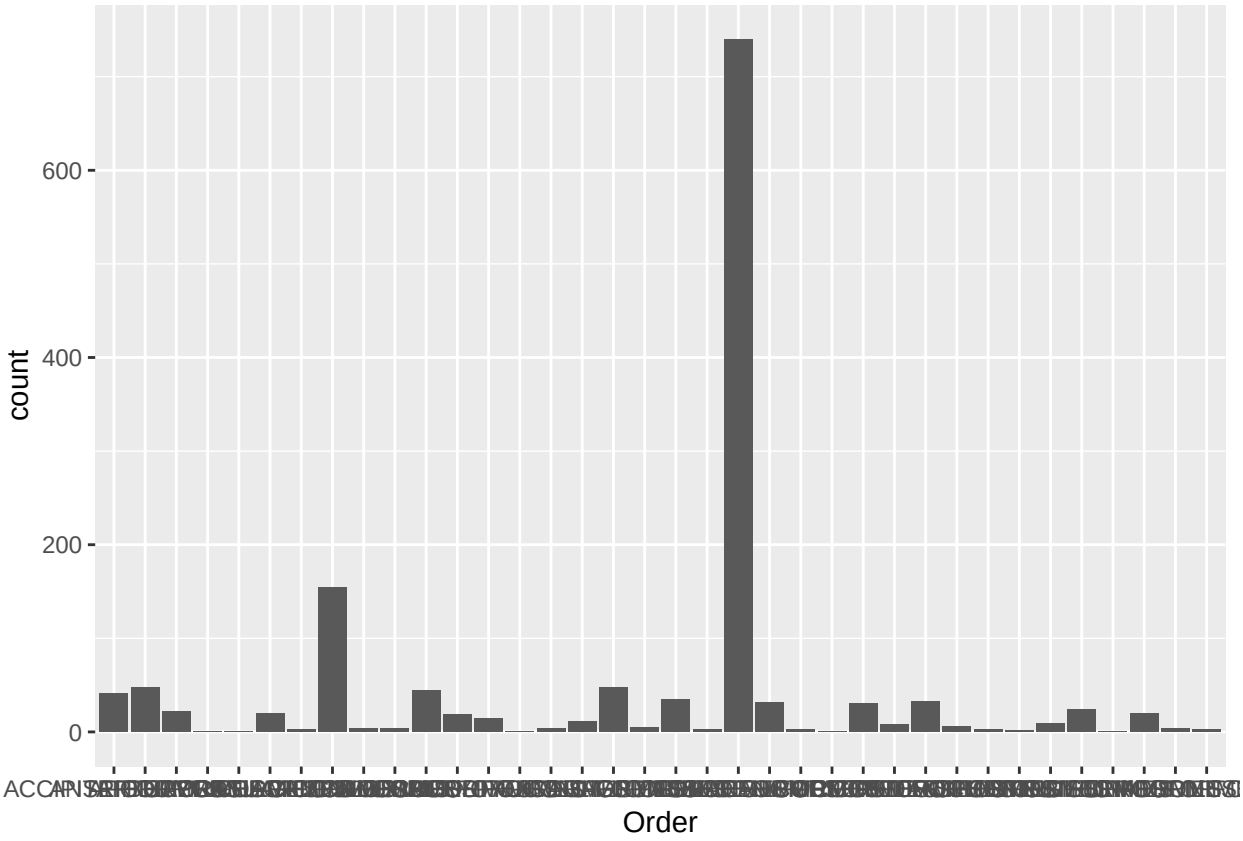
Let's try a bar chart now. We need a categorical X value.

```
ggplot(data=egg, mapping=aes(x=Order, y=Asymmetry)) +
  geom_bar()
```

```
## Error: stat_count() must not be used with a y aesthetic.
```

Well, it seems like it wants us to remove the Y variable, so let's try that.

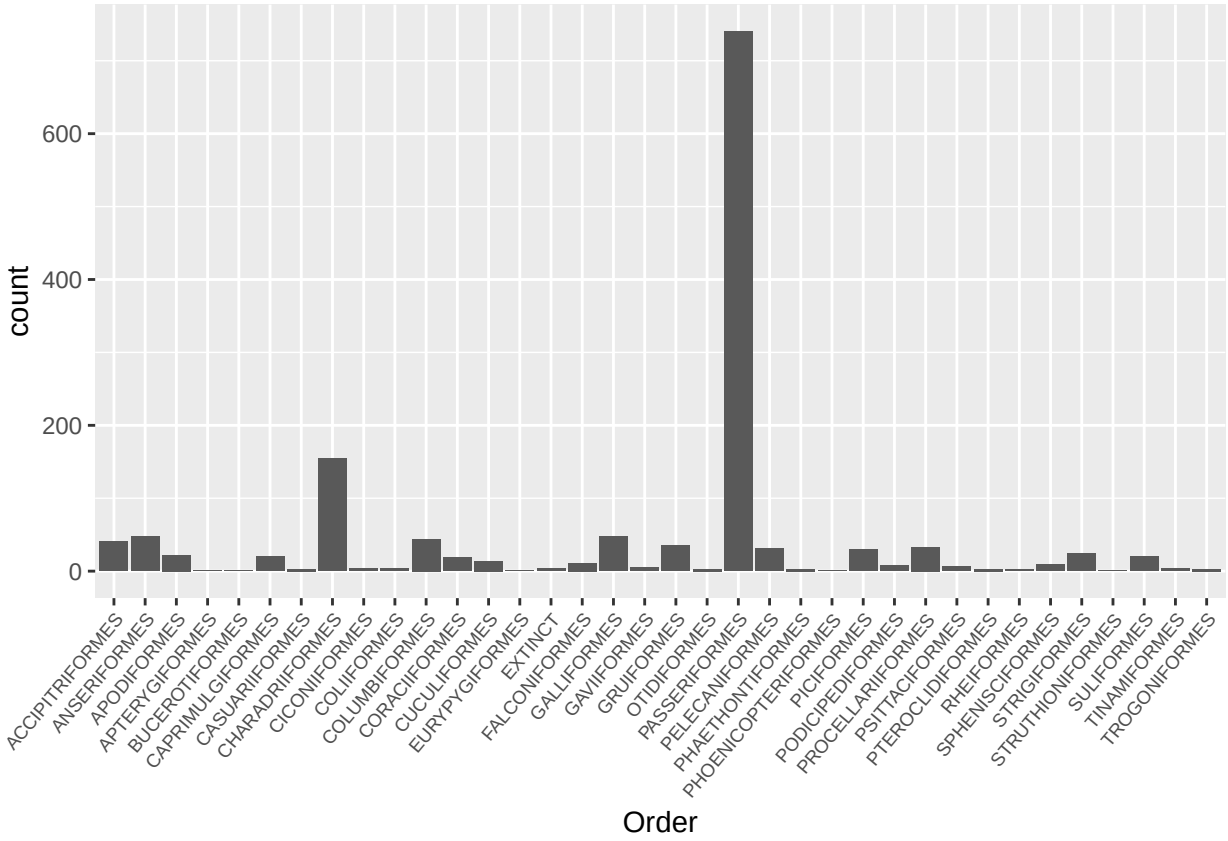
```
ggplot(data=egg, mapping=aes(x=Order)) +
  geom_bar()
```



