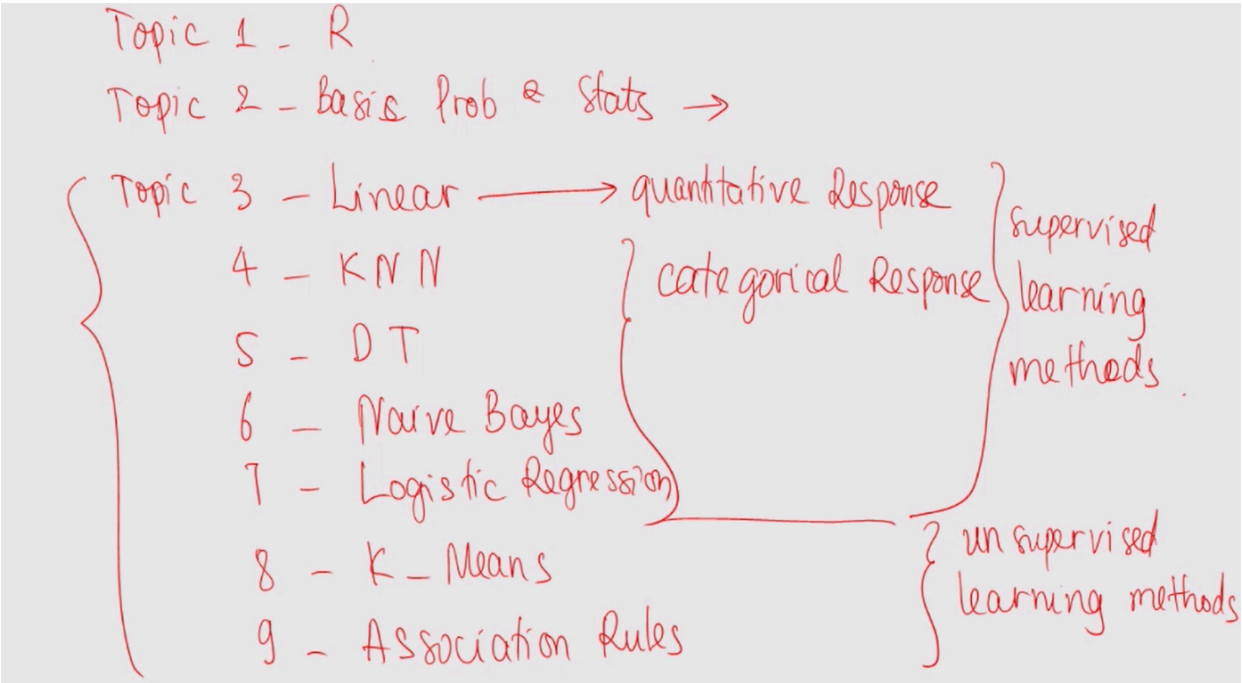


Histogram:
#for left skewed histograms, the left tail is longer than the right tail
#ie theres more values on the left edge than the right edge, some vid said the left side looks more squished than the right side

