Making figures in R

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Plotting the data

One of the most powerful parts of R besides the stats and packages is the ability to meaningfully plot data and show others what we see. There are many packages that can be used in R to plot data and the goal of this tutorial is to go over a few to get started making publication quality figures.

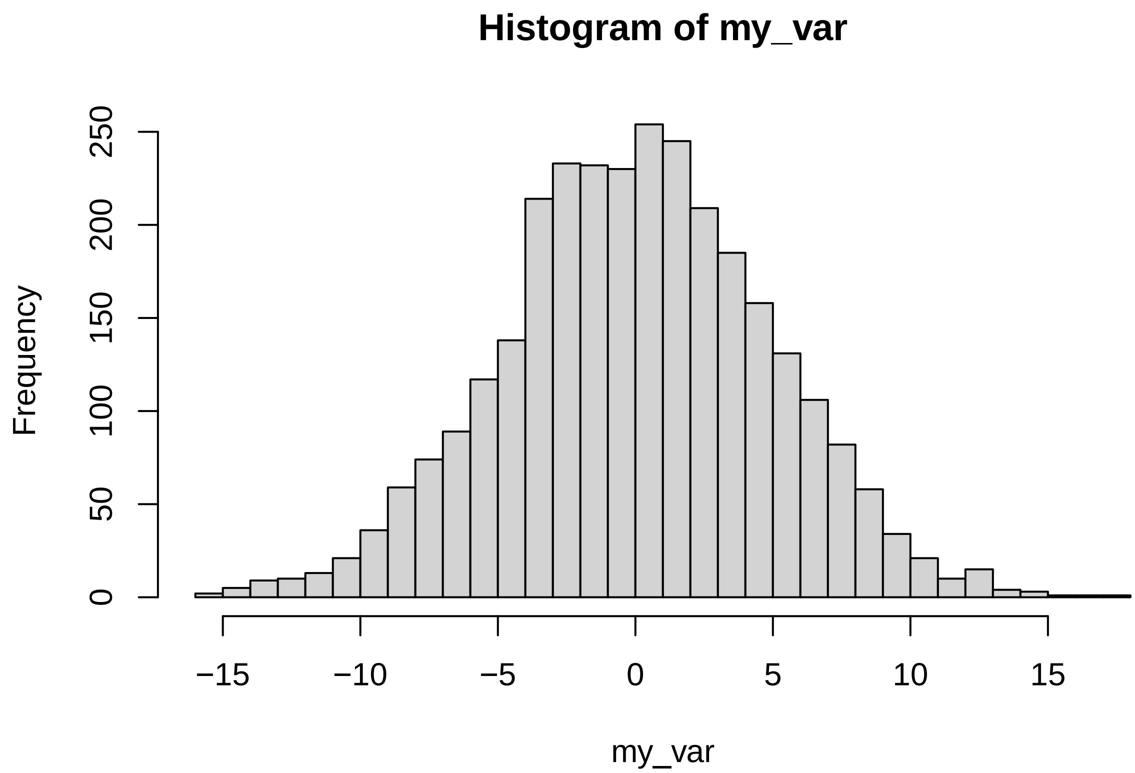
Plotting with base R no packages

In R there are base functions, those that come with R without the need to upload any packages. Since R is a statistical package it of course comes with its own plotting functions to reveal data patterns of interest. Here we will plot some synthetic data using base R only no packages.

Histograms and density plots

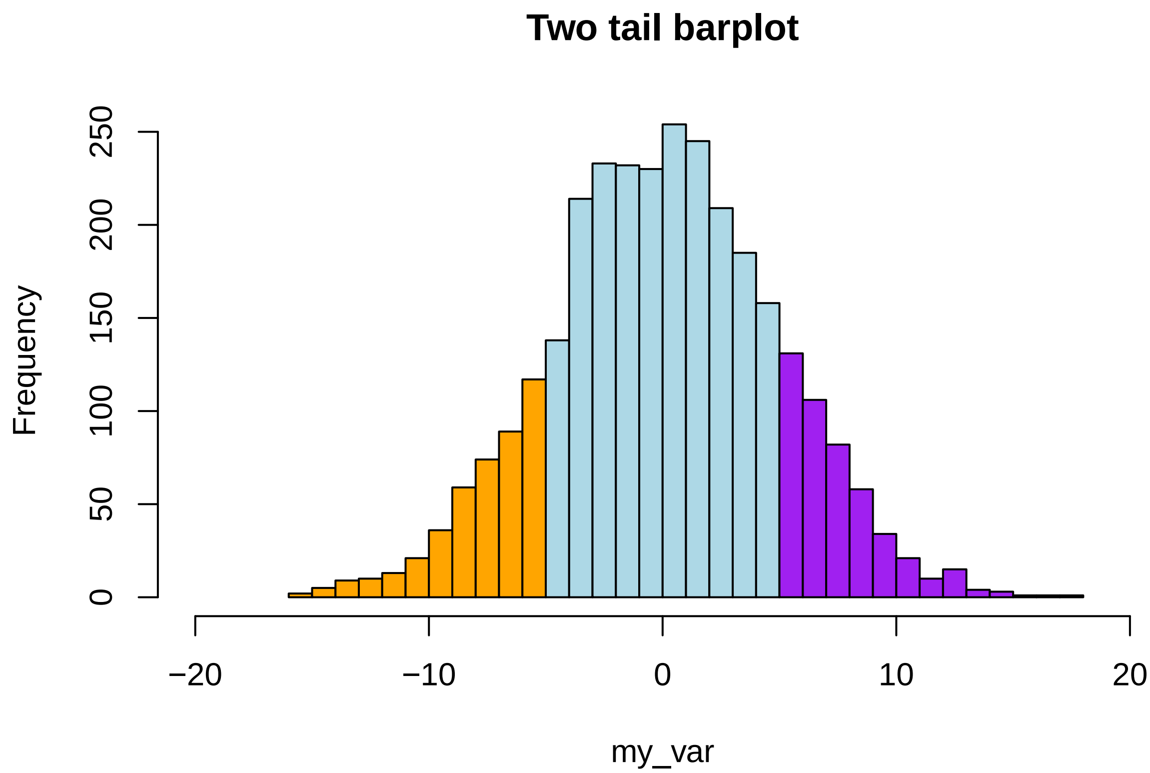
First we will make some synthetic data to play with using `rnorm()`. We will use `set.seed()` to set the random generator starting point, this will make the randomness reproducible and should only be used to teach debug code involving random numbers. This will generate a random normal distribution with the mean and standard deviation chosen. Then we plot the histogram with `hist()`.

```
set.seed(543)
my_var <- rnorm(n = 3000,mean = 0,sd = 5)
histo <- hist(my_var,breaks = 40)
```



Now we will spice it up a bit and add colors to the tails. This would be a great way to highlight these data in a distribution of p-values for example. To accomplish this we need to create the histogram but not print it and then we can access the object created and use a conditional statement to create our colored ends to then plot using the `plot()` function.

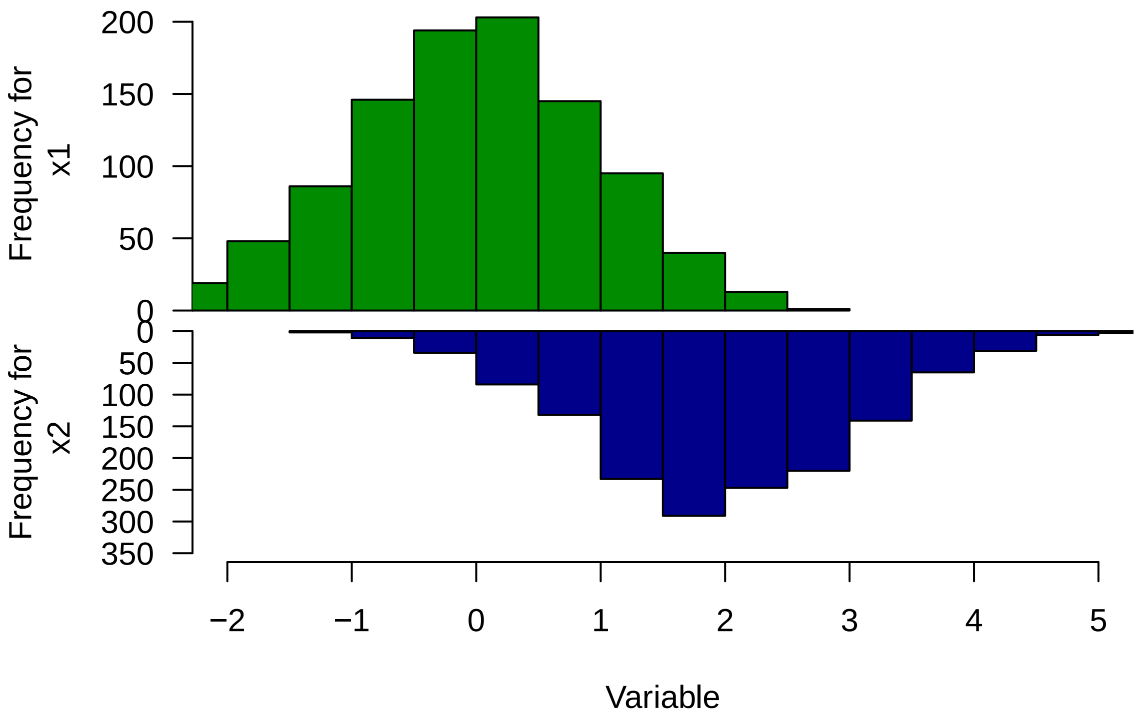
```
histo2 <- hist(my_var,breaks = 40, plot = F)
tail_colors <- ifelse(histo2$breaks < -5, "orange" ,
                       ifelse (histo2$breaks >=5, "purple","lightblue"))
plot(histo2, col=tail_colors , main="Two tail barplot" , xlim=c(-20,20))
```



Mirrored histogram

Now we will make a mirrored histogram, great for visually comparing the distributions of two datasets. We are using a new function here `par()`. This is a graphics function that controls graphical parameters like margins, background, size of text labels and much more. The `mfrow` parameter controls the layout of the graphs plotted by (number of rows, number of columns), this giving us two rows and one column. Next we use the `mar` parameter to set the margins on each plot so they do not overlap.

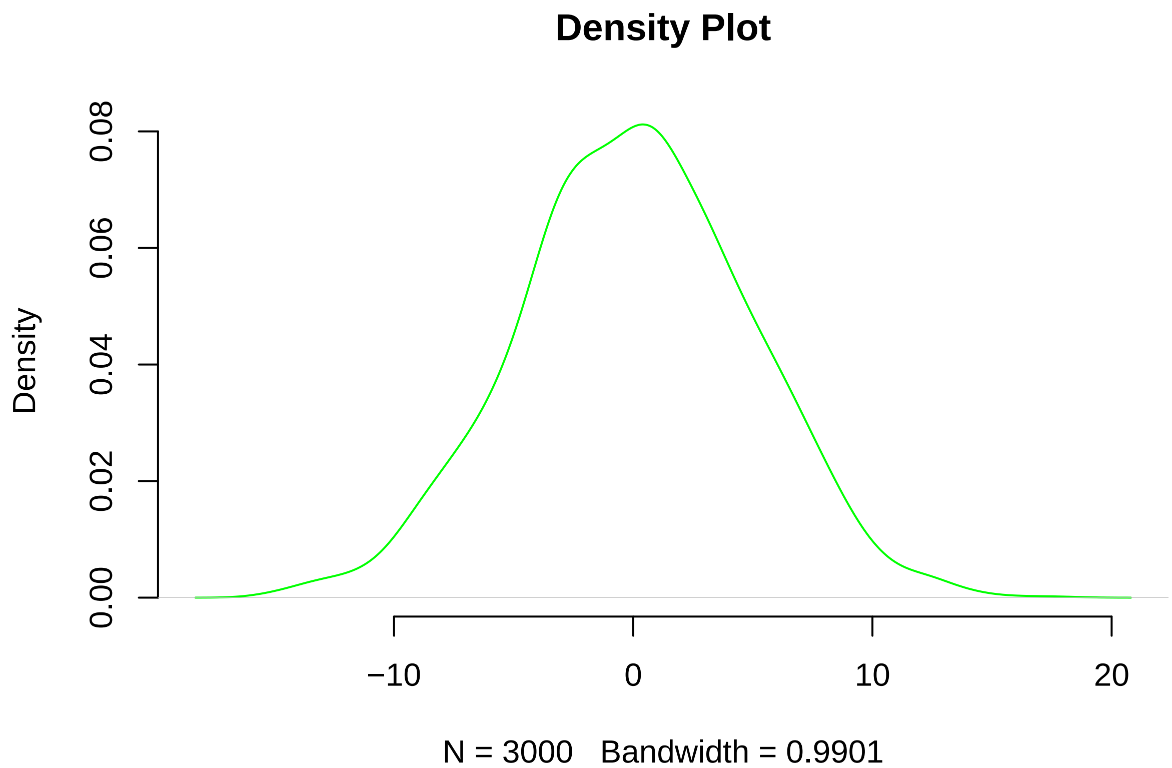
```
set.seed(567)
x1 = rnorm(n=1000,mean = 0)
x2 = rnorm(n=1500,mean = 2)
par(mfrow=c(2,1))

#Make the plot
par(mar=c(0,5,3,3))
hist(x1, main="", xlim=c(-2,5), ylab="Frequency for\n x1", xlab="",
     xaxt="n", las=1, col="green4", breaks=15)
par(mar=c(5,5,0,3))
hist(x2, main="", xlim=c(-2,5), ylab="Frequency for\n x2",
     xlab="Variable", ylim=c(350,0), las=1, col="blue4", breaks=10)
```