This gives us a histogram, which is not what we wanted, but let's work with it. The first issue is that we can't read the tick labels on the X axis (in `ggplot` terms, the axis label here is "Order" and the tick labels are the labels for the levels on that axis).

Let's rotate them and make them a bit smaller so we can see them.

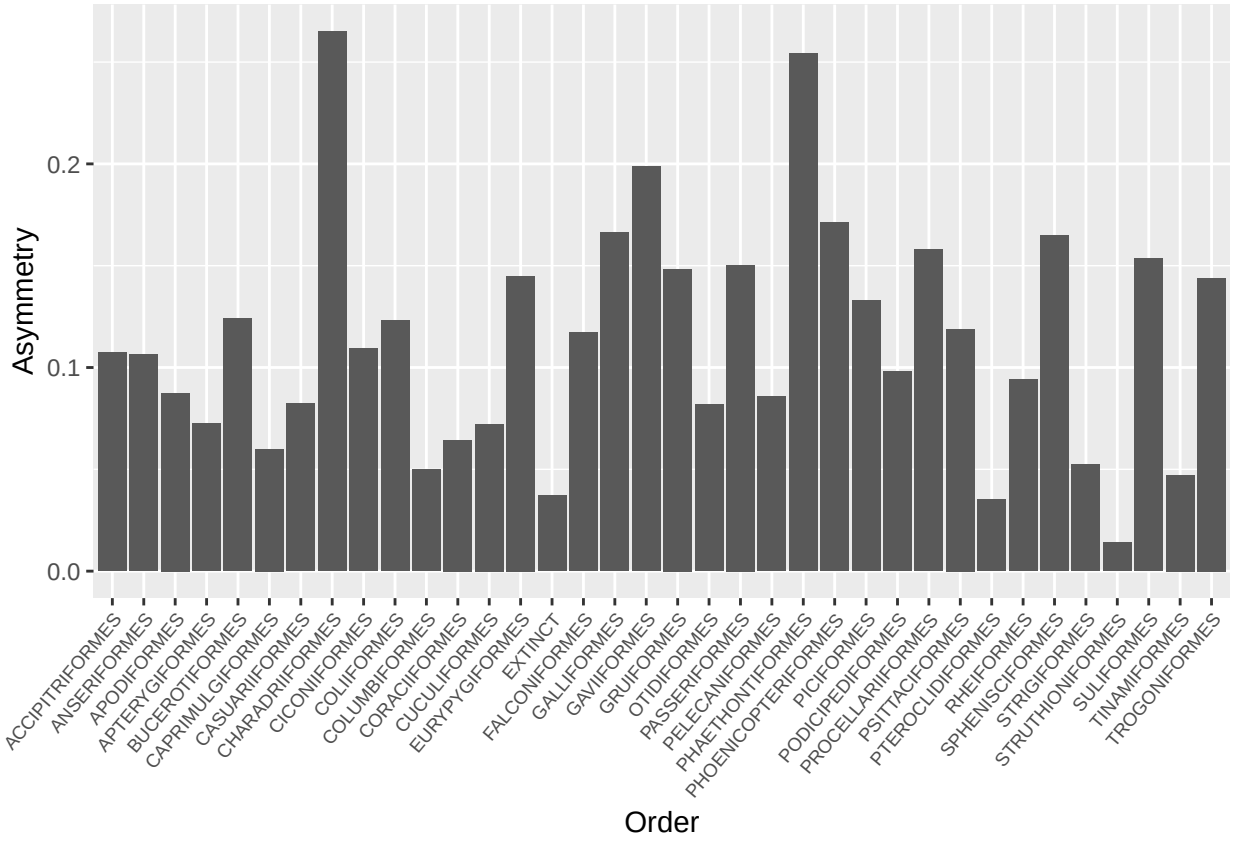
```
ggplot(data=egg, mapping=aes(x=Order)) +
  geom_bar() +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```



Looks better, for a histogram. But we wanted to see the `Asymmetry` value for each order.

Let's tell `ggplot` that we want to see the mean values. For this we need to change the `stat` argument of `geom_bar()` from `count` (its default, which produces a histogram) to `summary`, and specify that the function we want to use to calculate our Y axis values is `mean()`.

