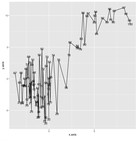
Packages and set data set

In [15]:
```
library(ggplot2)
library(dplyr)
setwd("/Users/danielkent/Desktop/Statistic_I/HW2/H2Rand00Walk.csv")
df2 <- read.csv("/Users/danielkent/Desktop/Statistic_I/HW2/HQ2.csv")
```

Q1 (2 points) Random walk [1] is a mathematical object, known as a stochastic or random pro- cess, it is easy to be understood by imaging that a drunk person walking. Random walk is used for simulating the price change in the finance application. Draw a 2-dimension random walk path plot using H2RandomWalk.csv data.

In [3]:
```
rw_plot1 = ggplot(df, aes(x=rw.axis, y=rw.axis)) + geom_text(aes(label=step)) + geom_line()
print(rw_plot1)
```



Q2 (5 points) Draw a diagram, a box plot and a pie plot that discribe the frequency of the data in HQ2.csv. (You may classify the data using the interval with range 5 if needed.)

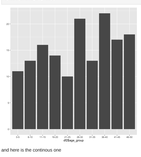
Here I classify the data using the interval with range 5 using dplyr package functions

In [4]:
```
df2 <- df2 %>%

                    mutate(
                      # Create categories
                      age_group = dplyr::case_when(
                        age < 5   ~ "0-5",
                        age > 5  & age <= 10 ~ "6-10",
                        age > 10 & age <= 15 ~ "11-15",
                                    age > 15 & age <= 20 ~ "16-20",
                        age > 20 & age <= 25 ~ "21-25",
                        age > 25 & age <= 30 ~ "26-30",
                        age > 30 & age <= 35 ~ "31-35",
                                    age > 35 & age <= 40 ~ "36-40",
                        age > 40 & age <= 45 ~ "41-45",
                                    age > 45 & age <= 50 ~ "46-50"

                      ),
                      # Convert to factor
                      age_group = factor(
                        age_group,
                        levels = c("0-5","6-10","11-15","16-20","21-25","26-30","31-35","36-40","41-45","46-50")
                      )
                    )

glimpse(df2)
```

```
Rows: 155
Columns: 3
$ id        <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 1…
$ age       <chr> 41.18, 5.89, 12.53, 43.67, 11.08, 2.79, 4.46, 17.34, 14.15, …
$ age_group <fct> 41-45, 6-10, 11-15, 41-45, 11-15, 0-5, 0-5, 16-20, 11-15, 46…
```

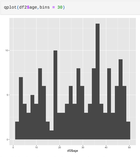
Draw a diagram(interpreted # as histograms to know the frequency) and here is the discrete one because I group it

In [5]:
```
qplot(df2$age_group)
```



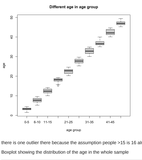
and here is the continous one

In [6]:
```
qplot(df2$age,bins = 30)
```



box plot (to show the age distribution in each group)

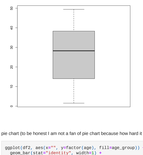
In [7]:
```
boxplot(age~age_group,data=df2,main="Different age in age group",xlab="age group",ylab="age")
```



there is one outlier there because the assumption people >15 is 16 already for convenient so if his/her 15th birthday already past then I assume he/she is doing his/her 16th year

Booplot showing the distribution of the age in the whole sample

In [8]:
```
boxplot(df2$age)
```



pie chart (to be honest I am not a fan of pie chart because how hard it is to tell if there is more than 3 groups)

In [9]:
```
ggplot(df2, aes(x="", y=factor(age), fill=age_group)) +
  geom_bar(stat="identity", width=1) +
  coord_polar("y", start=0)+
  theme_void()
```

Q3 (3 points) There is a 4-dimension dataset (y, x1, x2, x3) where x1 is the categorical data (e.g species, sex...) and y, x2, x3 are continuous data (e.g temperture, age...). How would you visualize the data?

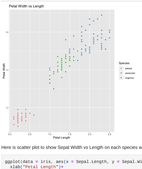
Here I use one of the most common dataset in R which is Iris dataset which have categorical data (Species) and continous data (Sepal length, Sepal width,Petal Length, Petal Width

In [10]:
```
glimpse(iris)
```

```
Rows: 150
Columns: 5
$ Sepal.Length <dbl> 5.1, 4.9, 4.7, 4.6, 5.0, 5.4, 4.6, 5.0, 4.4, 4.9, 5.4, 4.…
$ Sepal.Width  <dbl> 3.5, 3.0, 3.2, 3.1, 3.6, 3.9, 3.4, 3.4, 2.9, 3.1, 3.7, 3.…
$ Petal.Length <dbl> 1.4, 1.4, 1.3, 1.5, 1.4, 1.7, 1.4, 1.5, 1.4, 1.5, 1.5, 1.…
$ Petal.Width  <dbl> 0.2, 0.2, 0.2, 0.2, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1, 0.2, 0.…
$ Species      <fct> setosa, setosa, setosa, setosa, setosa, setosa, setosa, s…
```

Here is scatter plot to show Petal Width vs Length on each species

In [11]:
```
ggplot(data = iris, aes(x = Petal.Width, y = Petal.Length))+
  xlab("Petal Length")+
  ylab("Petal Width")+
  geom_point(aes(color = Species,shape=Species))+
  ggtitle("Petal Width vs Length")
```



Here is scatter plot to show Sepal Width vs Length on each species which seem to have cluster and linear relationship

In [12]:
```
ggplot(data = iris, aes(x = Sepal.Length, y = Sepal.Width))+
  xlab("Petal Length")+
  ylab("Petal Width")+
  geom_point(aes(color = Species,shape=Species))+
  ggtitle("Petal Width vs Length")
```

While the Petal is more diverse and harder to differenciate cluster and relationship

In [16]:
```
par(mfrow=c(2,2))
ggplot(iris, aes(Species, Petal.Width, fill=Species)) +
  geom_boxplot()+
  scale_y_continuous("Petal Width", breaks= seq(0,30, by=.5))+
  labs(title = "Iris Petal Width Box Plot", x = "Species")

ggplot(iris, aes(Species, Petal.Length, fill=Species)) +
  geom_boxplot()+
  scale_y_continuous("Petal Length", breaks= seq(0,30, by=.5))+
  labs(title = "Iris Petal Length Box Plot", x = "Species")

ggplot(iris, aes(Species, Sepal.Width, fill=Species)) +
  geom_boxplot()+
  scale_y_continuous("Sepal Width", breaks= seq(0,30, by=.5))+
  labs(title = "Iris Sepal Width Box Plot", x = "Species")

ggplot(iris, aes(Species, Sepal.Length, fill=Species)) +
  geom_boxplot()+
  scale_y_continuous("Sepal Length", breaks= seq(0,30, by=.5))+
  labs(title = "Iris Sepal Length Box Plot", x = "Species")
```