Density plots

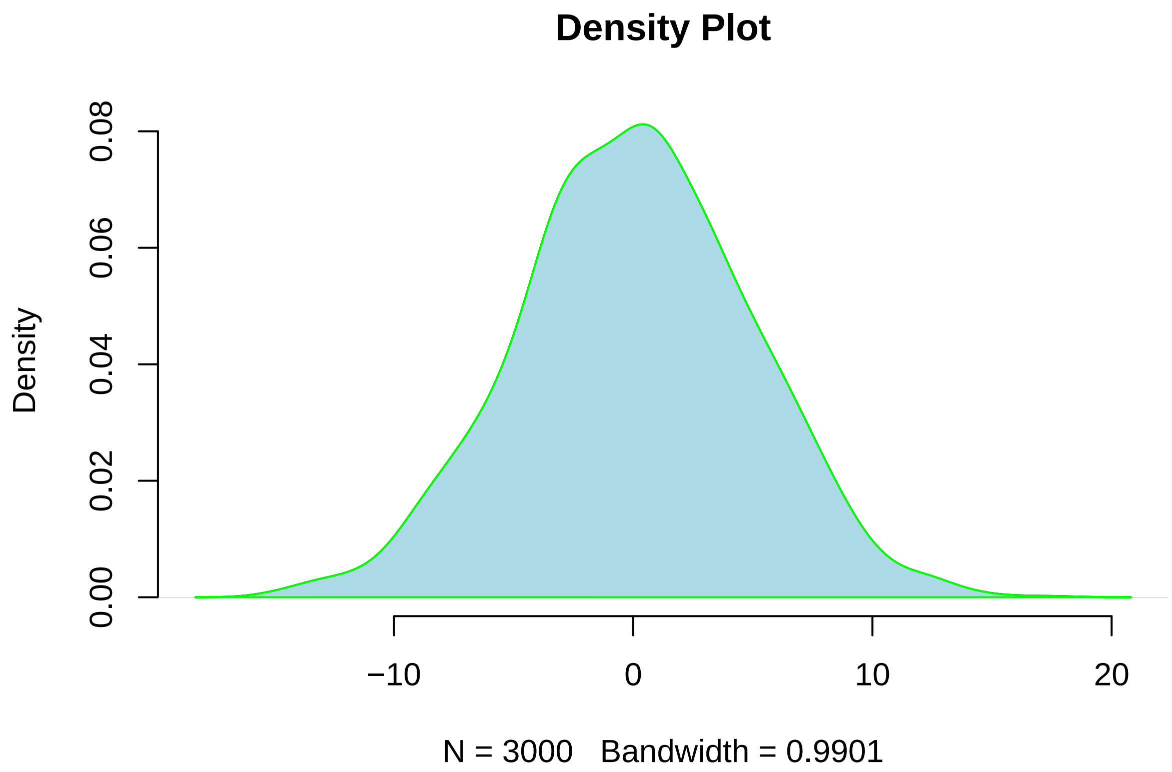
Here we can use the `density()` function to estimate the kernel density of a dataset. We can reuse the `my_var` variable we made previously.

```
dens <- density(my_var,bw = "sj")
plot(dens, main = "Density Plot",col="green",frame=F)
```



Then we can add color beneath the line graph generated for the density.

```
plot(dens, main = "Density Plot",frame=F)
polygon(dens,col="lightblue",border = "green")
```



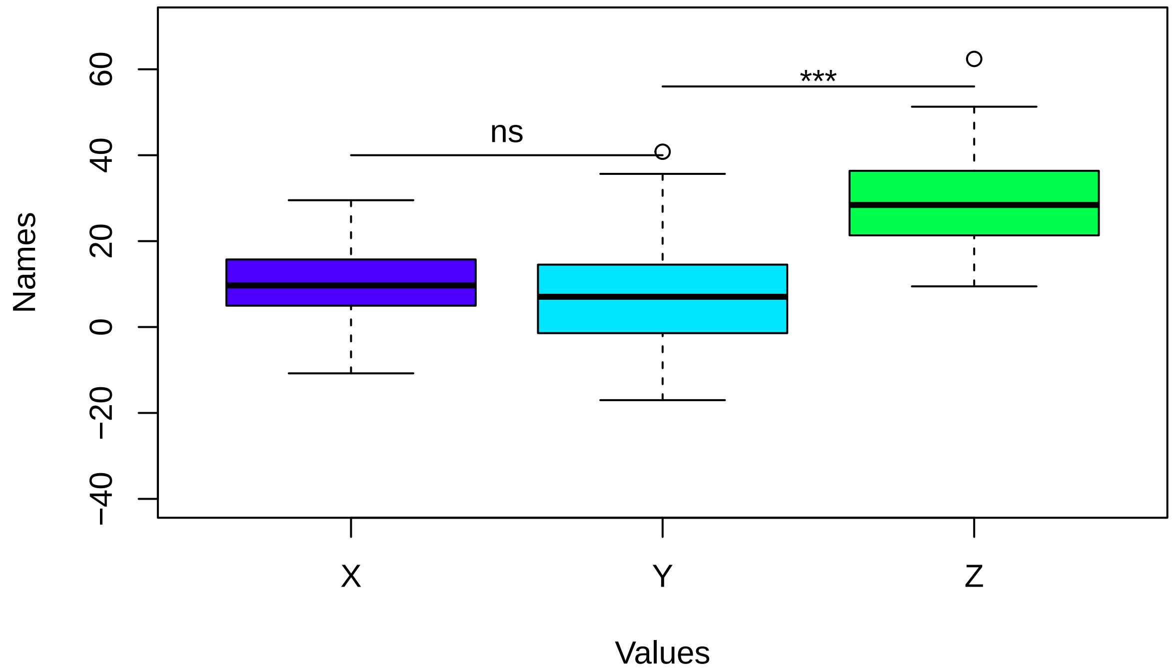
Boxplots and Barplots

Boxplots

Box and whisker plots can be made with the base R `boxplot()` function. Here we make a example dataset. We can use box plots to understand the mean differences between groups. Then we can calculate the p-values between each group using an ANOVA method, `aov()`.

```
set.seed(123)
names <- c(rep("X", 80), rep("Y", 50), rep("Z", 70))
value <- c( rnorm(80, mean=10, sd=9) , rnorm(50, mean=8, sd=15),
            rnorm(70, mean=30, sd=10))
data <- data.frame(names,value)

# Perform ANOVA and extract the p-value
anova_result <- aov(value ~ names, data = data)
p_value_anova <- summary(anova_result)[[1]]$`Pr(>F)`[1]
pvals <- TukeyHSD(anova_result)
pvals <- data.frame(pvals[[1]])

# Basic boxplot
boxplot(data$value ~ data$names , col=topo.colors(4),
        xlab = "Values",ylab = "Names",ylim=c(-40,70))
text(x=1.5,y = 45,labels="ns")
segments(1,40,2,40)
```

```
text(x=2.5,y = 59,labels="***")
segments(2,56,3,56)
```

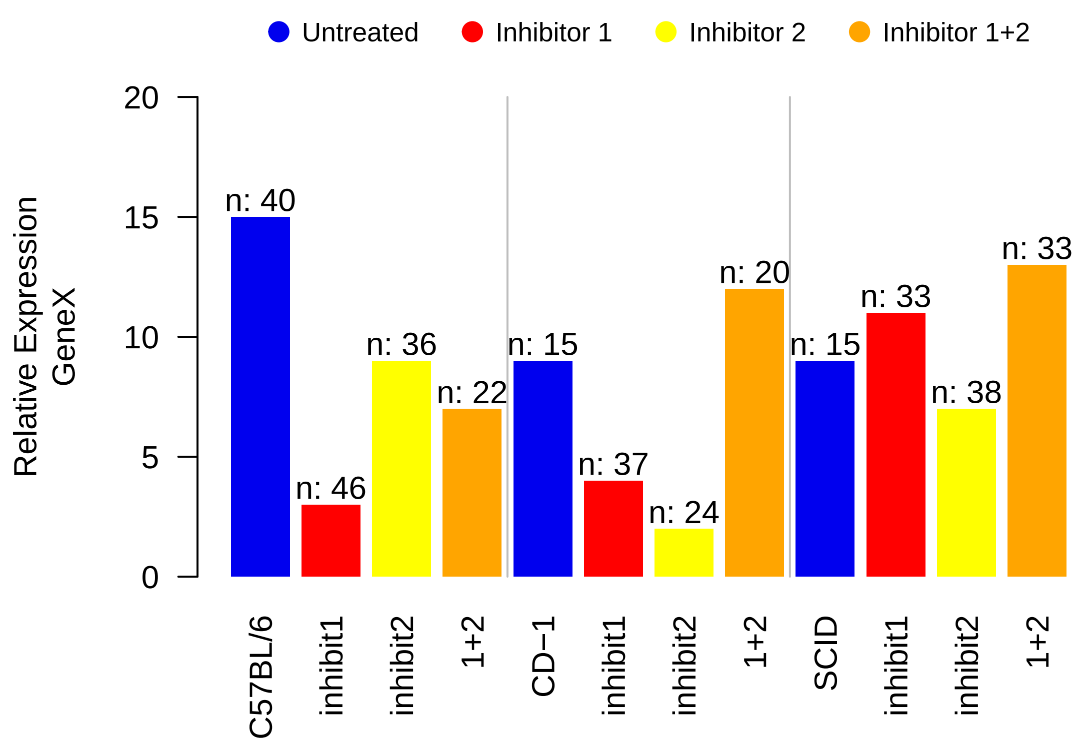


Barplots

Here we make some random data and plot using the `barplot()` function. The example is supposed to represent an experiment measuring geneX expression for three different mouse strains when treated with two different inhibitors.

```
# Data
treatment_data <- data.frame(
  name = c("C57BL/6","inhibit1","inhibit2","1+2" ,"CD-1",
           "inhibit1","inhibit2","1+2" ,"SCID","inhibit1","inhibit2","1+2"),
  average = sample(seq(1,19) , 12 , replace=T),
  number = sample(seq(4,59) , 12 , replace=T))

# Make room in the bottom margin
par(mar=c(6,5,4,4),xpd=TRUE)


# Basic Barplot
my_bar <- barplot(treatment_data$average, border=F, names.arg=treatment_data$name,
                  las=2,
                  col=c("blue2","red","yellow","orange"),
```

```
                   ylim=c(0,20),
                   main="",
                   ylab="Relative Expression\nGeneX")


segments(4.9,0,4.9,20,col="grey")
segments(9.7,0,9.7,20, col = "grey")
text(my_bar, treatment_data$average+0.7, paste("n: ",treatment_data$number, sep=""),cex=1)

legend("top", legend = c("Untreated","Inhibitor 1","Inhibitor 2","Inhibitor 1+2"),
     col = c("blue2","red","yellow","orange"),
     bty = "n", pch=20 , pt.cex = 2, cex = 0.8, horiz = T,inset=c(-0.2,-0.2))
```

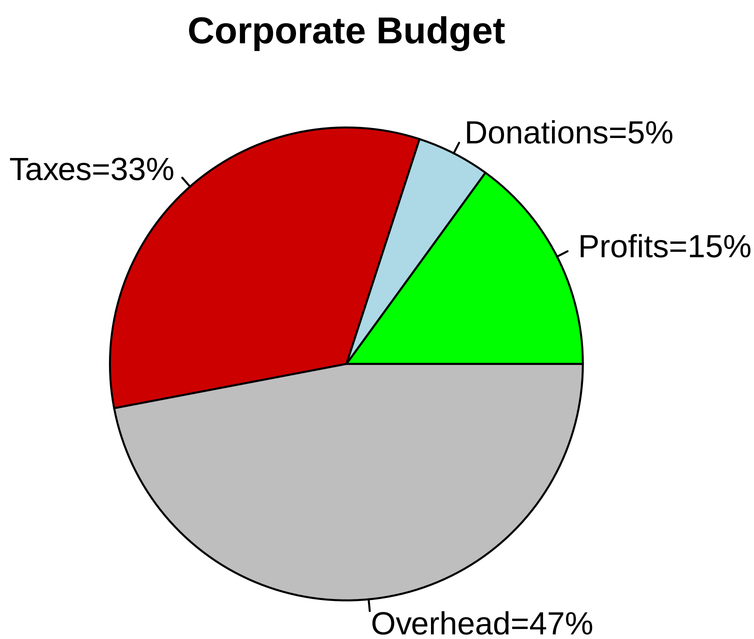


Pie charts

Next we use the `pie()` function to plot the expenses of an imaginary business. Something that would be quickly understood by anyone in the room and informative enough to spark discussion, like should we reduce donations since they make up a fourth of our profits.

```
df <- data.frame(
  group = c("Profits", "Donations", "Taxes", "Overhead"),
  prop = c(15,5,33,47)
  )
```

```r
# Create labels
pie_labels <- paste0(df$group, "=", df$prop, "%")
# Choose colors for the chart
pie_colors <- c("green","lightblue","red3","grey")

pie(df$prop, labels = pie_labels,col = pie_colors, radius = 1,main = "Corporate Budget")
```



There are even more base plots in R that can be used including the `qqnorm()`, `curve()`, and `stripchart()`. These base R plots are great but next we will look into a very powerful R package `ggplot2`.

