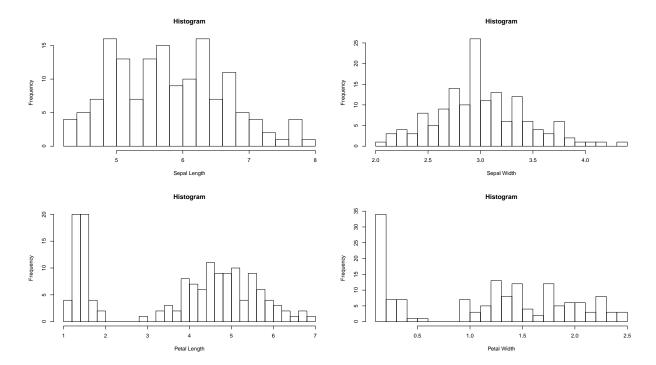
MSc Bioinformatics

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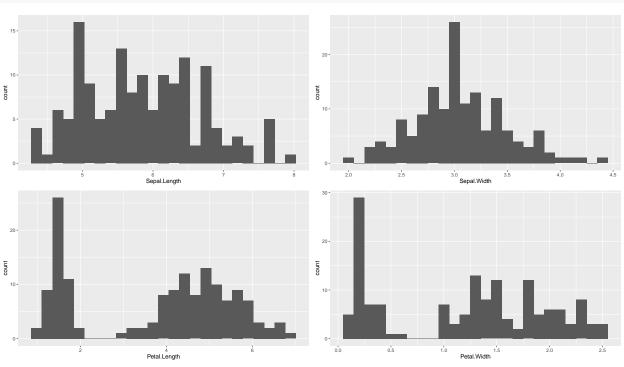
Session 7 - Practical (Solutions)

- 1. Using the iris dataset (type ?iris to get more information about this dataset) that comes pre-loaded with R, produce the following figures:
 - Produce histograms for each of Sepal.Length, Sepal.Width, Petal.Length, Petal.Width. Try using both the graphics (base R) and ggplot2 (tidyverse R) libraries.
 - Produce a bar plot for Species.
 - Produce box and whisker plots for each of the 4 continuous variables. Put them all on a single, multi-panel figure.
 - Repeat for just Sepal.Length using a violin plot, stratifying by Species.
 - Produce a single graph (not multi-panel) that has histograms for Sepal.Length for each of the 3 flower species.
 - There are 4 continuous variables. This means there are 6 possible pairs of these. For each such pair, produce a scatter plot of one variable against the other and highlight the different flower species by using a different colour for each species.
 - For one of these 6 scatter plots: estimate the bivariate probability density and add density contour lines to the figure.
- Histograms using base R:



• Histograms using ggplot2:

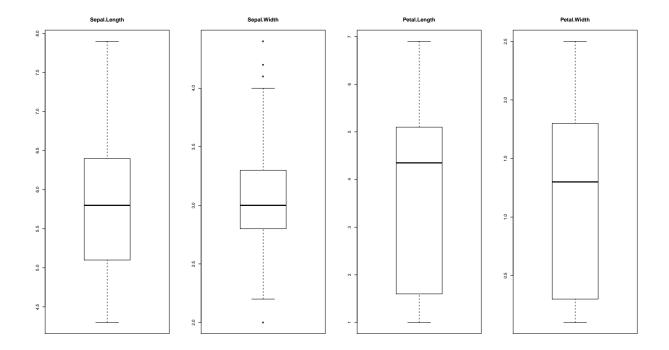
```
g<-list()
g[[1]]<-ggplot(data=iris,mapping=aes(x=Sepal.Length)) + geom_histogram(bins=25)
g[[2]]<-ggplot(data=iris,mapping=aes(x=Sepal.Width)) + geom_histogram(bins=25)
g[[3]]<-ggplot(data=iris,mapping=aes(x=Petal.Length)) + geom_histogram(bins=25)
g[[4]]<-ggplot(data=iris,mapping=aes(x=Petal.Width)) + geom_histogram(bins=25)
grid.arrange(g[[1]],g[[2]],g[[3]],g[[4]],nrow=2)</pre>
```