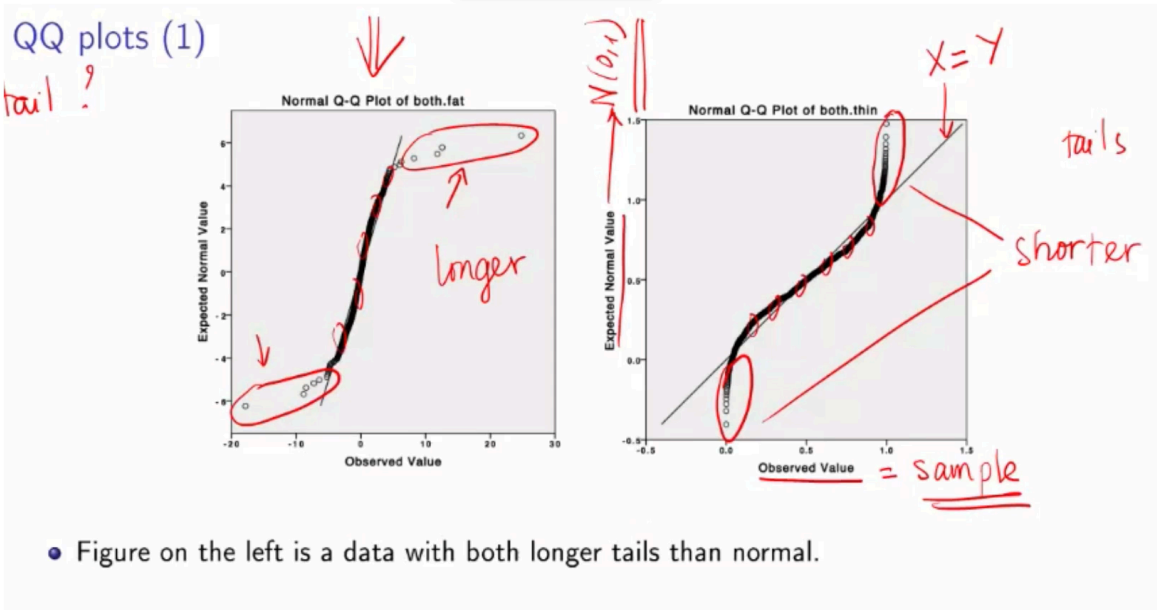
#vice versa for right skew

$$\text{outlier} = \begin{cases} > Q_3 + 1.5\,IQR \\ < Q_1 - 1.5\,IQR \end{cases}$$

$$IQR = Q_3 - Q_1$$

QQ Plots:

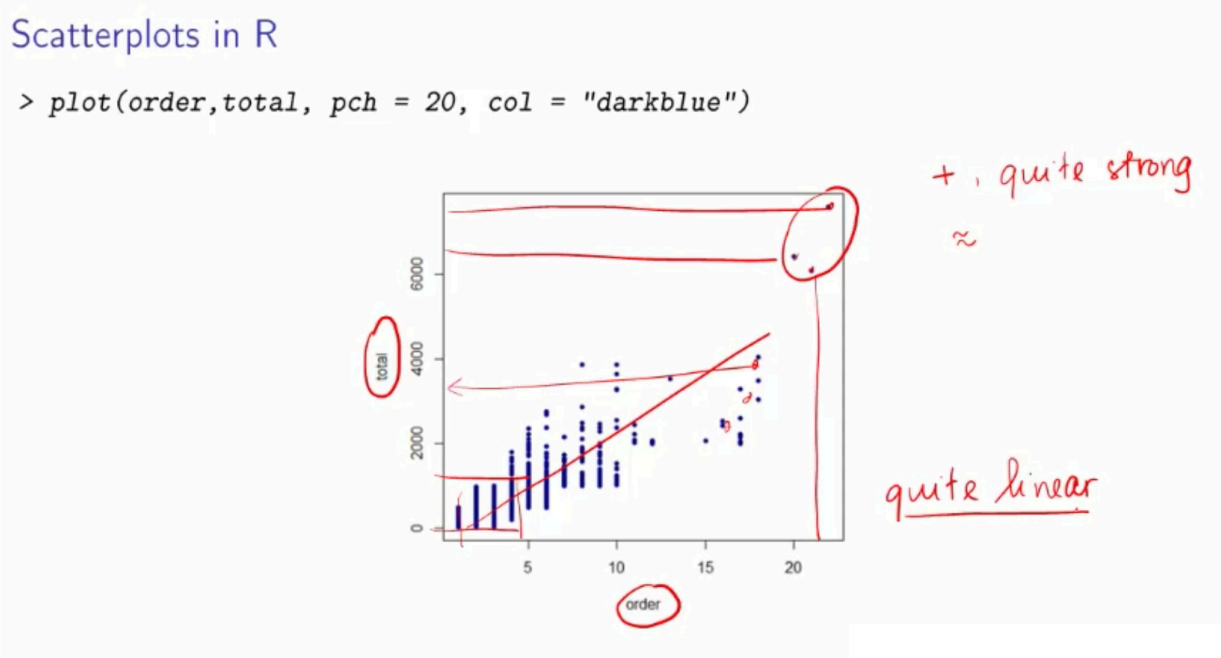
- Stands for “Quantile-Quantile” Plot
- Used to see if the sample follows (approx) a normal distribution or not
    - So the plot matches the sample sample quantiles against the theoretical quantiles of a N(0,1) distribution