Beautiful reproducible plots with `ggplot2`

Here we will make a few figures using a `ggplot2`, a powerful package for making publication quality figures. First we will need some data to play with,the `datasets` library should do, and then we can explore some data using `ggplot()`.

```r
library("datasets")
library("ggplot2")
```

To do this effectively we will try and look at 2-3 datasets that have interesting data that we need to find a way to present to an average audience. This is a great real world example of what you would want to do for a job or school work.

```
sleep_data <- sleep
```

The sleep data will be our first study to understand, because sleep is sooooo important!! It is student sleep data as described by the datasets package, but lets see what data they have collected. This can be accomplished by viewing the column and row names usually. Here the row names are just the index of the rows.

```
colNames <- colnames(sleep_data)
rowNames <- rownames(sleep_data)

colNames
```

```
## [1] "extra" "group" "ID"
```

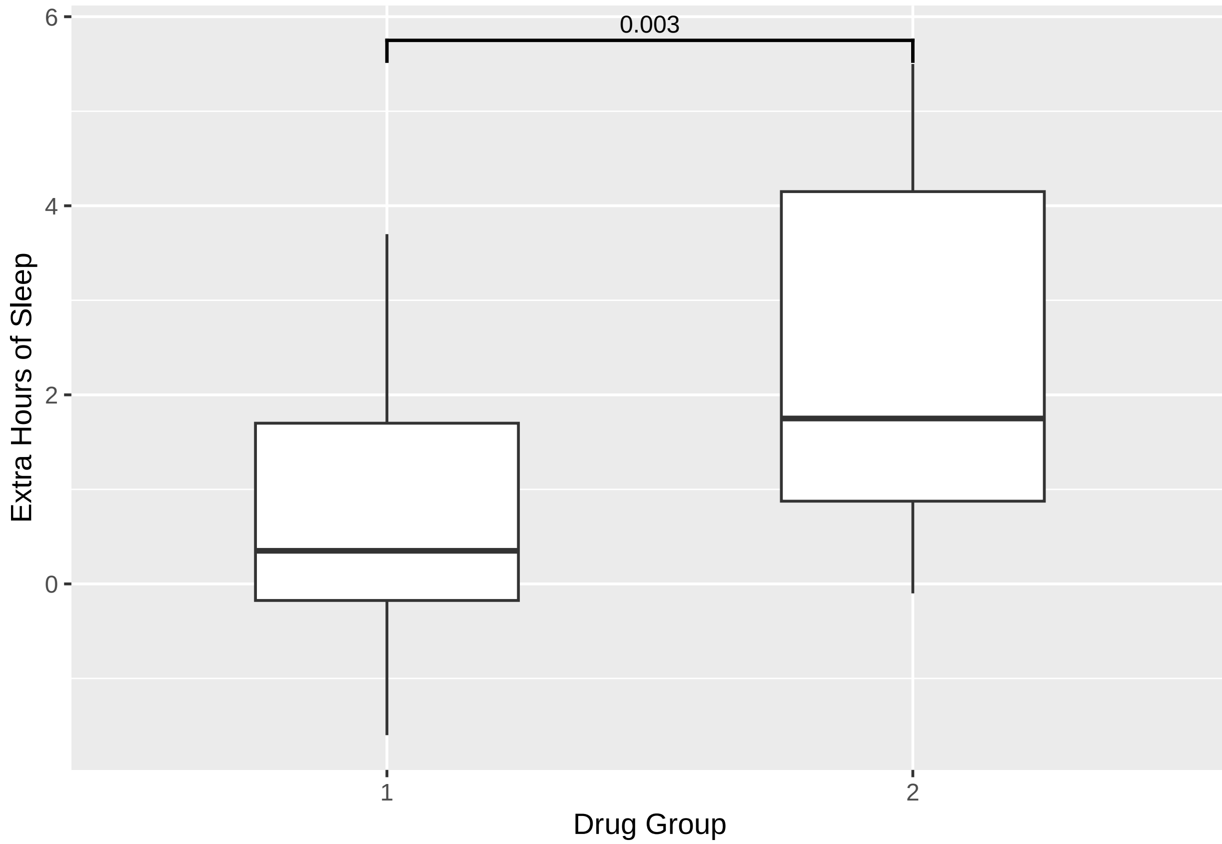
```
rowNames
```

```
##  [1] "1"  "2"  "3"  "4"  "5"  "6"  "7"  "8"  "9"  "10" "11" "12" "13" "14" "15"
## [16] "16" "17" "18" "19" "20"
```

We can look up what these column names actually mean for this dataset, which is testing two drugs to see the influence on sleep. The `extra` column is the extra sleep the patients got vs control patients. The `group` column separates the drugs used and the `ID` column is of course for an ID for each patient. So now you need to come up with a way to look at this data to answer certain questions made by you or your boss. One good question is how much on average extra sleep did patients get for each group/drug treatment?

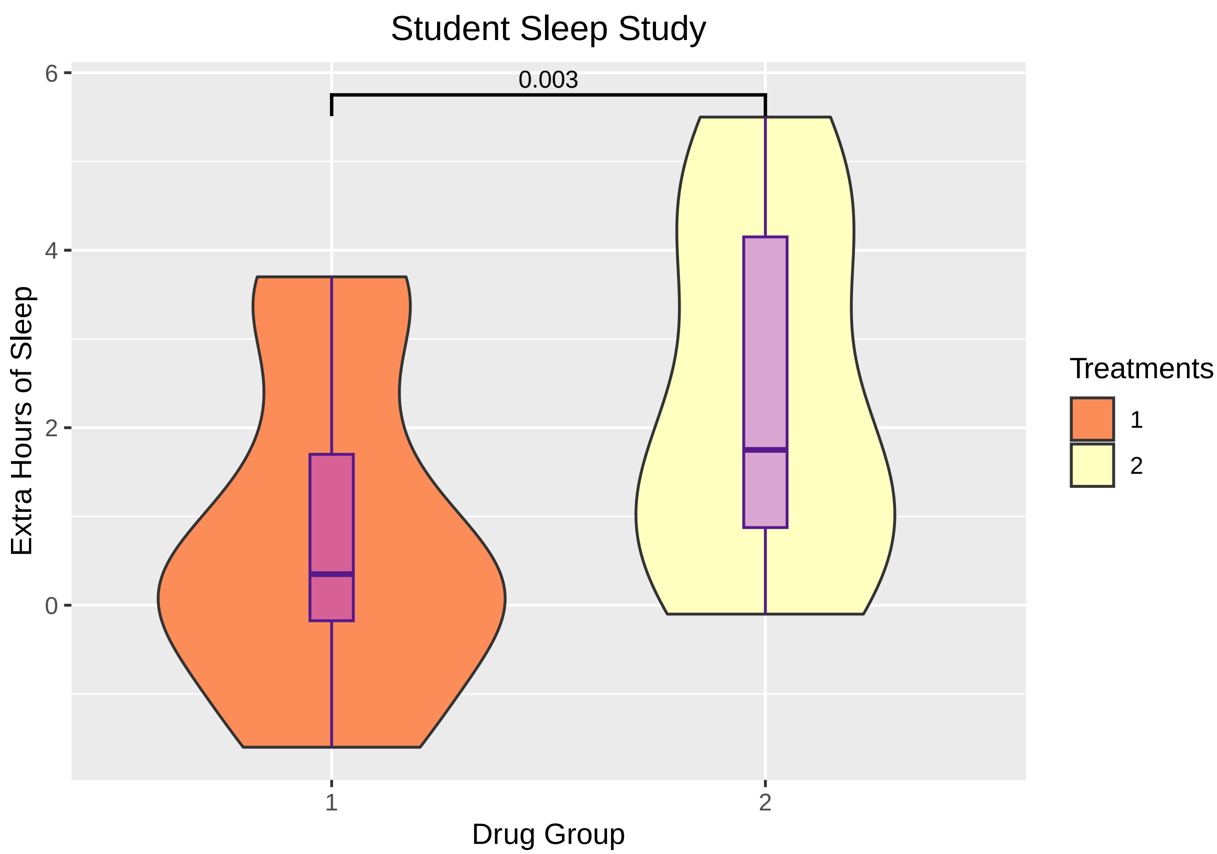
First how do we plot the data so we can see the trends between group 1 and group 2. A `boxplot()` from `ggplot2` works well to show an overview of the data. Here we will also add the pvalue using the `ggprism` package `add_pvalue()` function.

```
library(ggprism)
sleep2 <- reshape(sleep, direction = "wide",
                  idvar = "ID", timevar = "group")

# Pair ttest for pvalue
ttest_result <- t.test(Pair(extra.1, extra.2) ~ 1, data = sleep2)

df_pval <- data.frame(
  group1 = "1",
  group2 = "2",
  label = round(ttest_result$p.value,3),
  y.position = 5.75)

ggplot(sleep_data, aes(x=group, y=extra))+
  geom_boxplot(width = 0.5)+
  xlab("Drug Group")+ylab("Extra Hours of Sleep")+
  add_pvalue(df_pval)
```



Or we can do this with a combination plot to show the spread of the data with a violin plot and the minimum, first quartile, median, third quartile, and maximum with a box plot at once.

```
ggplot(sleep_data, aes(x=group, y=extra))+
  geom_violin(width=0.8,aes(fill=group))+
  geom_boxplot(width = 0.1, color="purple4",fill = "purple", alpha =0.4)+
  scale_fill_brewer(palette ="Spectral")+
  xlab("Drug Group")+ylab("Extra Hours of Sleep")+
  ggtitle("Student Sleep Study")+labs(fill="Treatments")+
  theme(plot.title = element_text(hjust = 0.5))+ #Adjusts the title to center of graph
  add_pvalue(df_pval)
```



And now that we have a few plots to see the data. It is clear that group/drug 1 do not provide as much of a benefit to sleep with a median close to 0hrs while group/drug 2 has a median closer to 2hrs of sleep. The pvalue lower than 0.05 would also suggest the difference it real between the two groups. The sleep dataset is fairly simple and doesn't require any extra sorting or data cleaning, so let's move onto something a little more complex and challenging.

A better dataset

Another dataset that contains the daily air quality measurements in New York from May to September in 1973. This dataset is missing some Ozone and solar radiation (Solar.R) values. What to do when data has missing values is a debated topic. Some users just remove the data with missing values and others will imputate to replace the data with the median or mean of the column as this should have little influence on downstream analyses. Here we will try removing the `NAs` and mean imputation.

```
air <- data.frame(airquality)
head(air)
```

```
##   Ozone Solar.R Wind Temp Month Day
## 1    41     190  7.4   67     5   1
## 2    36     118  8.0   72     5   2
## 3    12     149 12.6   74     5   3
## 4    18     313 11.5   62     5   4
## 5    NA      NA 14.3   56     5   5
## 6    28      NA 14.9   66     5   6
```

Check the dimensions of the data.

```
dim(air)
```

```
## [1] 153   6
```

Data removal for `NAs` Here we make some`cleanAir`. Removing all rows that contain any`NA` values. This takes us down to just 111 rows out of the original 153.