```
ggplot(data=egg, mapping=aes(x=Order, y=Asymmetry)) +
  geom_bar(stat="summary", fun.y="mean") +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```



Looks good. But for bar plots it's always good to have error bars. We'll need to use `geom_errorbar()`.

```
?geom_errorbar
```

What if we want to use confidence intervals for those bars? How do we calculate them? Well, one way is:

```
?mean_cl_normal
```

But for this, it shows we need to load the `Hmisc` package.

```
install.packages("Hmisc")
```

```
library(Hmisc)
```

```
## Loading required package: lattice
```

```
## Loading required package: survival
```

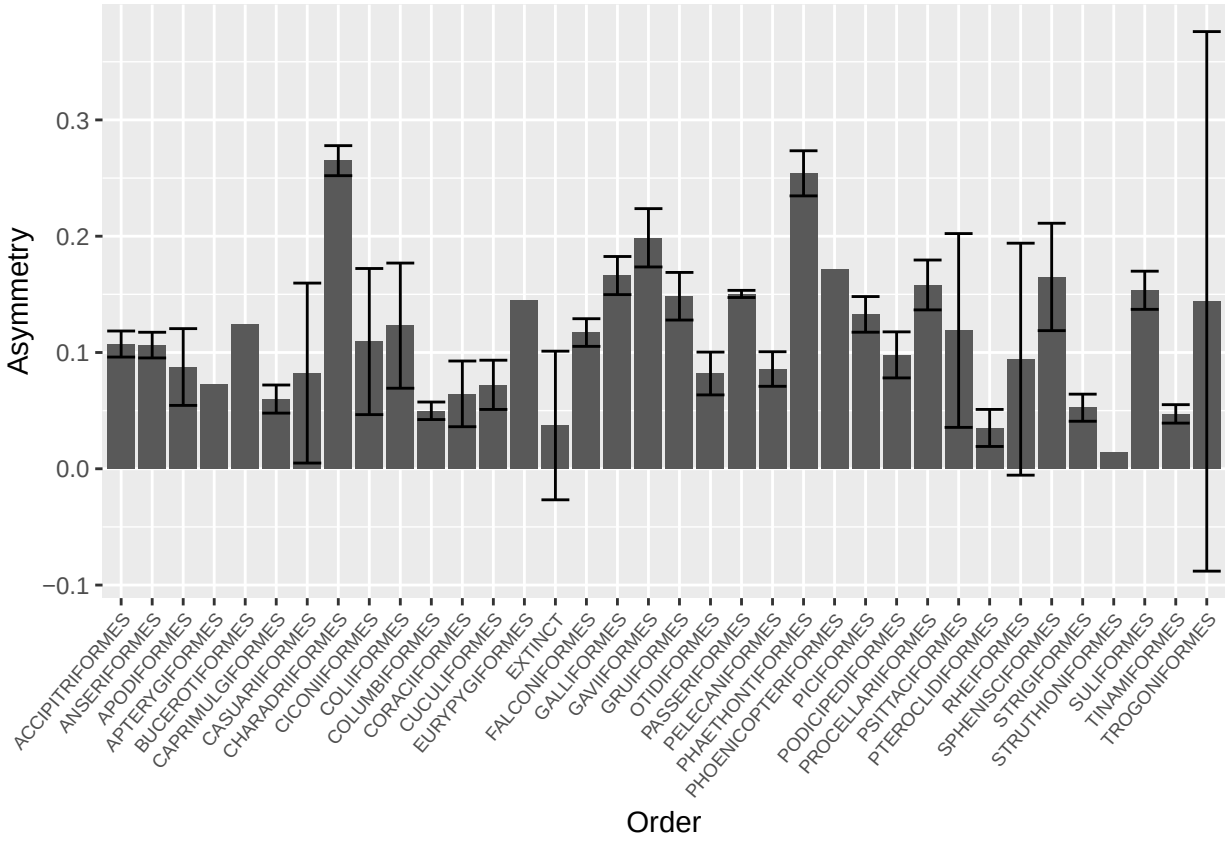
```
## Loading required package: Formula
```

```
##
## Attaching package: 'Hmisc'
```

```
## The following objects are masked from 'package:base':
##
##     format.pval, units
```

```
ggplot(data=egg, mapping=aes(x=Order, y=Asymmetry)) +
  geom_bar(stat="summary", fun.y="mean") +
  geom_errorbar(stat="summary", fun.data="mean_cl_normal") +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```



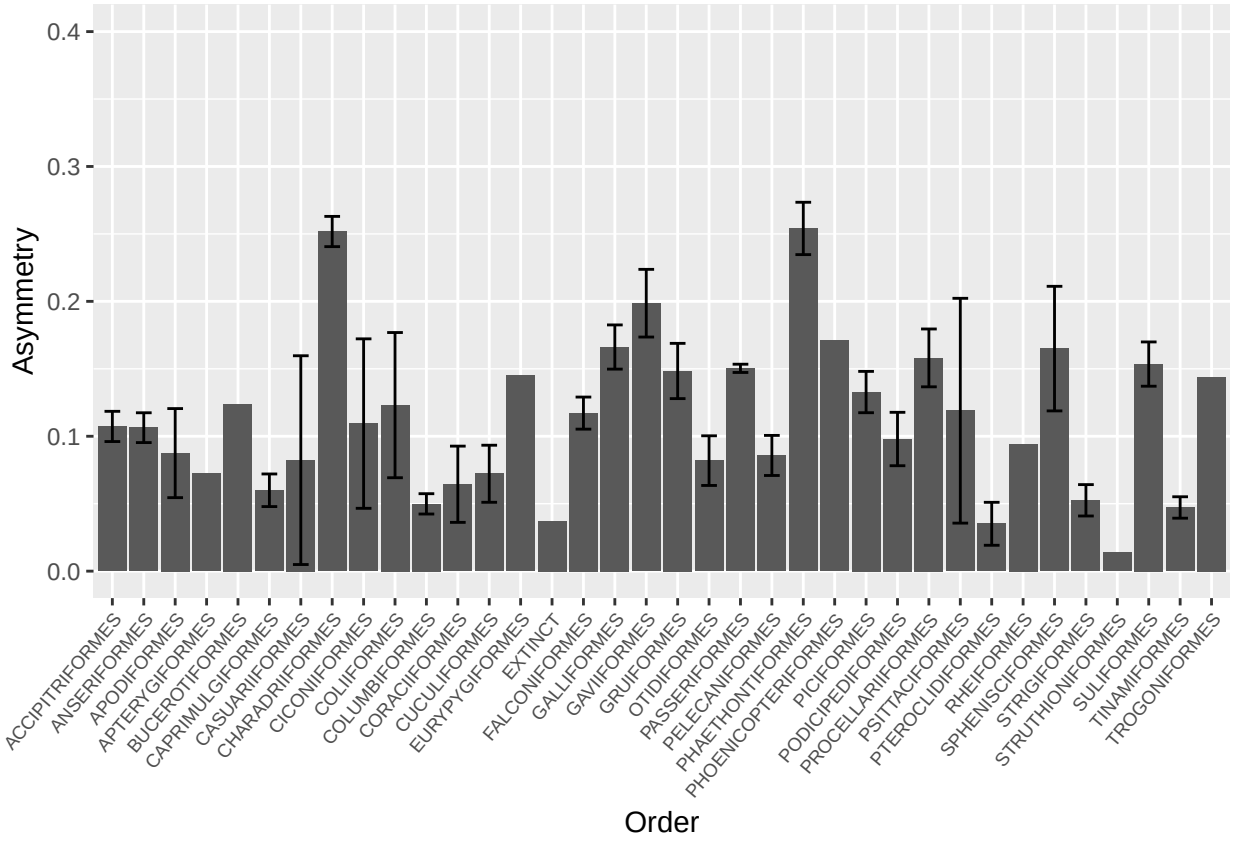
This put our axes out of whack. Let's fix them, and reduce the width of the error bars.