- Figure on the right is for data with both tails shorter than normal

- For figure on the right, notice there are some plots not *on* the line, but does not show a strong trend that deviates from the straight line (ie not suddenly curving up or smth), so be flexible on it lol

SCATTERPLOT

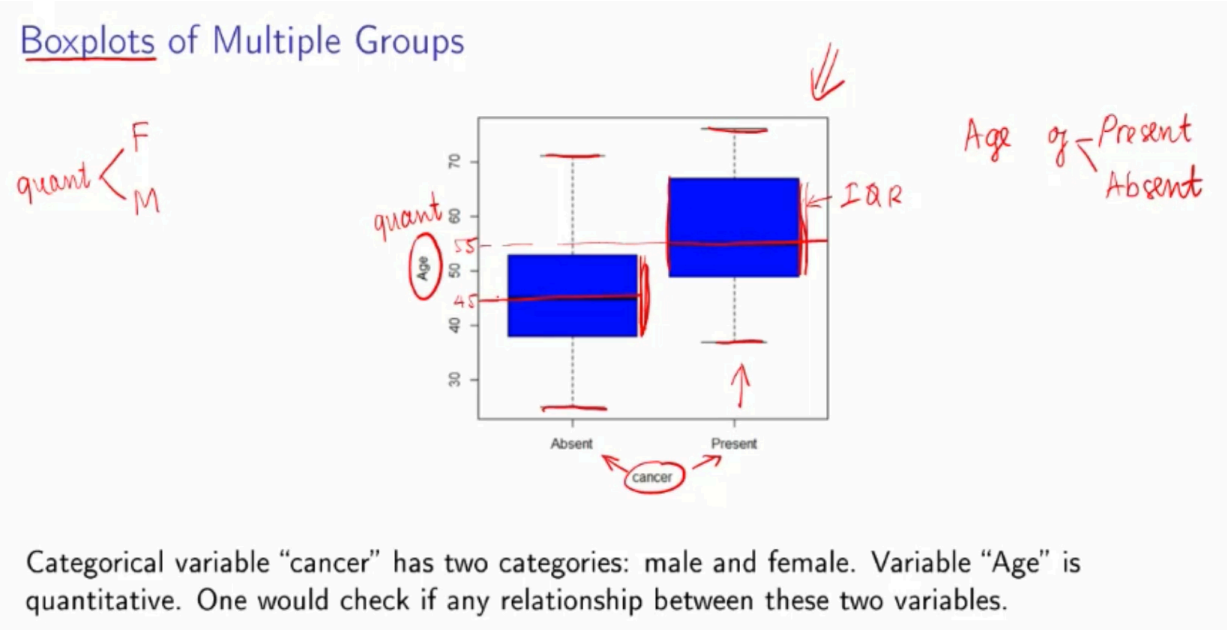


- X is the number of orders and Y is the number of sales
- Points are not random; seems like forming a trend => 2 variables are associated

    - Association is positive:
      when order is small => total sales is small,
      when order is large => total sales is large
    - Points do not form a straight line nicely, but approx it is quite straight => linear
    - Does not form any pattern of non-linear (eg quadratic/sin curve)
- Outliers: Some obvs that deviate from the rest ie the circled region, extremely large number of orders & large number of sales
- **TLDR the association is approximately linear, with a few extremely large values**

- **"plot of gender by align" => y by x => gender is y and align is x**

BOXPLOT



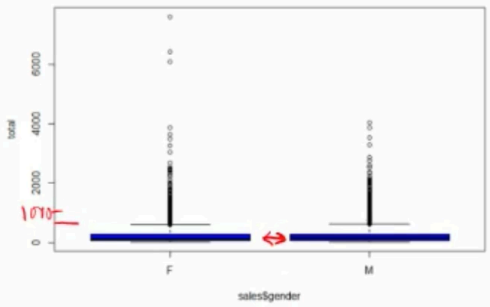
Categorical variable "cancer" has two categories: male and female. Variable "Age" is quantitative. One would check if any relationship between these two variables.