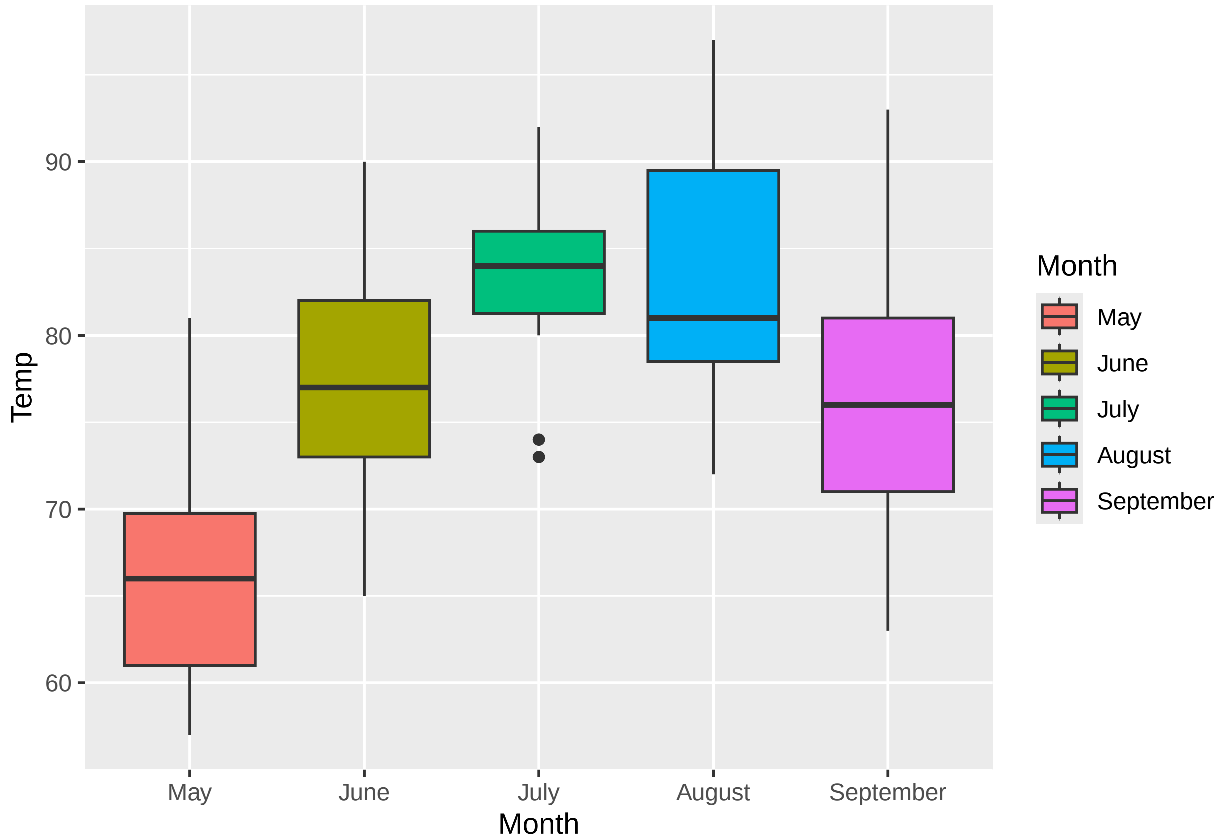
```
cleanAir <- na.omit(air) # Removes rows with NA in all columns
dim(cleanAir)
```

```
## [1] 111   6
```

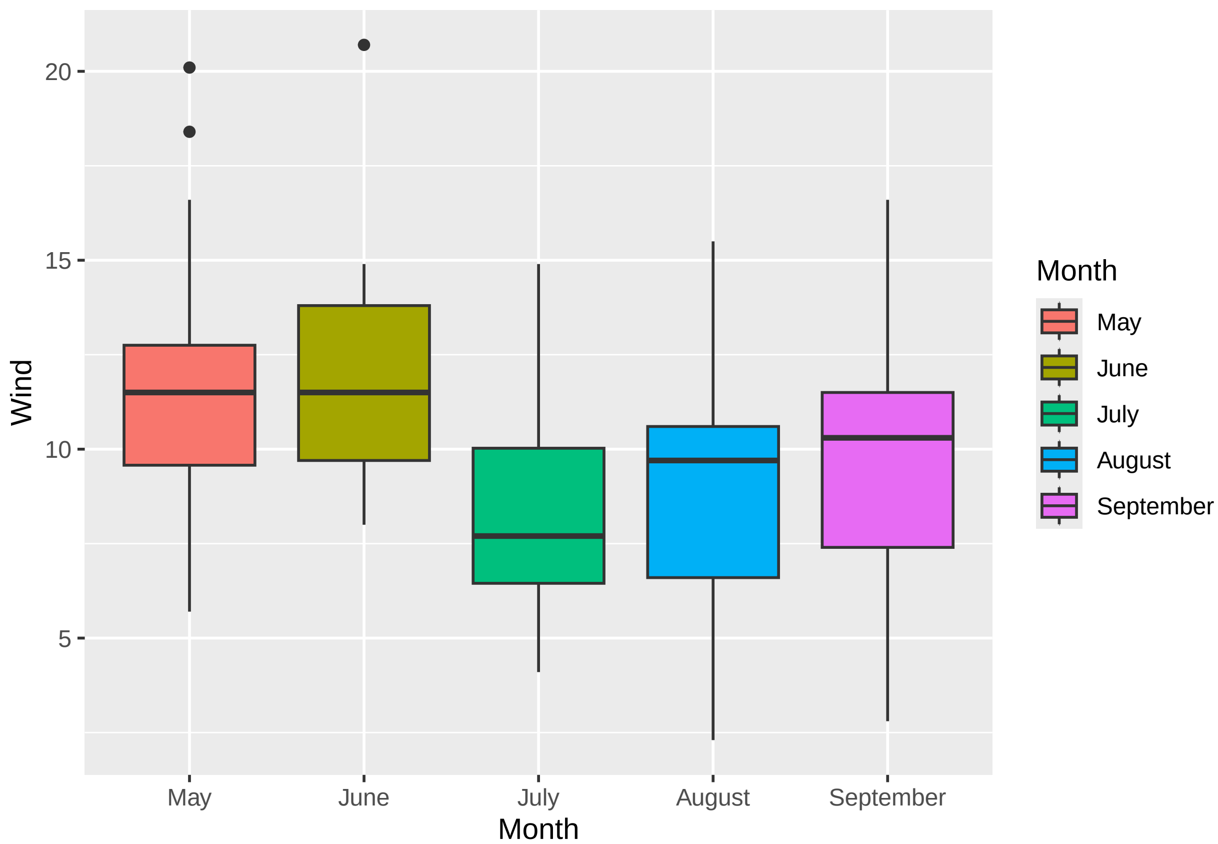
Quick graph to see the data

```
cleanAir$Month[cleanAir$Month == 5]<- "May"
cleanAir$Month[cleanAir$Month == 6]<- "June"
cleanAir$Month[cleanAir$Month == 7]<- "July"
cleanAir$Month[cleanAir$Month == 8]<- "August"
cleanAir$Month[cleanAir$Month == 9]<- "September"

cleanAir$Month<-factor(cleanAir$Month,
                         levels=c("May", "June", "July", "August", "September"))
```

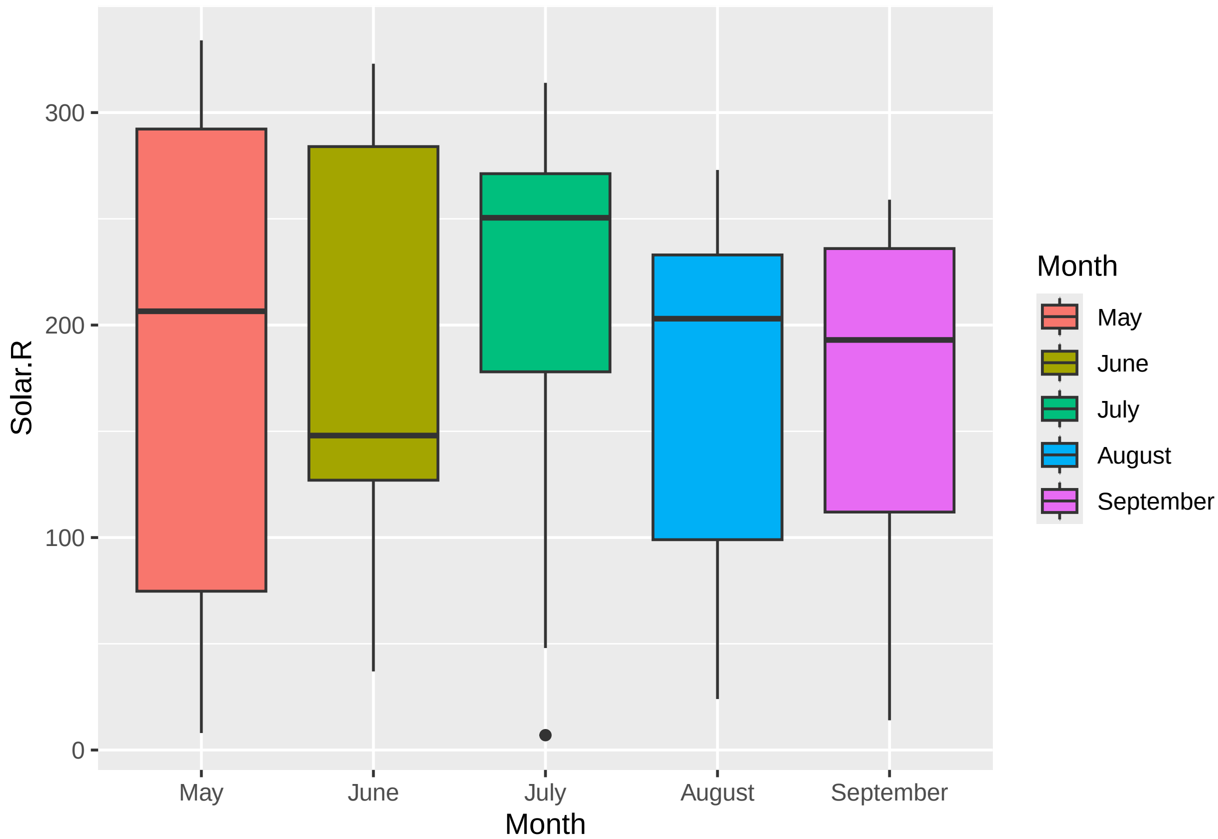
```
tempPlot <- ggplot(cleanAir, aes(x=Month,y=Temp,fill=Month))+
  geom_boxplot()+
  scale_fill_discrete(name = "Month",
                      labels = c("May", "June", "July", "August", "September"))
tempPlot
```



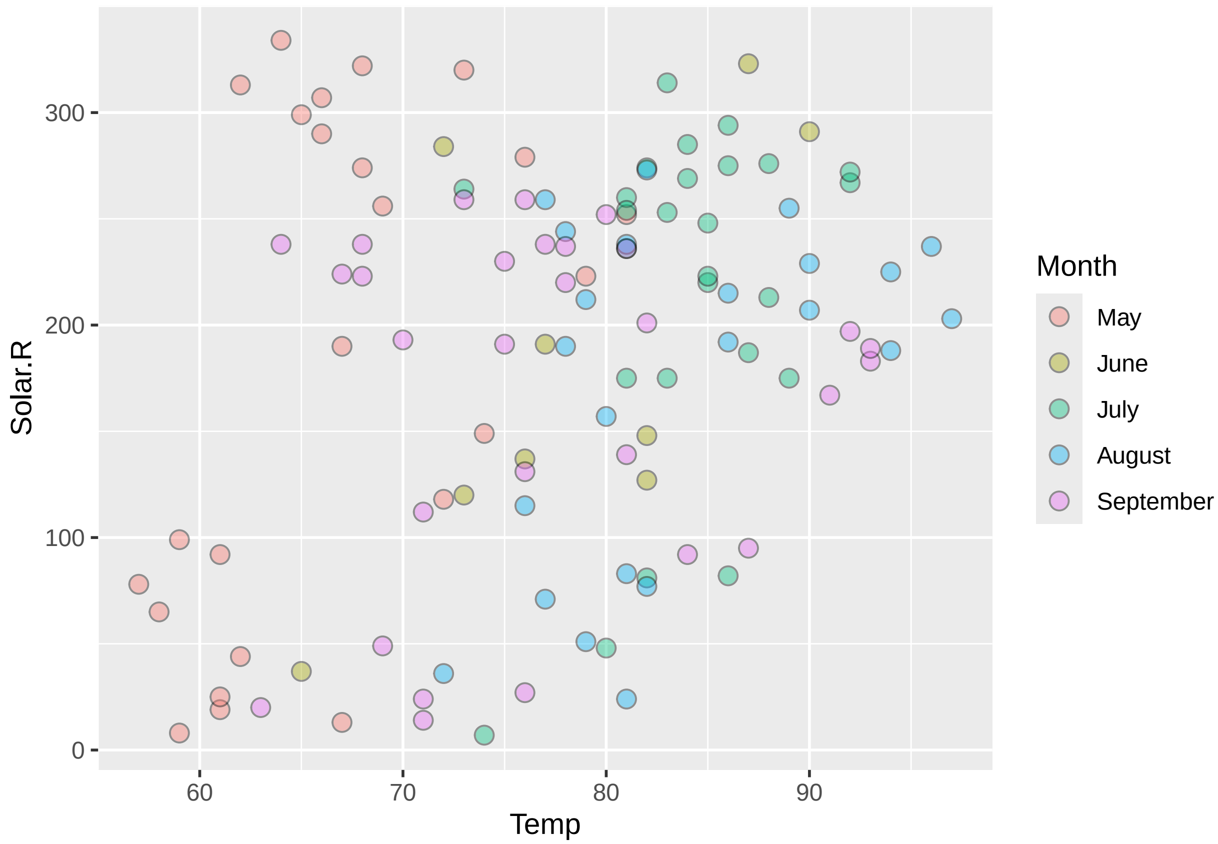

```
windPlot <- ggplot(cleanAir, aes(x=Month,y=Wind,fill=Month))+
  geom_boxplot()+
  scale_fill_discrete(name = "Month",
                      labels = c("May", "June", "July", "August", "September"))
windPlot
```