```
ggplot(data=egg, mapping=aes(x=Order, y=Asymmetry)) +
  geom_bar(stat="summary", fun.y="mean") +
  geom_errorbar(stat="summary", fun.data="mean_cl_normal",
                width=0.5) +
  ylim(c(0,0.4)) +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```

```
## Warning: Removed 11 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 11 rows containing non-finite values (stat_summary).
```

```
## Warning: Removed 8 rows containing missing values (geom_errorbar).
```



Hm. What happened?

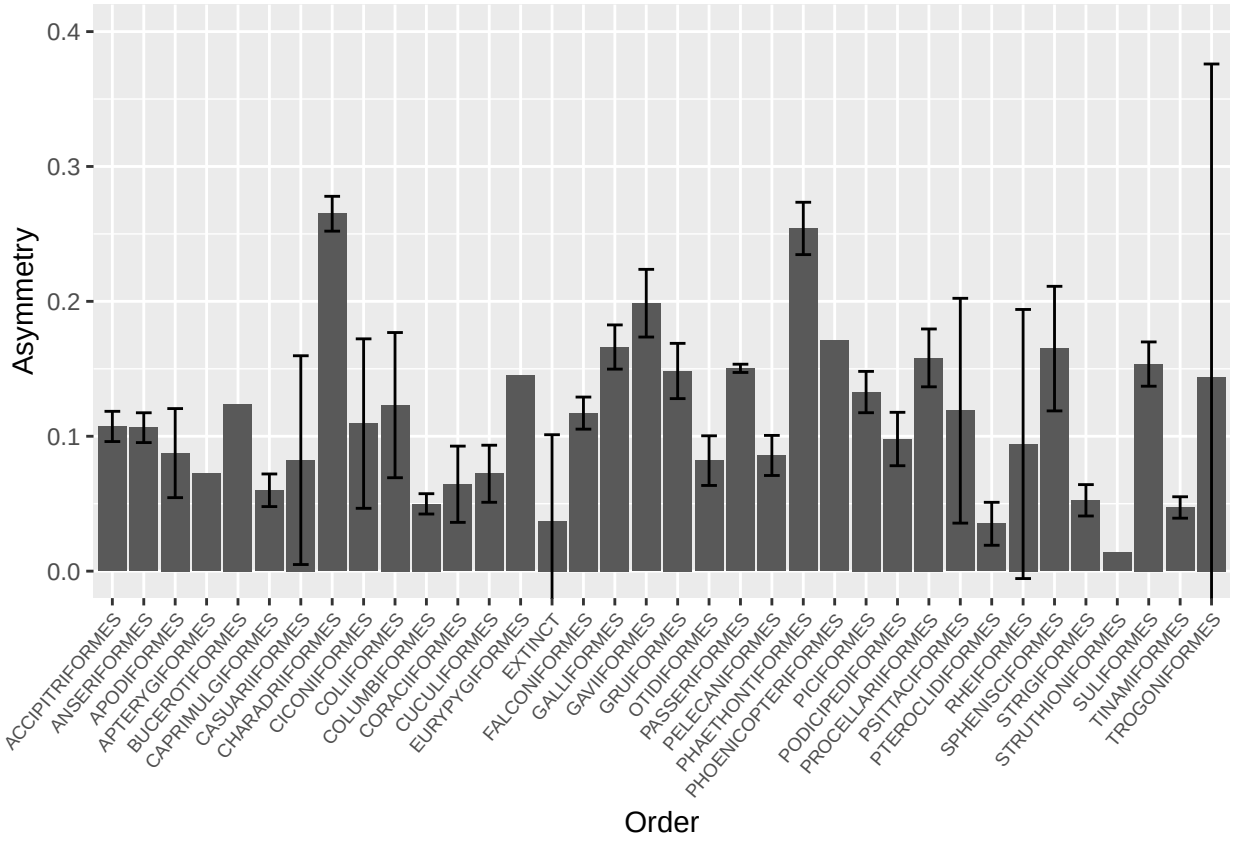
Instead of just "zooming in" on the area we wanted, it also dropped the confidence intervals that went outside that range.

```
?ylim
```

```
?coord_cartesian
```

```
ggplot(data=egg, mapping=aes(x=Order, y=Asymmetry)) +
  geom_bar(stat="summary", fun.y="mean") +
  geom_errorbar(stat="summary", fun.data="mean_cl_normal",
                width=0.5) +
  coord_cartesian(ylim=c(0,0.4)) +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```

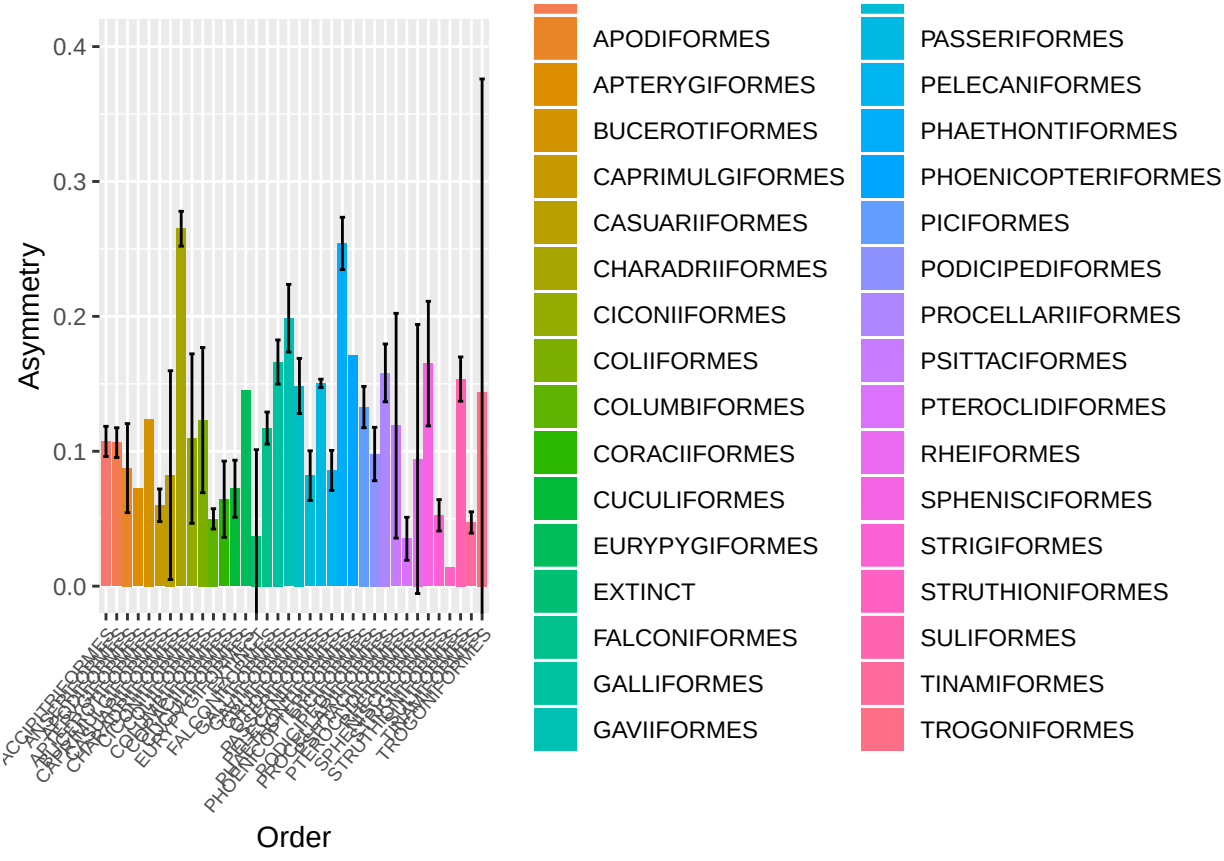


Good. We could do more to try to bring the lower intervals up to zero, but we can leave that for now (it would be easier to do using the `summarySE()` method shown later).

Gray on gray is boring. Let's add some fill colors (even though, in this case, they don't add anything meaningful to the plot).