• Barplot

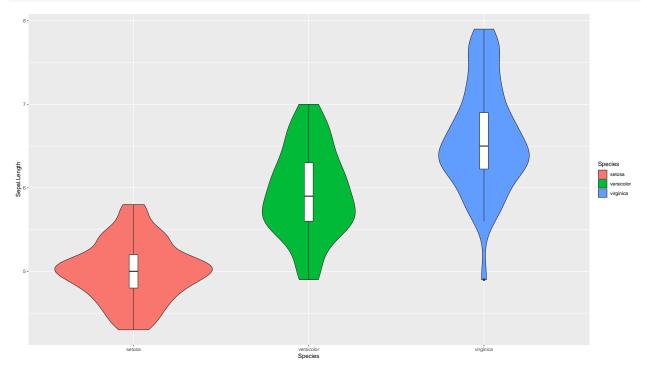
• Box plots

```
par(mfrow=c(1,4))
for(i in 1:4) {
  boxplot(iris[,i], main=names(iris)[i])
}
```



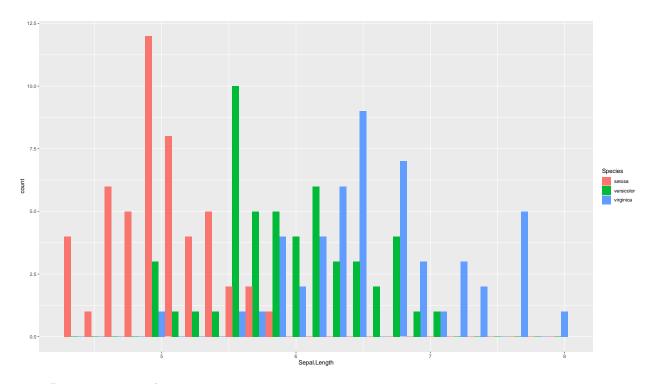
• Violin plot of Sepal.Length

```
ggplot(data=iris,mapping=aes(x=Species,y=Sepal.Length,fill=Species)) +
  geom_violin() +
  geom_boxplot(width=0.05, fill="white")
```



• Histograms for Sepal.Length

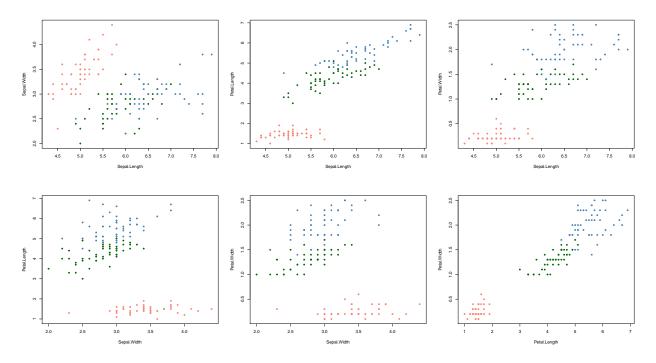
```
ggplot(data=iris,mapping=aes(x=Sepal.Length,fill=Species)) +
  geom_histogram(binwidth=0.15,position="dodge")
```



• Pair-wise scatterplots

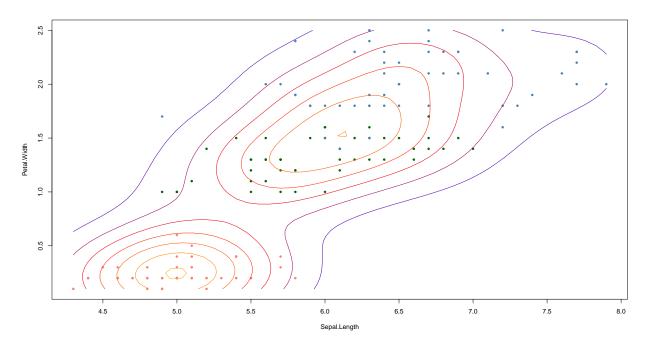
[1] 2 4 ## [1] 3 4

```
par(mfrow=c(2,3))
for(i in 1:3){
  for(j in min(c(i+1),4):4){
    print(c(i,j))
    plot(iris[,i],
         iris[,j],
         pch=20,
         col=ifelse(iris$Species=="setosa", "salmon", ifelse(iris$Species=="versicolor", "darkgreen", "stee
         xlab=colnames(iris)[i],
         ylab=colnames(iris)[j])
  }
}
## [1] 1 2
## [1] 1 3
## [1] 1 4
## [1] 2 3
```