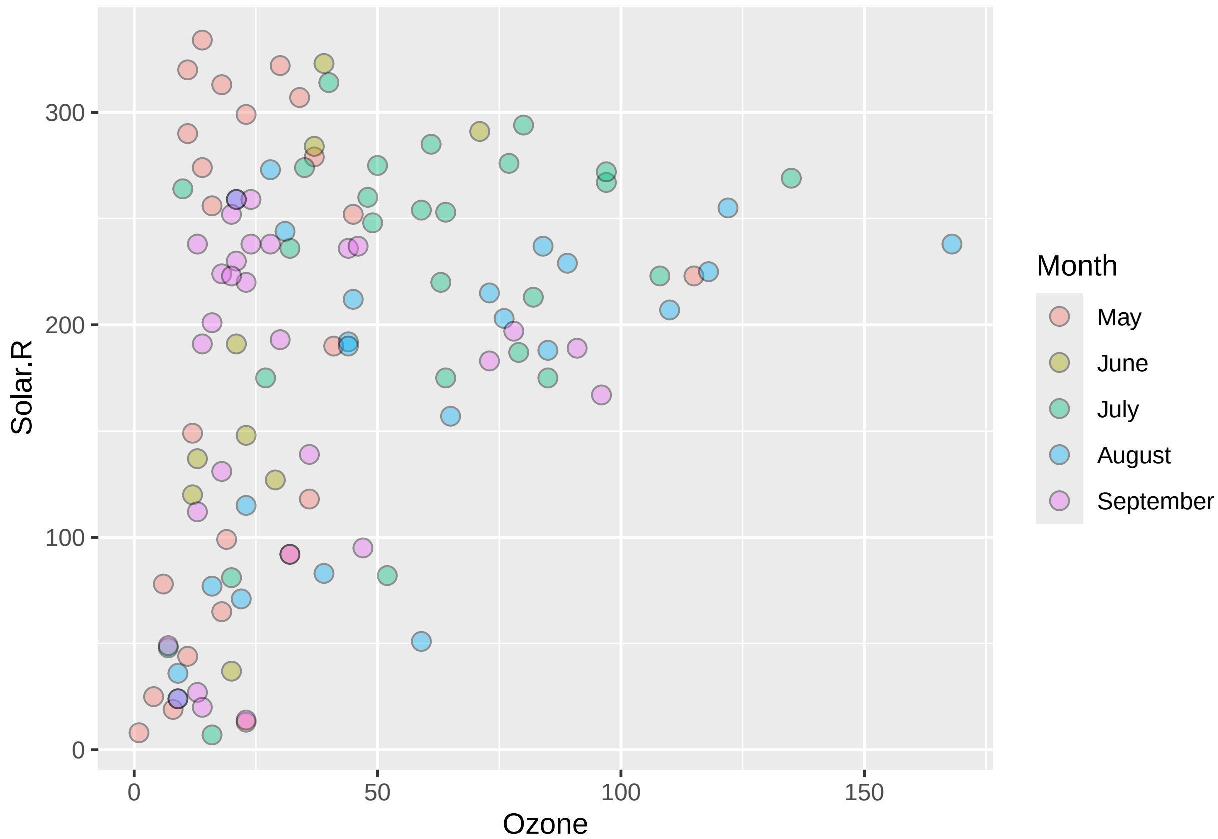

```
radPlot <- ggplot(cleanAir, aes(x=Month,y=Solar.R,fill=Month))+
  geom_boxplot()+
  scale_fill_discrete(name = "Month",
                      labels = c("May", "June", "July", "August", "September"))
radPlot
```




```
radpoint <- ggplot(cleanAir, aes(x=Temp,y=Solar.R,fill=Month))+
  geom_point(shape = 21, size = 3,alpha=0.4)+
  scale_fill_discrete(name = "Month",
                      labels = c("May", "June", "July", "August", "September"))
radpoint
```




```
ozonepoint <- ggplot(cleanAir, aes(x=Ozone,y=Solar.R,fill=Month))+
  geom_point(shape = 21, size = 3,alpha=0.4)+
  scale_fill_discrete(name = "Month",
                      labels = c("May", "June", "July", "August", "September"))
ozonepoint
```

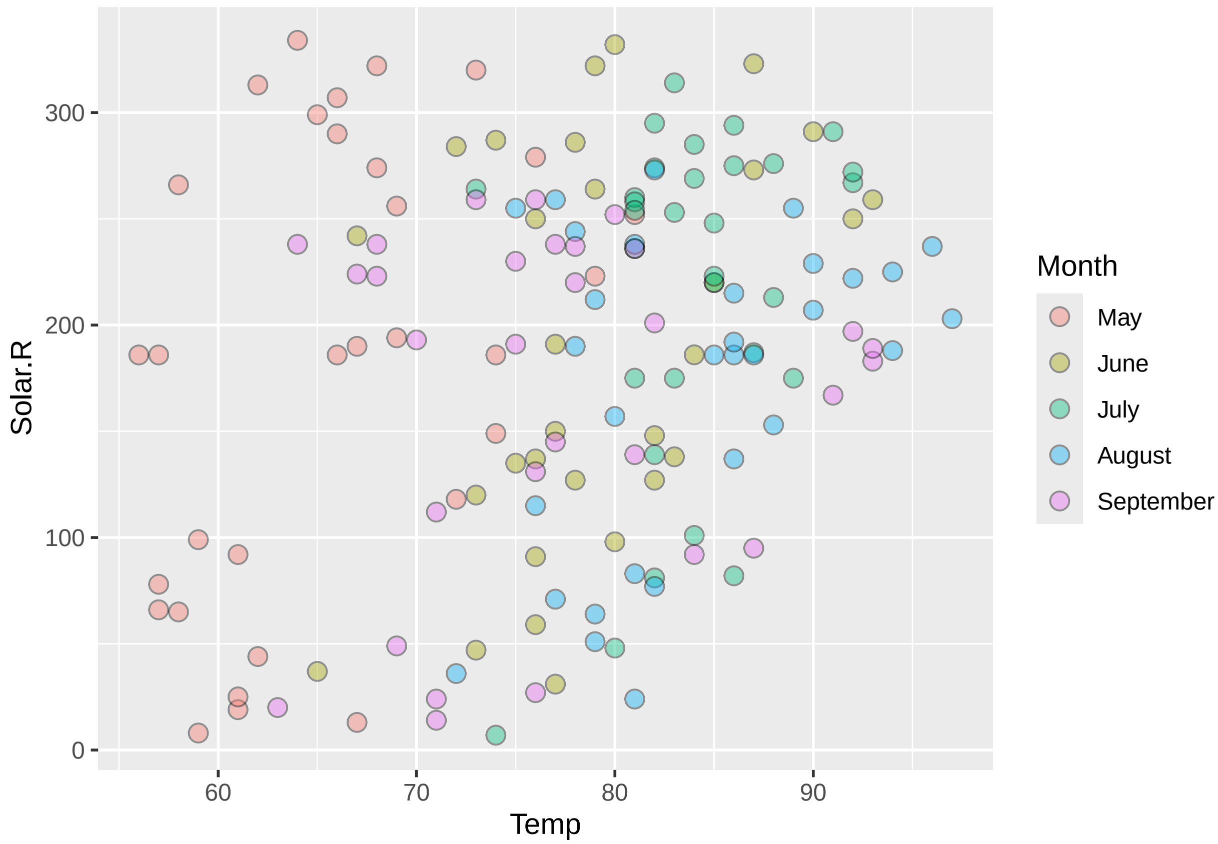


Mean imputation for `NA` data

```
cleanAir_mean <- air
cleanAir_mean$Ozone[is.na(cleanAir_mean$Ozone)] <- mean(cleanAir_mean$Ozone,
                                                         na.rm = TRUE)
cleanAir_mean$Solar.R[is.na(cleanAir_mean$Solar.R)] <- mean(cleanAir_mean$Solar.R,
                                                             na.rm = TRUE)

cleanAir_mean$Month[cleanAir_mean$Month == 5]<- "May"
cleanAir_mean$Month[cleanAir_mean$Month == 6]<- "June"
cleanAir_mean$Month[cleanAir_mean$Month == 7]<- "July"
cleanAir_mean$Month[cleanAir_mean$Month == 8]<- "August"
cleanAir_mean$Month[cleanAir_mean$Month == 9]<- "September"

cleanAir_mean$Month<-factor(cleanAir_mean$Month,
                         levels=c("May", "June", "July", "August", "September"))
```

All the True values in this list are the position of the `NA`s in this dataset. So say you want to make all the `NA`s a different value or you want to ignore them when plotting.

```
ggplot(cleanAir_mean, aes(x=Temp,y=Solar.R,fill=Month))+
  geom_point(shape = 21, size = 3,alpha=0.4)+
  scale_fill_discrete(name = "Month",
                      labels = c("May", "June", "July", "August", "September"))
```



A bigger dataset

We used a dataset from kaggle.com you can find it (here)[https://www.kaggle.com/datasets/soylevbeytullah/ds4work-human-resources/data]

```
hrdat <- read.csv("data/Human_Resources.csv",header = T)
head(hrdat)
```

```
##   Age Attrition    BusinessTravel DailyRate             Department
## 1  41       Yes     Travel_Rarely      1102                  Sales
## 2  49        No Travel_Frequently       279 Research & Development
## 3  37       Yes     Travel_Rarely      1373 Research & Development
## 4  33        No Travel_Frequently      1392 Research & Development
## 5  27        No     Travel_Rarely       591 Research & Development
## 6  32        No Travel_Frequently      1005 Research & Development
##   DistanceFromHome Education EducationField EmployeeCount EmployeeNumber
## 1                1         2  Life Sciences             1              1
## 2                8         1  Life Sciences             1              2
## 3                2         2          Other             1              4
## 4                3         4  Life Sciences             1              5
## 5                2         1        Medical             1              7
## 6                2         2  Life Sciences             1              8
##   EnvironmentSatisfaction Gender HourlyRate JobInvolvement JobLevel
## 1                       2 Female         94              3        2
## 2                       3   Male         61              2        2
```

```
## 3                       4   Male         92             2        1
## 4                       4 Female         56             3        1
## 5                       1   Male         40             3        1
## 6                       4   Male         79             3        1
##                JobRole JobSatisfaction MaritalStatus MonthlyIncome MonthlyRate
## 1      Sales Executive               4        Single          5993       19479
## 2   Research Scientist               2       Married          5130       24907
## 3 Laboratory Technician               3        Single          2090        2396
## 4   Research Scientist               3       Married          2909       23159
## 5 Laboratory Technician               2       Married          3468       16632
## 6 Laboratory Technician               4        Single          3068       11864
##   NumCompaniesWorked Over18 OverTime PercentSalaryHike PerformanceRating
## 1                  8      Y      Yes                11                 3
## 2                  1      Y       No                23                 4
## 3                  6      Y      Yes                15                 3
## 4                  1      Y      Yes                11                 3
## 5                  9      Y       No                12                 3
## 6                  0      Y       No                13                 3
##   RelationshipSatisfaction StandardHours StockOptionLevel TotalWorkingYears
## 1                        1            80                0                 8
## 2                        4            80                1                10
## 3                        2            80                0                 7
## 4                        3            80                0                 8
## 5                        4            80                1                 6
## 6                        3            80                0                 8
##   TrainingTimesLastYear WorkLifeBalance YearsAtCompany YearsInCurrentRole
## 1                     0               1              6                  4
## 2                     3               3             10                  7
## 3                     3               3              0                  0
## 4                     3               3              8                  7
## 5                     3               3              2                  2
## 6                     2               2              7                  7
##   YearsSinceLastPromotion YearsWithCurrManager
## 1                       0                    5
## 2                       1                    7
## 3                       0                    0
## 4                       3                    0
## 5                       2                    2
## 6                       3                    6
```

```r
dim(hrdat)
```

```
## [1] 1470   35
```