```
ggplot(data=egg, mapping=aes(x=Order, y=Asymmetry, fill=Order)) +
  geom_bar(stat="summary", fun.y="mean") +
  geom_errorbar(stat="summary", fun.data="mean_cl_normal",
                width=0.5) +
  coord_cartesian(ylim=c(0,0.4)) +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```

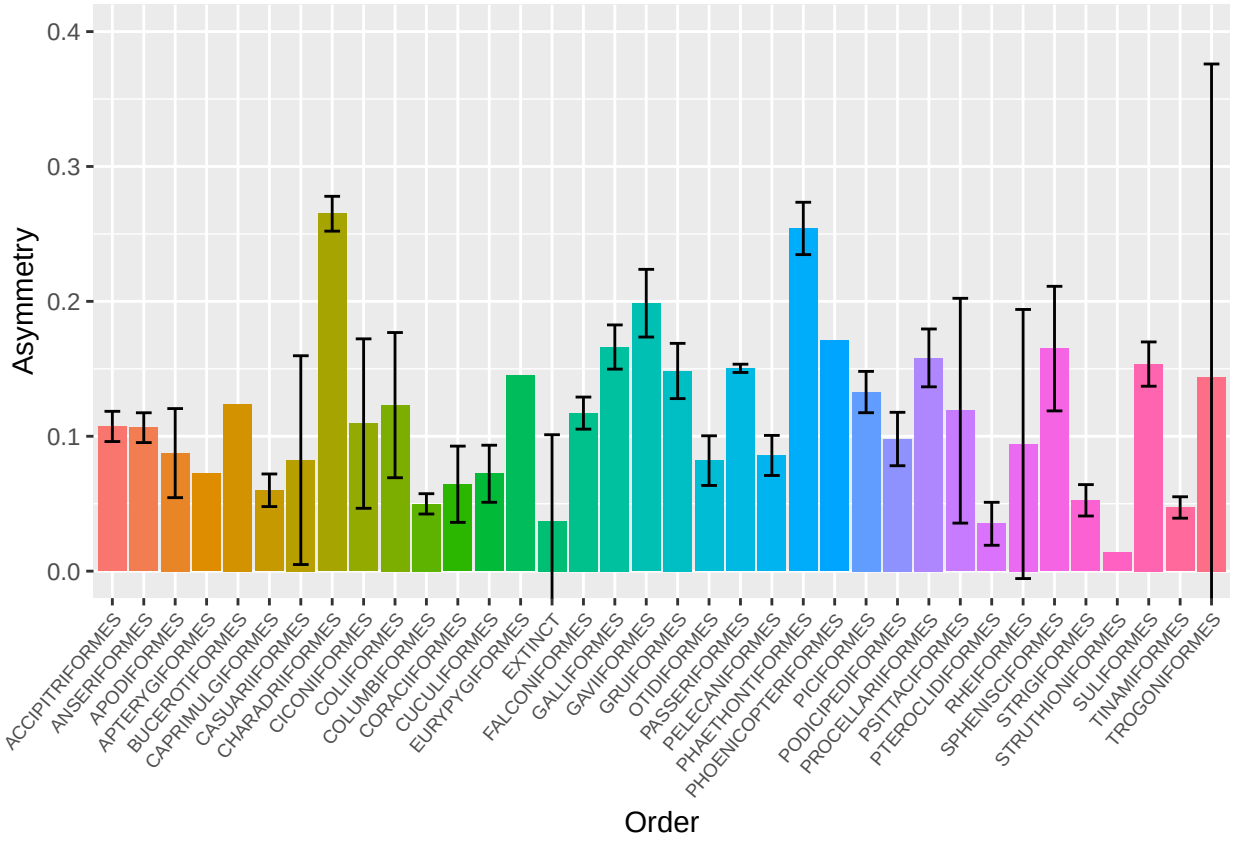
```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```



The legend takes up half the plot. Let's remove it.