- **Compare: are the medians similar, and are the boxes overlapping or not (ie is the IQR within similar ranges)**
- **Both groups no outliers**
- **If the distribution of each group is unimodal, they both could be quite normal**
- **Range is quite similar**
- **Boxes are overlapping but not much**
    - **IQR or the group Present is larger than the group Absent**
      I.e spread in age in the center part of Present is larger
- **Median age of Present > median age of Absent**
    - **Indicates that age could affect cancer status**

Boxplots of Multiple Groups in R

gender < F, M

```
> attach(sales)
> boxplot(total ~ gender)
```



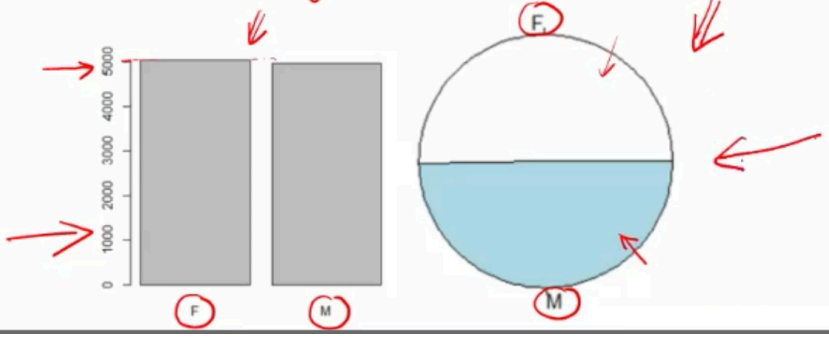
There is no obvious difference in the total sales of the customer's gender. The median of two groups are similar, and the IRQ are about the same.

- **Gender is categorical, sales is quantitative**
- **Both have majority of datapoints below 1,000**
- **Both have many outliers**
- **Both boxes are overlapping and similar in size**
- **Median values are similar**
- **HENCE no obvious difference**