This dataset is large and we should probably try to understand the 35 columns and what they mean.First we can checkout the column names with the `names()` function and then check the data types for all the columns with `lapply()`.

```r
names(hrdat)
```

```
##  [1] "Age"                      "Attrition"
##  [3] "BusinessTravel"           "DailyRate"
##  [5] "Department"               "DistanceFromHome"
```

```
##  [7] "Education"                "EducationField"
##  [9] "EmployeeCount"            "EmployeeNumber"
## [11] "EnvironmentSatisfaction"  "Gender"
## [13] "HourlyRate"               "JobInvolvement"
## [15] "JobLevel"                 "JobRole"
## [17] "JobSatisfaction"          "MaritalStatus"
## [19] "MonthlyIncome"            "MonthlyRate"
## [21] "NumCompaniesWorked"       "Over18"
## [23] "OverTime"                 "PercentSalaryHike"
## [25] "PerformanceRating"        "RelationshipSatisfaction"
## [27] "StandardHours"            "StockOptionLevel"
## [29] "TotalWorkingYears"        "TrainingTimesLastYear"
## [31] "WorkLifeBalance"          "YearsAtCompany"
## [33] "YearsInCurrentRole"       "YearsSinceLastPromotion"
## [35] "YearsWithCurrManager"
```

```r
lapply(hrdat, typeof)
```

```
## $Age
## [1] "integer"
##
## $Attrition
## [1] "character"
##
## $BusinessTravel
## [1] "character"
##
## $DailyRate
## [1] "integer"
##
## $Department
## [1] "character"
##
## $DistanceFromHome
## [1] "integer"
##
## $Education
## [1] "integer"
##
## $EducationField
## [1] "character"
##
## $EmployeeCount
## [1] "integer"
##
## $EmployeeNumber
## [1] "integer"
##
## $EnvironmentSatisfaction
## [1] "integer"
##
## $Gender
## [1] "character"
##
```

```
## $HourlyRate
## [1] "integer"
##
## $JobInvolvement
## [1] "integer"
##
## $JobLevel
## [1] "integer"
##
## $JobRole
## [1] "character"
##
## $JobSatisfaction
## [1] "integer"
##
## $MaritalStatus
## [1] "character"
##
## $MonthlyIncome
## [1] "integer"
##
## $MonthlyRate
## [1] "integer"
##
## $NumCompaniesWorked
## [1] "integer"
##
## $Over18
## [1] "character"
##
## $OverTime
## [1] "character"
##
## $PercentSalaryHike
## [1] "integer"
##
## $PerformanceRating
## [1] "integer"
##
## $RelationshipSatisfaction
## [1] "integer"
##
## $StandardHours
## [1] "integer"
##
## $StockOptionLevel
## [1] "integer"
##
## $TotalWorkingYears
## [1] "integer"
##
## $TrainingTimesLastYear
## [1] "integer"
##
```

```
## $WorkLifeBalance
## [1] "integer"
##
## $YearsAtCompany
## [1] "integer"
##
## $YearsInCurrentRole
## [1] "integer"
##
## $YearsSinceLastPromotion
## [1] "integer"
##
## $YearsWithCurrManager
## [1] "integer"
```

Some of the columns are described below, these will be ordinal data. Those columns with characters are most likely categorical data and the rest will be values recorded or measured meaning continuous data. This will be important to what statistical tests and plotting we perform below.

- Education: 1=Below College, 2=College, 3=Bachelor, 4=Master, 5=Doctor
- EnvironmentSatisfaction: 1=Low, 2=Medium, 3=High, 4=Very High
- JobInvolvement: 1=Low, 2=Medium, 3=High, 4=Very High
- JobSatisfaction: 1=Low, 2=Medium, 3=High, 4=Very High
- PerformanceRating: 1=Low, 2=Good, 3=Excellent, 4=Outstanding
- RelationshipSatisfaction: 1=Low, 2=Medium, 3=High, 4=Very High
- WorkLifeBalance: 1=Bad, 2=Good, 3=Better, 4=Best
- Attrition: 0=Stayed, 1=Left

Asking questions of our data

We have an interesting data set here we can try to answer some questions. What does life balance correlate with? Do higher salaries correlate with high retention rates? Do performance ratings correlate with better salaries? We can investigate this by calculating R^2 values for two continuous variables or use spearman's or polyserial correlations.

To calculate the R^2 value you can use the `lm()` function stands for linear model and `summary()`.

```r
model <- lm(MonthlyRate ~ DailyRate, data = hrdat)
modelSum <- summary(model)
modelSum$r.squared
```

```
## [1] 0.001035655
```

Then we can use Spearman's correlation for ordinal and continuous data comparisons.

```r
corre <- cor(as.numeric(hrdat$WorkLifeBalance),as.numeric(hrdat$Education),
             method ="spearman")
corre
```

```
## [1] 0.01735044
```

```r
corre2 <- cor(as.numeric(hrdat$WorkLifeBalance),hrdat$MonthlyIncome,
              method ="spearman")
corre2
```

```
## [1] 0.03075915
```

```r
corre3 <- cor(as.numeric(hrdat$WorkLifeBalance),hrdat$YearsInCurrentRole,
              method ="spearman")
corre3
```

```
## [1] 0.02321426
```

There is a positive weak monotonic relationship between work life balance and education, monthly income, and years in the current role.

Another test for ordinal and continuous data is the polyserial correlation instead of Spearman's. The polyserial correlation value assumes an underlying bivariate normal distribution for a latent continuous variable that the ordinal variable represents. But still only a weak correlation between monthly income and work life balance. I guess it is true money can not buy happiness.

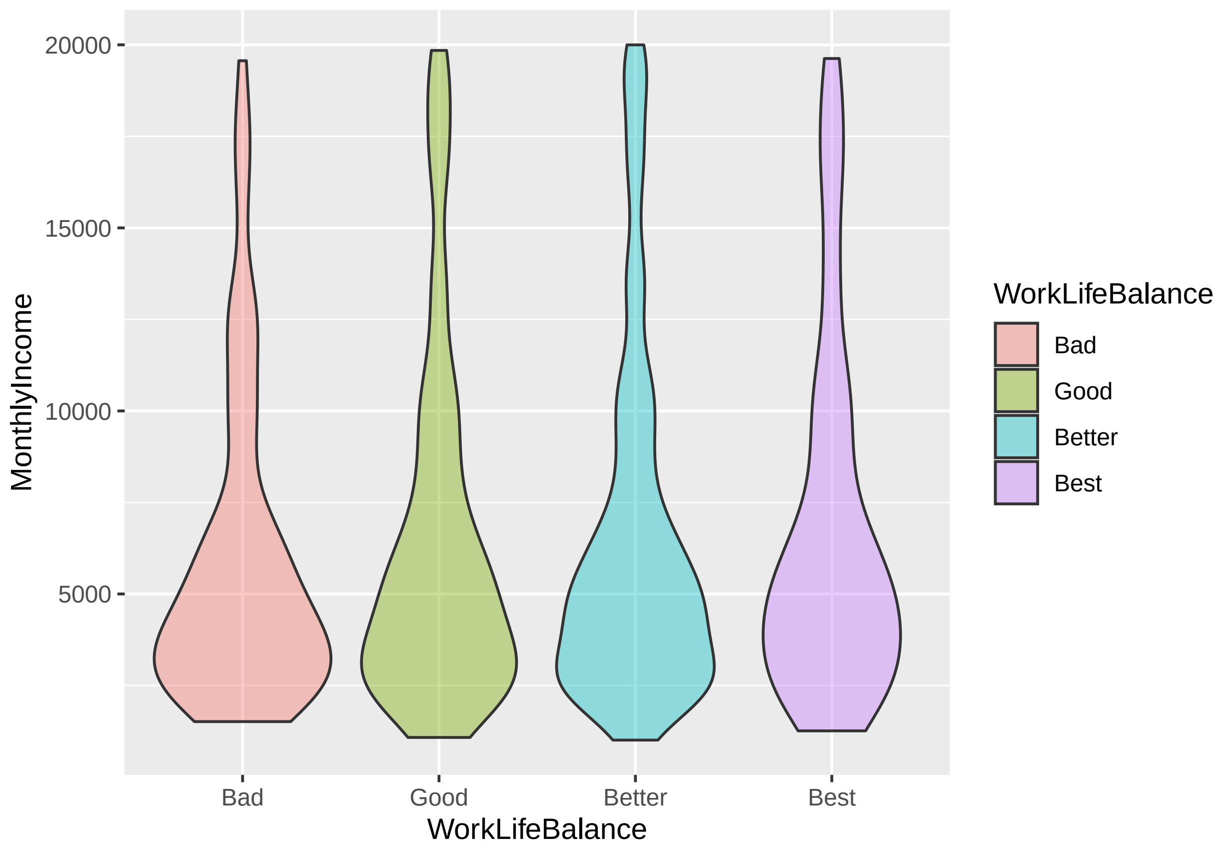
```r
# install.packages("polycor")
library(polycor)

# x=ordinal_var y=continuous_var
polyserial(hrdat$MonthlyIncome,hrdat$WorkLifeBalance)
```

```
## [1] 0.03426368
```

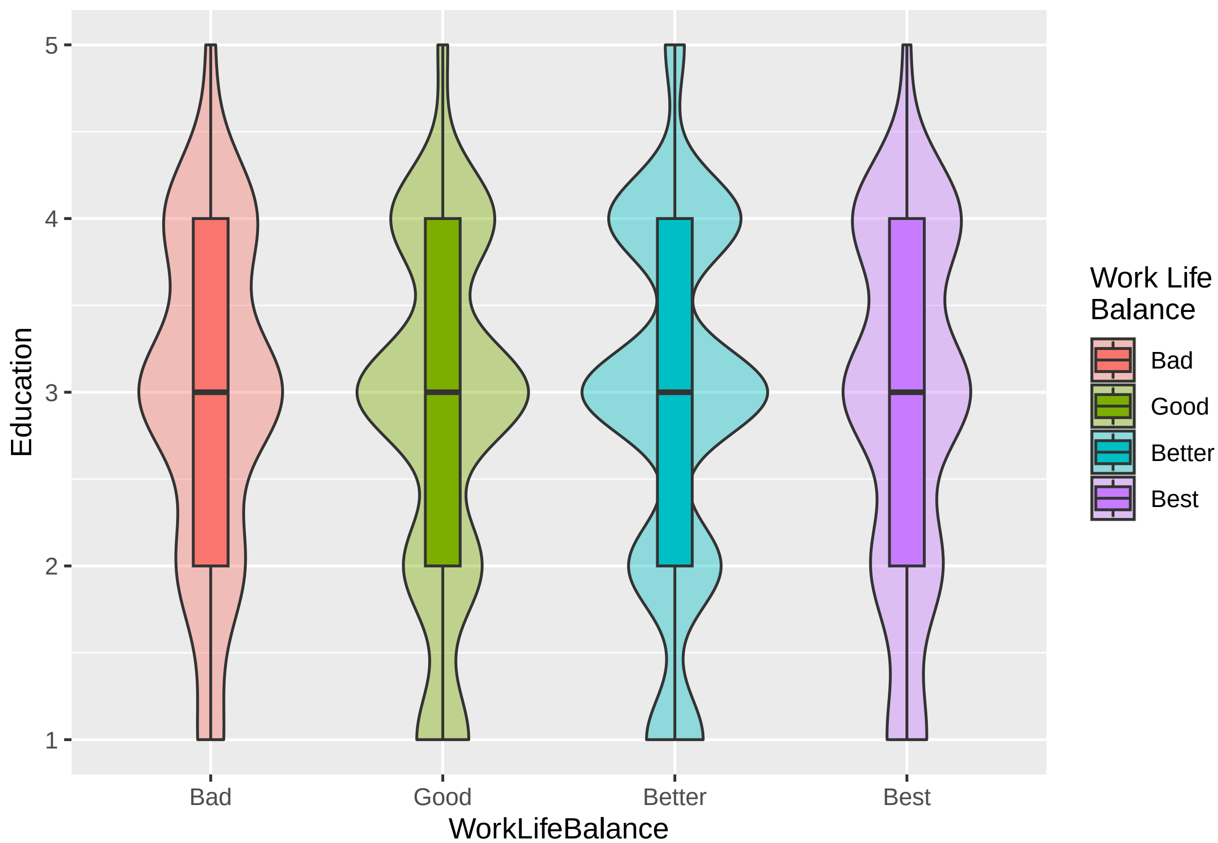
Making the work life balance column a factor with levels and changing the values for plotting.

```r
hrdat$WorkLifeBalance[hrdat$WorkLifeBalance == 1]<- "Bad"
hrdat$WorkLifeBalance[hrdat$WorkLifeBalance == 2]<- "Good"
hrdat$WorkLifeBalance[hrdat$WorkLifeBalance == 3]<- "Better"
hrdat$WorkLifeBalance[hrdat$WorkLifeBalance == 4]<- "Best"

hrdat$WorkLifeBalance<-factor(hrdat$WorkLifeBalance,
                         levels=c("Bad", "Good", "Better", "Best"))
```