```
ggplot(data=egg, mapping=aes(x=Order, y=Asymmetry, fill=Order)) +
  geom_bar(stat="summary", fun.y="mean") +
  geom_errorbar(stat="summary", fun.data="mean_cl_normal",
                width=0.5) +
  coord_cartesian(ylim=c(0,0.4)) +
  guides(fill=FALSE) +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```

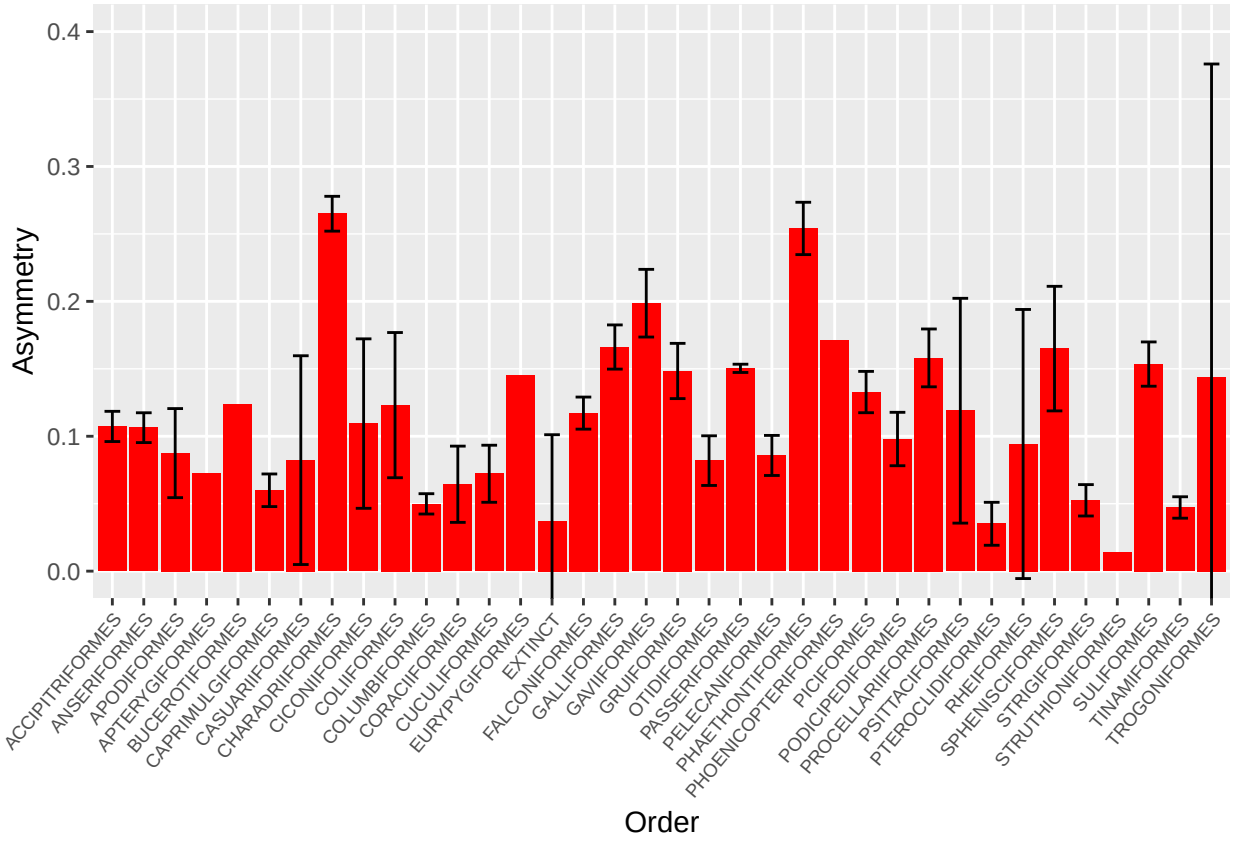


If we want to specify a single color, we can move our `fill` argument to the `geom_bar()` function and specify what color we want (either by name or hexadecimal value, e.g. "#FF0000").