• Bivariate density contours

```
library(MASS)
```



- 2. Install the package nycflights13, then load it. This has data on flights that took off in the US during 2013. There are 5 data tables:
 - airlines, data on airlines
 - airports, data on airports
 - planes, data on planes
 - weather, hourly weather data at NYC airports for 2013
 - flights, data on flights leaving NYC airports during 2013
- Compute the average delay by destination, then join the airports data frame to get the longitude and latitude of delays. Plot this (if you are using ggplot2, then the functions borders() and coord_quickmap() can be useful for a nicer figure).
- Construct data frames giving average delay per wind speed / temperature / precipitation / visibility. Produce scatter plots of each of these against delay and add an average trend line.

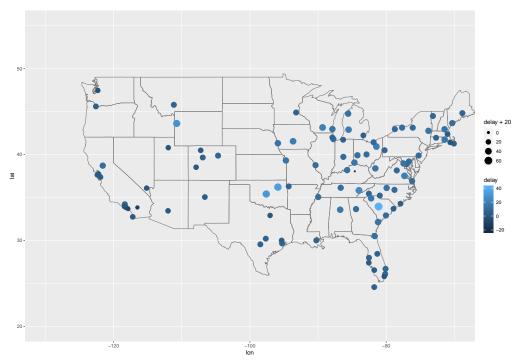
```
library(nycflights13)

# Compute the average delay by destination, then join the airports data frame
# to get the longitude and latitude of delays.
avg_dest_delays <-
    flights %>%
    group_by(dest) %>%
    summarise(delay = mean(arr_delay, na.rm = TRUE)) %>% # arrival delay NA's are cancelled flights
    inner_join(airports, by = c(dest = "faa"))

# stratify by origin airport
avg_dest_delays_by_origin <-
    flights %>%
    group_by(origin,dest) %>%
    group_by(origin,dest) %>%
    summarise(delay = mean(arr_delay, na.rm = TRUE)) %>% # arrival delay NA's are cancelled flights
    inner_join(airports, by = c(dest = "faa"))

# plotting this
```

```
ggplot(data=avg_dest_delays,mapping=aes(lon,lat,colour=delay,size=delay+20)) +
borders("state") +
geom_point() +
coord_quickmap(xlim=c(-130,-70),ylim=c(20,55)) # xlim, ylim to hide Alaska and Hawaii
```



```
flights_weather <-flights %>% left_join(weather,by=c("year","month","day","hour"))
flights_precip <- flights_weather %>%
  group_by(precip) %>%
  summarise(delay=mean(dep_delay,na.rm=T))
flights_wind <- flights_weather %>%
  group_by(wind_speed) %>%
  summarise(delay=mean(dep_delay,na.rm=T))
flights_temp <- flights_weather %>%
  group_by(temp) %>%
  summarise(delay=mean(dep_delay,na.rm=T))
flights_visib <- flights_weather %>%
  group_by(visib) %>%
  summarise(delay=mean(dep_delay,na.rm=T))
g1<-ggplot(data=flights_precip,mapping=aes(x=precip,y=delay)) +</pre>
  geom_point() +
  geom_smooth()
g2<-ggplot(data=flights_wind,mapping=aes(x=wind_speed,y=delay)) +</pre>
  geom_point() +
  geom_smooth()
```

```
g3<-ggplot(data=flights_temp,mapping=aes(x=temp,y=delay)) +
  geom_point() +
  geom_smooth()

g4<-ggplot(data=flights_visib,mapping=aes(x=visib,y=delay)) +
  geom_point() +
  geom_smooth()

grid.arrange(g1,g2,g3,g4)</pre>
```