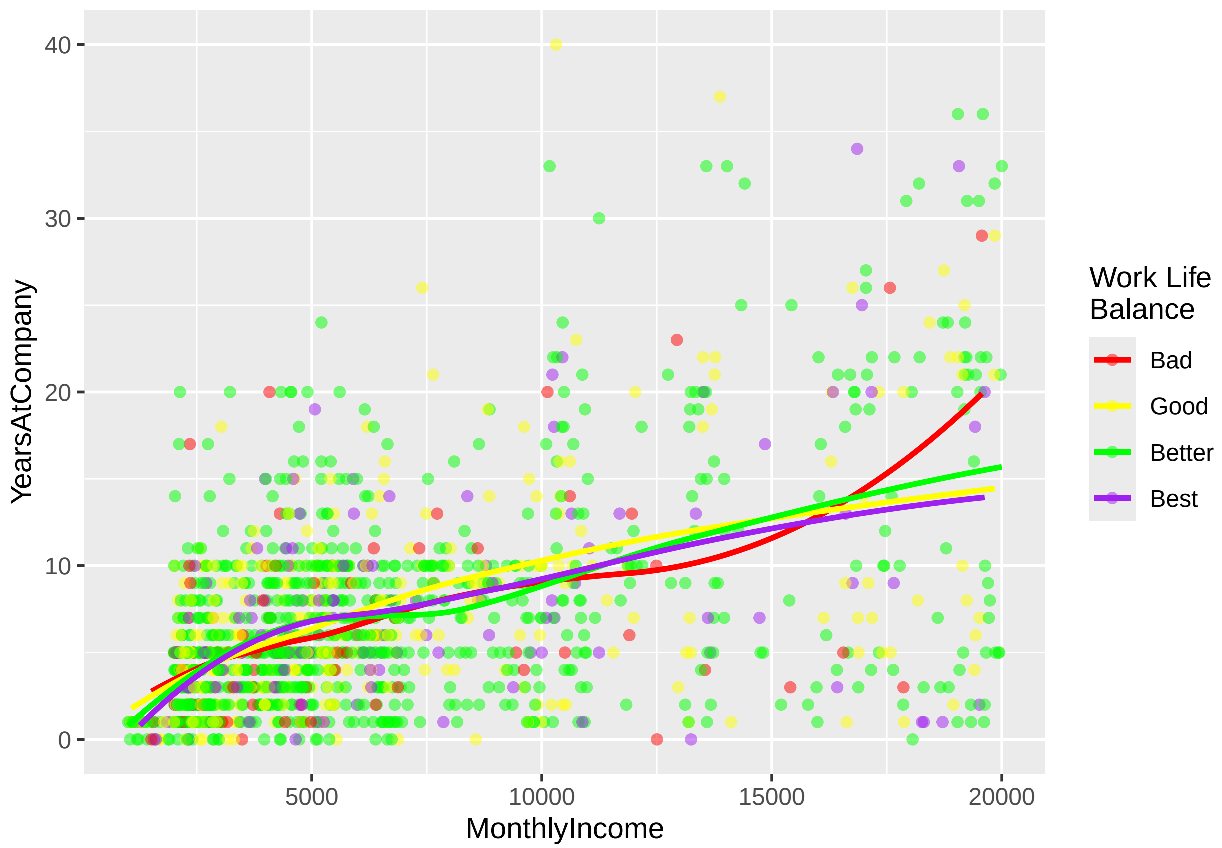
```r
ggplot(hrdat, aes(x=WorkLifeBalance,y=MonthlyIncome,fill=WorkLifeBalance))+
  geom_violin(alpha=0.4)
```



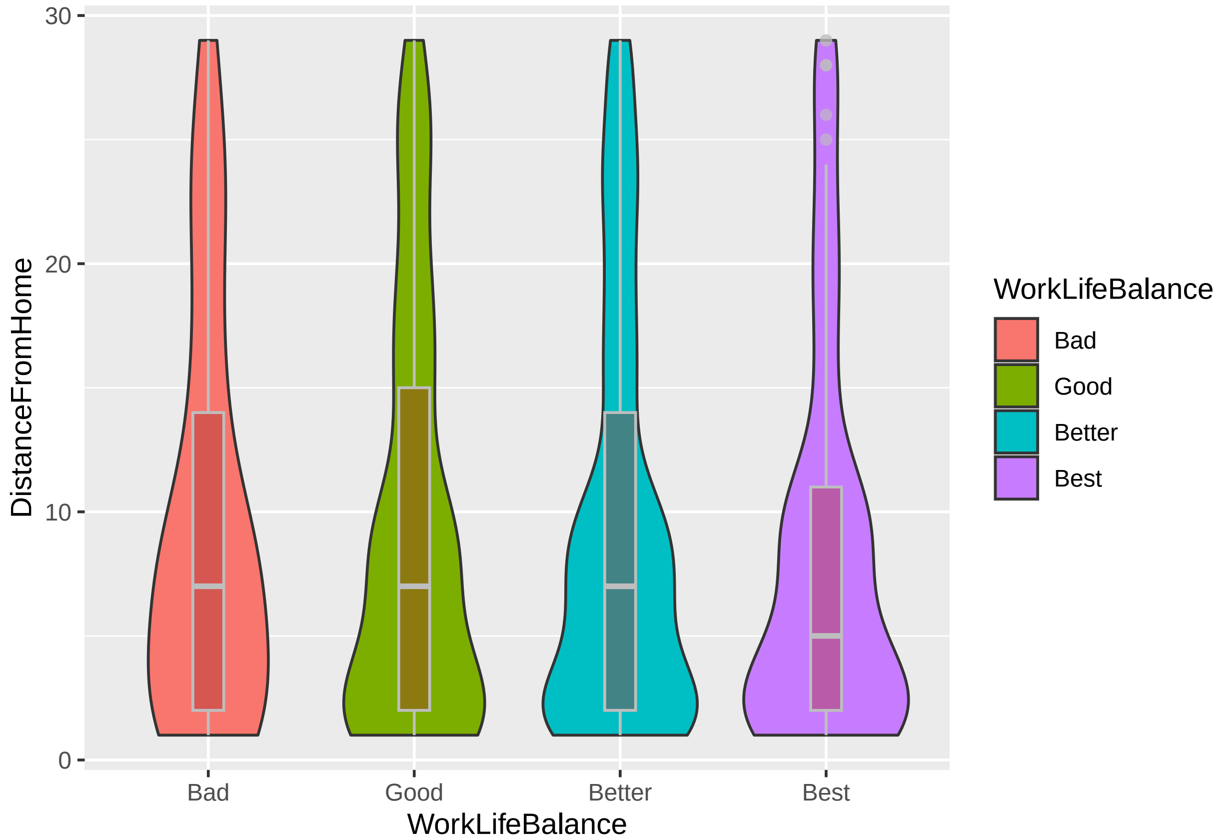

```
ggplot(hrdat, aes(x=WorkLifeBalance,y=Education,fill=WorkLifeBalance))+
  geom_violin(width=0.8,alpha=0.4)+
  geom_boxplot(width=0.15)+
  scale_fill_discrete(name = "Work Life\nBalance",
                      labels = c("Bad", "Good", "Better", "Best"))
```



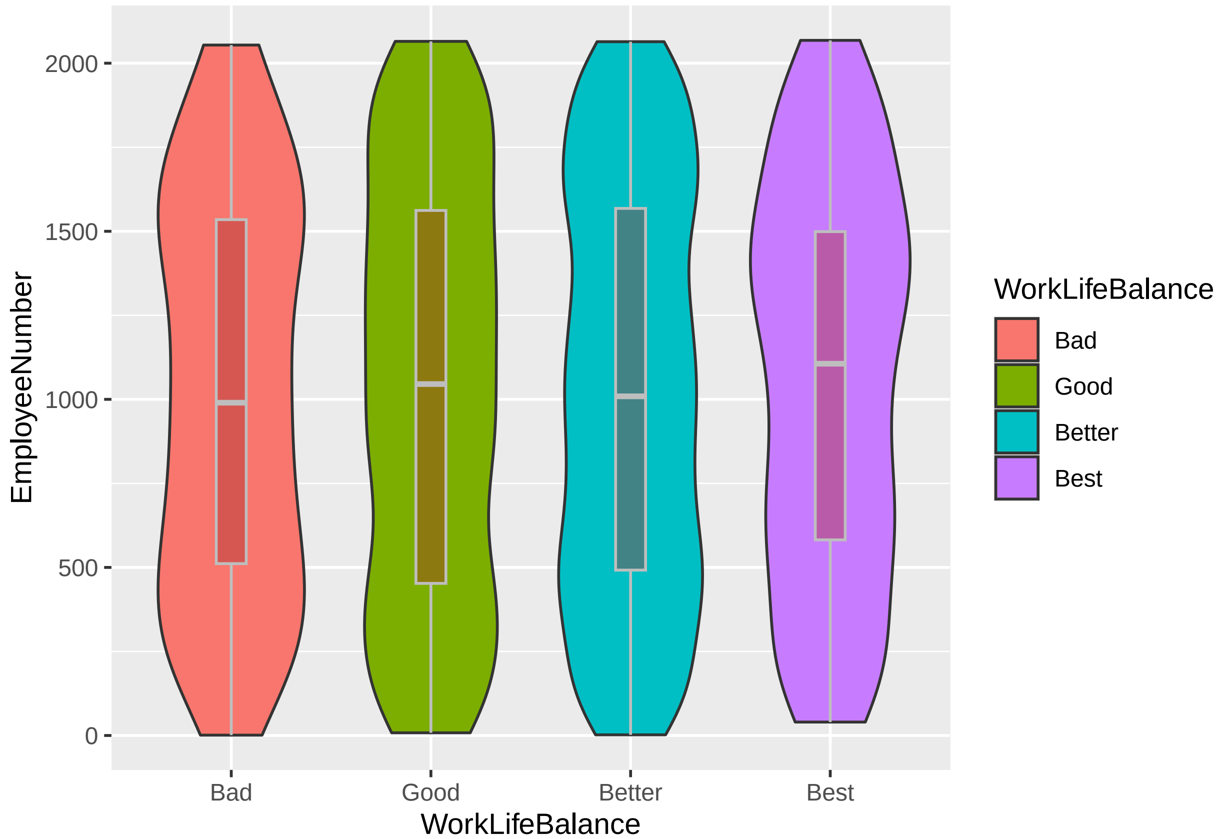

```
ggplot(hrdat, aes(x=MonthlyIncome,y=YearsAtCompany,colour = WorkLifeBalance))+
  geom_point(alpha=0.5)+
  geom_smooth(aes(x=MonthlyIncome),se=F,method = "loess",formula = 'y ~ x')+
  scale_color_discrete(name = "Work Life\nBalance",
                       labels = c("Bad", "Good", "Better", "Best"),
                       palette = c("red","yellow","green","purple"))
```




```
ggplot(hrdat, aes(x=WorkLifeBalance,y=DistanceFromHome,fill=WorkLifeBalance))+
  geom_violin(width=0.8)+
  geom_boxplot(width = 0.15, color="grey",fill = "brown", alpha =0.4)+
  scale_colour_brewer(name = "Work Life\nBalance",
                      labels = c("Bad", "Good", "Better", "Best")
                      ,palette = "Set1")
```



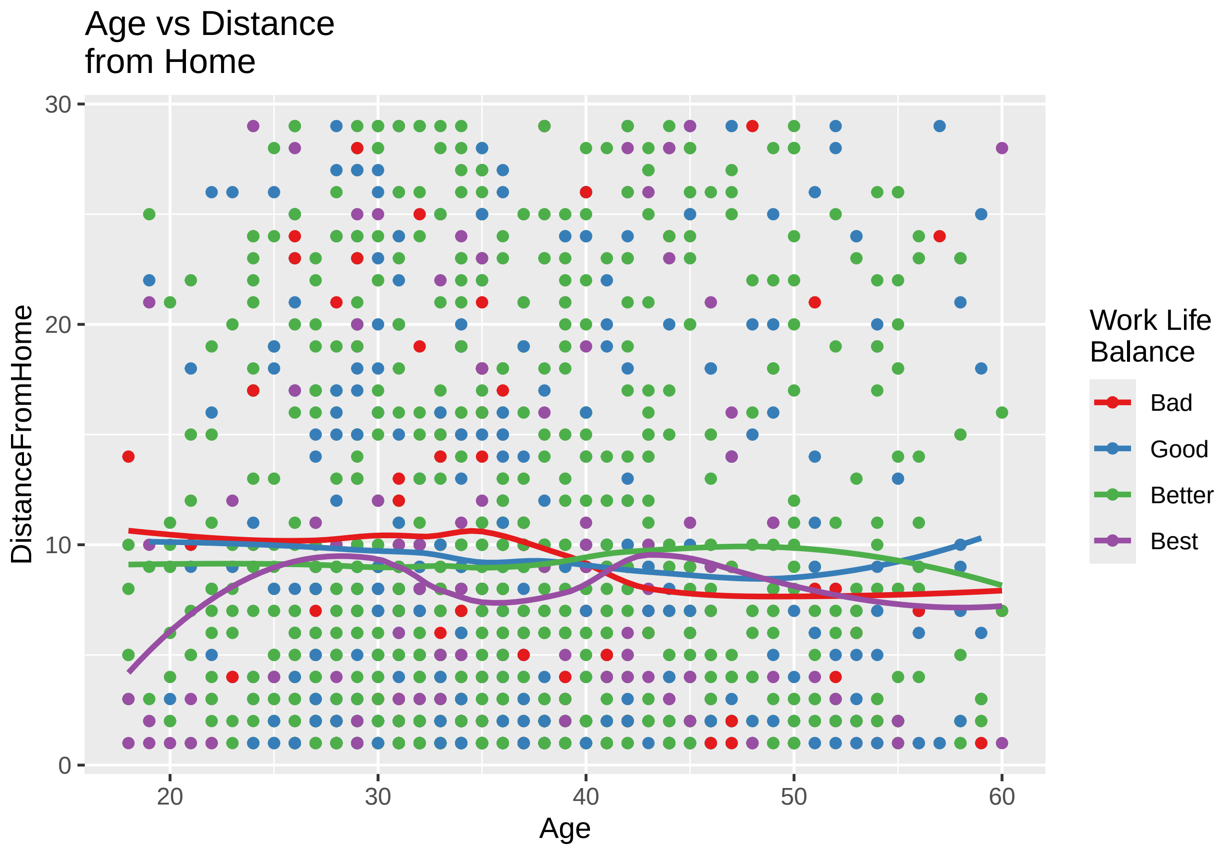

```
ggplot(hrdat, aes(x=WorkLifeBalance,y=EmployeeNumber,fill=WorkLifeBalance))+
  geom_violin(width=0.8)+
  geom_boxplot(width = 0.15, color="grey",fill = "brown", alpha =0.4)+
  scale_colour_brewer(name = "Work Life\nBalance",
                     labels = c("Bad", "Good", "Better", "Best")
                    ,palette = "Set1")
```