You can find a list of colors defined in R here: http://www.stat.columbia.edu/~tzheng/files/Rcolor.pdf

```
ggplot(data=egg, mapping=aes(x=Order, y=Asymmetry)) +
  geom_bar(stat="summary", fun.y="mean", fill="red") +
  geom_errorbar(stat="summary", fun.data="mean_cl_normal",
                width=0.5) +
  coord_cartesian(ylim=c(0,0.4)) +
  guides(fill=FALSE) +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```

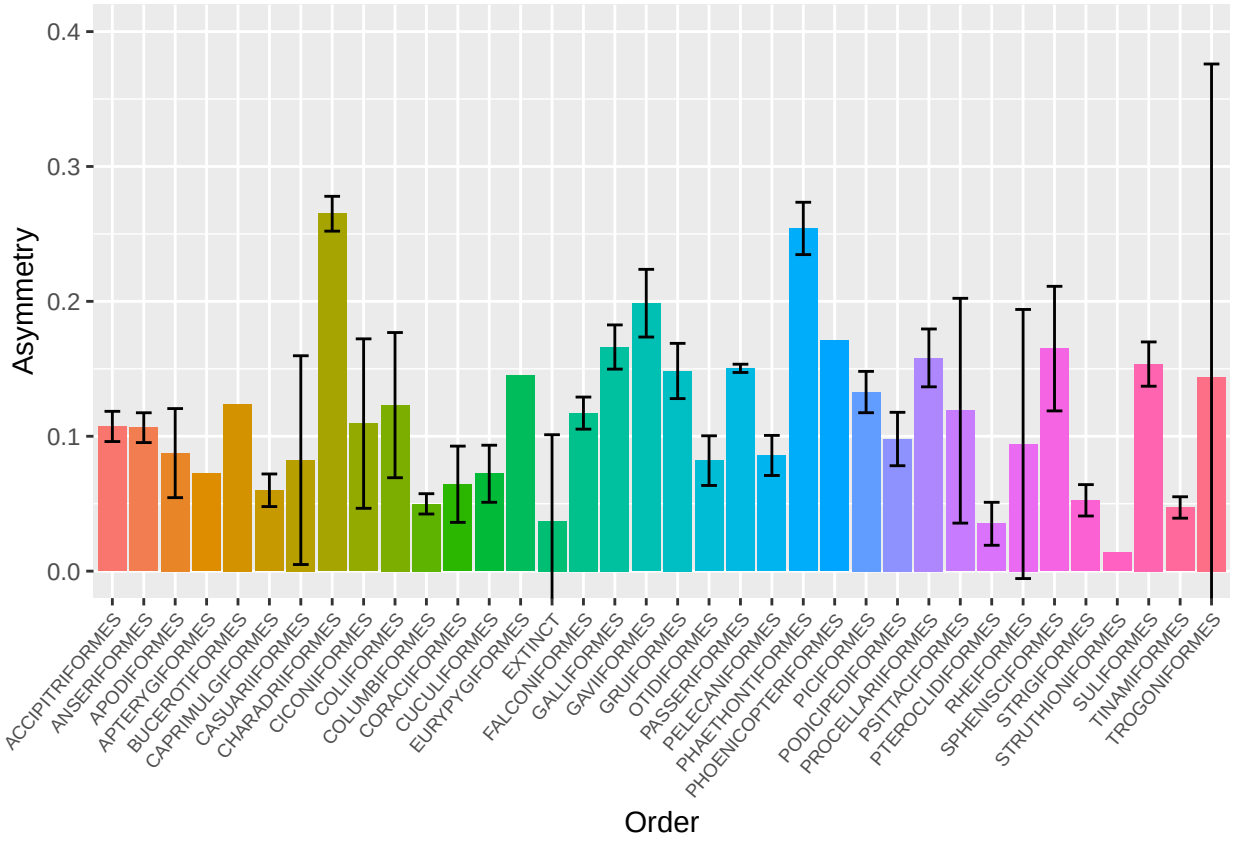


As with everything in R, there are multiple ways to do the same thing.

We can use the `stat_summary()` function instead of the `geom` functions, and specify the `geom` in the arguments:

```
ggplot(data=egg, mapping=aes(x=Order, y=Asymmetry, fill=Order)) +
  stat_summary(geom="bar", fun.y=mean) +
  stat_summary(geom="errorbar", fun.data=mean_cl_normal,
               width=0.5) +
  coord_cartesian(ylim=c(0,0.4)) +
  guides(fill=FALSE) +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```



Another, more useful way is to use the `summarySE()` function to make a new data frame with the information we need.

If I know a function that I want to use but can't remember what package it's in, I can search from it (as long as I have that package installed).

```
??summarySE  # Will only search packages that you have installed
```

It's in `Rmisc`, from the creator of the R Companion website.

```
install.packages("Rmisc")
```

```
library(Rmisc)
```

```
## Loading required package: plyr
```

```
##
## Attaching package: 'plyr'
```

```
## The following objects are masked from 'package:Hmisc':
##
##     is.discrete, summarize
```

Now we can read the help file for the function.

```
?summarySE
```

And use it to make a new data frame:

(Note: Pay attention to the arguments. Variable names need to be given as characters, and the `groupvars` argument wants a vector.)

```
eggAsymByOrder = summarySE(data=egg,
                           measurevar="Asymmetry",
                           groupvars=c("Order"))
```

```
## Warning in qt(conf.interval/2 + 0.5, datac$N - 1): NaNs produced
```

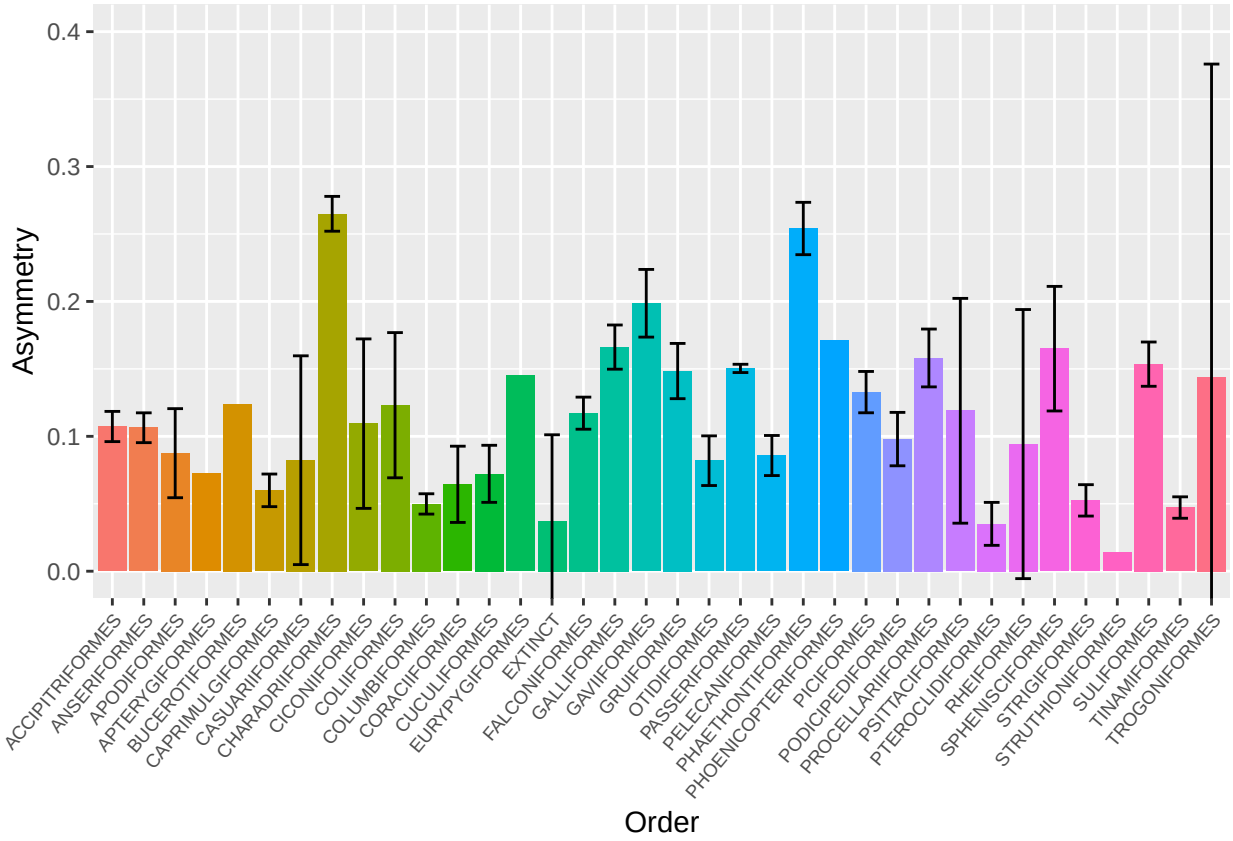
```
eggAsymByOrder
```

```
##                   Order   N  Asymmetry          sd          se          ci
## 1      ACCIPITRIFORMES  41 0.10728049 0.035478530 0.005540816 0.011198406
## 2         ANSERIFORMES  48 0.10635625 0.038055373 0.005492820 0.011050129
## 3          APODIFORMES  22 0.08750455 0.074462579 0.015875475 0.033014858
## 4       APTERYGIFORMES   1 0.07250000          NA          NA         NaN
## 5       BUCEROTIFORMES   1 0.12400000          NA          NA         NaN
## 6     CAPRIMULGIFORMES  20 0.05995500 0.025815366 0.005772491 0.012081963
## 7       CASUARIIFORMES   3 0.08230000 0.031153009 0.017986198 0.077388366
## 8      CHARADRIIFORMES 154 0.26496948 0.081065790 0.006532467 0.012905480
## 9        CICONIIFORMES   4 0.10940000 0.039479699 0.019739850 0.062821012
## 10         COLIIFORMES   4 0.12307500 0.033823697 0.016911849 0.053821050
## 11       COLUMBIFORMES  44 0.04987955 0.024793300 0.003737731 0.007537852
## 12       CORACIIFORMES  19 0.06442632 0.058624870 0.013449468 0.028256283
## 13        CUCULIFORMES  14 0.07220000 0.036647300 0.009794403 0.021159521
## 14      EURYPYGIFORMES   1 0.14500000          NA          NA         NaN
## 15             EXTINCT   4 0.03722500 0.040169174 0.020084587 0.063918119
## 16       FALCONIFORMES  11 0.11716364 0.017703122 0.005337692 0.011893120
## 17         GALLIFORMES  48 0.16615625 0.056425141 0.008144268 0.016384153
## 18         GAVIIFORMES   5 0.19864000 0.020200322 0.009033859 0.025082012
## 19          GRUIFORMES  35 0.14838571 0.059621774 0.010077919 0.020480796
## 20         OTIDIFORMES   3 0.08193333 0.007409678 0.004277980 0.018406661
## 21       PASSERIFORMES 740 0.15035392 0.042467665 0.001561142 0.003064802
## 22      PELECANIFORMES  31 0.08577097 0.040492791 0.007272720 0.014852876
## 23    PHAETHONTIFORMES   3 0.25406667 0.007811743 0.004510112 0.019405446
## 24 PHOENICOPTERIFORMES   1 0.17120000          NA          NA         NaN
## 25          PICIFORMES  30 0.13277667 0.041035751 0.007492069 0.015323001
## 26    PODICIPEDIFORMES   8 0.09795000 0.023687369 0.008374749 0.019803136
## 27   PROCELLARIIFORMES  33 0.15808788 0.060472038 0.010526831 0.021442452
## 28      PSITTACIFORMES   6 0.11893333 0.079404576 0.032416782 0.083329992
## 29    PTEROCLIDIFORMES   3 0.03510000 0.006409368 0.003700450 0.015921753
## 30          RHEIFORMES   2 0.09425000 0.011101576 0.007850000 0.099743707
## 31     SPHENISCIFORMES   9 0.16497778 0.060067790 0.020022597 0.046172191
## 32        STRIGIFORMES  24 0.05252083 0.027568413 0.005627379 0.011641120
## 33    STRUTHIONIFORMES   1 0.01400000          NA          NA         NaN
## 34          SULIFORMES  20 0.15350500 0.035058905 0.007839409 0.016408073
## 35        TINAMIFORMES   4 0.04720000 0.004989990 0.002494995 0.007940188
## 36       TROGONIFORMES   3 0.14396667 0.093391988 0.053919889 0.231998558
```

We can see some of these are missing values (`NA` or `NaN`, "not a number") because those orders only had one observation (see the `N` column) and you can't get a confidence interval from one value.

```
ggplot(data=eggAsymByOrder, mapping=aes(x=Order, y=Asymmetry, fill=Order)) +
  geom_bar(stat="identity") +
  geom_errorbar(aes(ymin=Asymmetry-ci, ymax=Asymmetry+ci),
                width=0.5) +
  coord_cartesian(ylim=c(0,0.4)) +
  guides(fill=FALSE) +
  theme(axis.text.x=element_text(angle=50, hjust=1, size=7))
```

```
## Warning: Removed 5 rows containing missing values (geom_errorbar).
```



(pdf / Rmd)