Rproducible graphs with ggplot

Next we will introduce `theme()` a useful function that allows you to change all the aspects of the graph itself and gives you reproducible graphs across types. In science we will sometimes need to change the text to italics or we like to bold important data, but to do this for each graph is unnecessary with `theme()`. A quick example will illustrate this. Take any plot we have made previously.

```
ggplot(hrdat, aes(x=Age,y=DistanceFromHome,color=WorkLifeBalance))+
  geom_point()+ggtitle("Age vs Distance\nfrom Home")+
  geom_smooth(aes(x=Age),se=F,method = "loess",formula = 'y ~ x')+
  scale_colour_brewer(name = "Work Life\nBalance",
                      labels = c("Bad", "Good", "Better", "Best")
                      ,palette = "Set1")
```



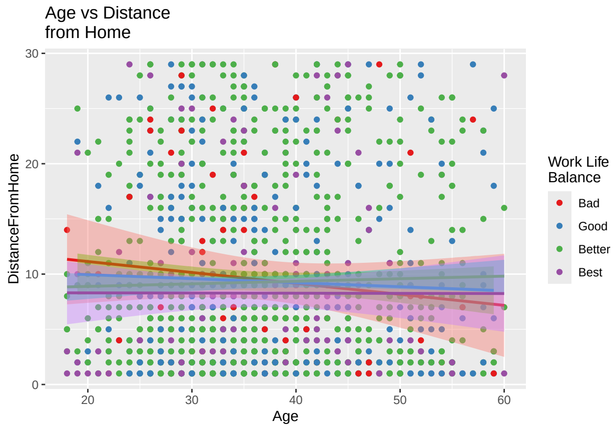
We will change the graph title and axis text size the axis titles to italics, center the graph title, then we will bold the legend text and increase the size and shrink the legend title.

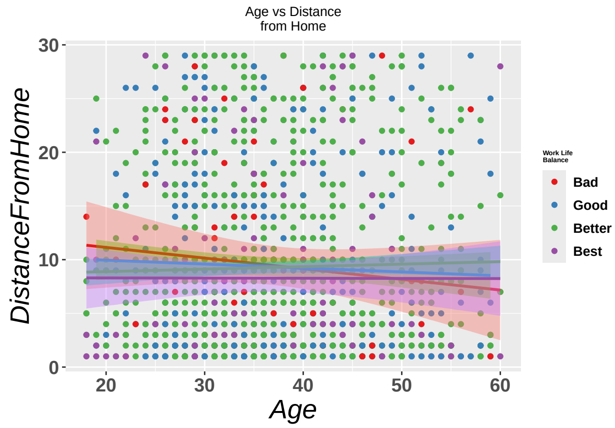
```
the_theme <- theme(plot.title = element_text(size=10,hjust = 0.5),
                   axis.title = element_text(face = "italic",size = 20),
                   axis.text = element_text(size = 14,face = "bold"),
                   legend.text = element_text(face = "bold",size = 10),
                   legend.title = element_text(face = "bold",size = 5))
```

Now add the theme to the graph.

```
p1<-ggplot(hrdat, aes(x=Age,y=DistanceFromHome,color=WorkLifeBalance))+
  geom_point()+ggtitle("Age vs Distance\nfrom Home")+
  stat_smooth(method = "lm",aes(fill=WorkLifeBalance),se=T,show.legend = F,
              formula = 'y ~ x')+
  scale_colour_brewer(name = "Work Life\nBalance",
                      labels = c("Bad", "Good", "Better", "Best"),
                      palette = "Set1")

p2<-ggplot(hrdat, aes(x=Age,y=DistanceFromHome,color=WorkLifeBalance))+
  geom_point()+ggtitle("Age vs Distance\nfrom Home")+
  stat_smooth(method = "lm",aes(fill=WorkLifeBalance),se=T,show.legend = F,
              formula = 'y ~ x')+
  scale_colour_brewer(name = "Work Life\nBalance",
                      labels = c("Bad", "Good", "Better", "Best"),
                      palette = "Set1")+
```

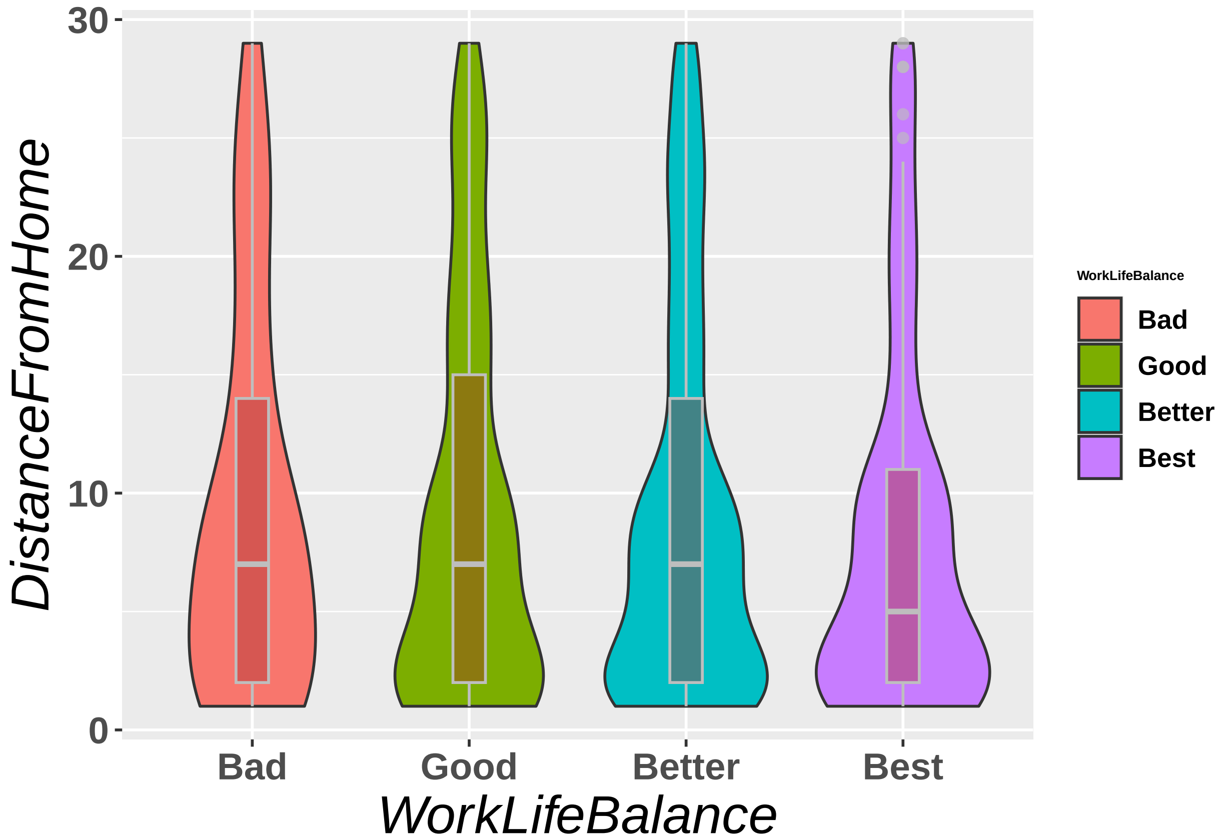
```
  the_theme
p1
p2
```





And this theme can be added to any graph you make, meaning all the graphs you make will have the same styling which is great for many projects including making figures for publication.

```
ggplot(hrdat, aes(x=WorkLifeBalance,y=DistanceFromHome,fill=WorkLifeBalance))+
  geom_violin(width=0.8)+
  geom_boxplot(width = 0.15, color="grey",fill = "brown", alpha =0.4)+
  scale_colour_brewer(name = "Work Life\nBalance",
                      labels = c("Bad", "Good", "Better", "Best")
                      ,palette = "Set1")+
  the_theme
```



The `theme()` function has many parameters that cover all aspects of a graph, use the `args()` function to get a look.

```
args(theme)
```

```
## function (..., line, rect, text, title, point, polygon, geom,
##     spacing, margins, aspect.ratio, axis.title, axis.title.x,
##     axis.title.x.top, axis.title.x.bottom, axis.title.y, axis.title.y.left,
##     axis.title.y.right, axis.text, axis.text.x, axis.text.x.top,
##     axis.text.x.bottom, axis.text.y, axis.text.y.left, axis.text.y.right,
##     axis.text.theta, axis.text.r, axis.ticks, axis.ticks.x, axis.ticks.x.top,
##     axis.ticks.x.bottom, axis.ticks.y, axis.ticks.y.left, axis.ticks.y.right,
##     axis.ticks.theta, axis.ticks.r, axis.minor.ticks.x.top, axis.minor.ticks.x.bottom,
##     axis.minor.ticks.y.left, axis.minor.ticks.y.right, axis.minor.ticks.theta,
##     axis.minor.ticks.r, axis.ticks.length, axis.ticks.length.x,
##     axis.ticks.length.x.top, axis.ticks.length.x.bottom, axis.ticks.length.y,
##     axis.ticks.length.y.left, axis.ticks.length.y.right, axis.ticks.length.theta,
##     axis.ticks.length.r, axis.minor.ticks.length, axis.minor.ticks.length.x,
##     axis.minor.ticks.length.x.top, axis.minor.ticks.length.x.bottom,
##     axis.minor.ticks.length.y, axis.minor.ticks.length.y.left,
##     axis.minor.ticks.length.y.right, axis.minor.ticks.length.theta,
##     axis.minor.ticks.length.r, axis.line, axis.line.x, axis.line.x.top,
##     axis.line.x.bottom, axis.line.y, axis.line.y.left, axis.line.y.right,
##     axis.line.theta, axis.line.r, legend.background, legend.margin,
##     legend.spacing, legend.spacing.x, legend.spacing.y, legend.key,
##     legend.key.size, legend.key.height, legend.key.width, legend.key.spacing,
```

```
##      legend.key.spacing.x, legend.key.spacing.y, legend.key.justification,
##      legend.frame, legend.ticks, legend.ticks.length, legend.axis.line,
##      legend.text, legend.text.position, legend.title, legend.title.position,
##      legend.position, legend.position.inside, legend.direction,
##      legend.byrow, legend.justification, legend.justification.top,
##      legend.justification.bottom, legend.justification.left, legend.justification.right,
##      legend.justification.inside, legend.location, legend.box,
##      legend.box.just, legend.box.margin, legend.box.background,
##      legend.box.spacing, panel.background, panel.border, panel.spacing,
##      panel.spacing.x, panel.spacing.y, panel.grid, panel.grid.major,
##      panel.grid.minor, panel.grid.major.x, panel.grid.major.y,
##      panel.grid.minor.x, panel.grid.minor.y, panel.ontop, panel.widths,
##      panel.heights, plot.background, plot.title, plot.title.position,
##      plot.subtitle, plot.caption, plot.caption.position, plot.tag,
##      plot.tag.position, plot.tag.location, plot.margin, strip.background,
##      strip.background.x, strip.background.y, strip.clip, strip.placement,
##      strip.text, strip.text.x, strip.text.x.bottom, strip.text.x.top,
##      strip.text.y, strip.text.y.left, strip.text.y.right, strip.switch.pad.grid,
##      strip.switch.pad.wrap, complete = FALSE, validate = TRUE)
## NULL
```

To make figure files (PNG, TIFF, and PDF)

R has the ability to make figures using built-in graphic devices like `png()`, `tiff()`, and `pdf()` and more. This can be great when making figure panels. Here is an example making a figure out of the plots we already made. It can take some time to find the right fit for the plot desired so some trial and error are required. This where using ggplot objects is convenient packaging all parts of the graph in one place. You should make an output folder for figures when making them, this will keep the working directory from being cluttered with images.

```
#Make a png
png(filename = "output/my_bar_test1.png",res=600,
    width=8,height=5,units="in",
    bg = "white",
    type ="cairo")
p1
dev.off()

#Make a tiff
tiff(filename = "output/my_bar_test2.tiff",res=600,
    width=8,height=5,units="in",
    bg = "white",
    type ="cairo")
p2
dev.off()

#Make a pdf
pdf(file = "output/my_bar_test3.pdf",
    width=8,height=5,
    bg = "white")
p2
dev.off()
```

Conclusions

Now you can plot data with base R and using the ggplot2 package and reproduce plots easily with themes. There are so many packages that extend ggplot2 even further and you should learn these as your plotting needs change.