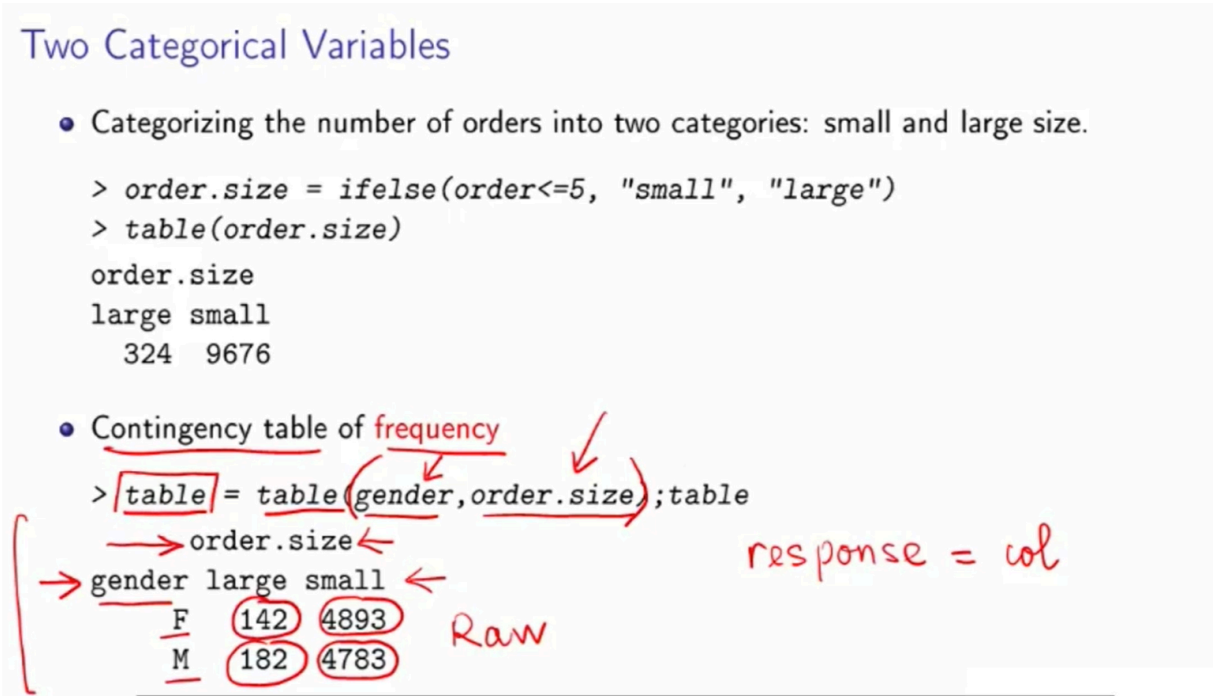
Barplot and Pie Chart

Sales → gender < F, M

```
> count = table(gender)
> count # frequency table
gender
   F    M
5035 4965
> barplot(count)
> pie(count)
```

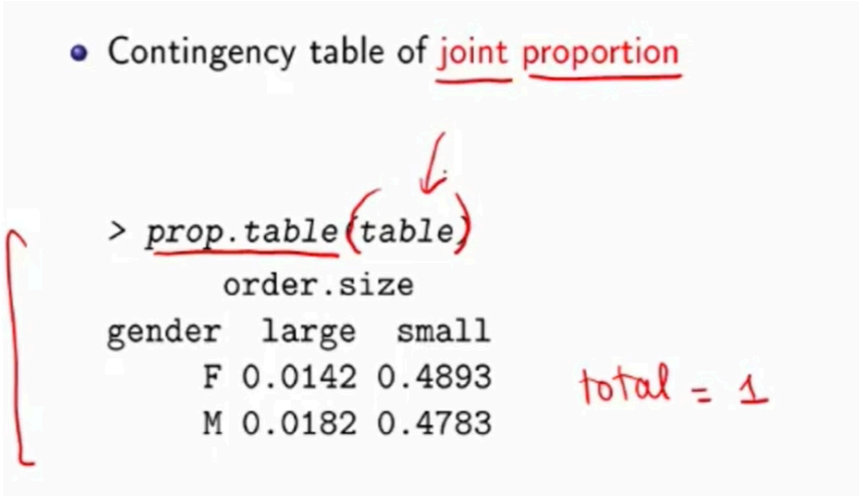


- **Females are the MODAL VALUE because they're the most frequent categorical value under gender**



- **Response variable is the dependent variable lol, cus it changes or 'responds' to changes in the independent variable**
- **Response variable is usually put as the 2nd parameter in table() so it becomes the column. Its like table(row, column)**

CONTINGENCY TABLE



- **Total of all the rows and columns is 1**
- **prop.table(frequency table created using table()) so 1 parameter only**

Contingency Tables

large for → M ↘ F ↘ larger ⇒

- Contingency table of proportion by gender * 100

```
> tab = prop.table(table, "gender") # proportion by gender
> tab
        order.size
gender       large       small
     F 0.02820258 0.97179742
     M 0.03665660 0.96334340
```

total: F → 1, M → 1

Among orders by females, 2.82% are large orders while 3.67% of orders by males are large.

There is difference, but the difference is not large.

```
> tab
       order.size
gender      large      small
     F 0.02820258 0.97179742
     M 0.03665660 0.96334340
>

> 0.028/0.972
[1] 0.02880658
> 0.037/0.963
[1] 0.0384216
> tab[1]
[1] 0.02820258
> tab[2]
[1] 0.0366566
> tab[3]
[1] 0.9717974
> tab[4]
[1] 0.9633434
> 
```

Odds Ratio

- Odds ratio is the ratio of two odds of success: odds of larger orders in the female group (0.029), and odds of larger orders in the male group (0.038).

$$OR = \frac{0.029}{0.038} = 0.76. \rightarrow OR = \frac{1}{0.76} \approx 1.3$$

odds of large in F

What does this value mean?

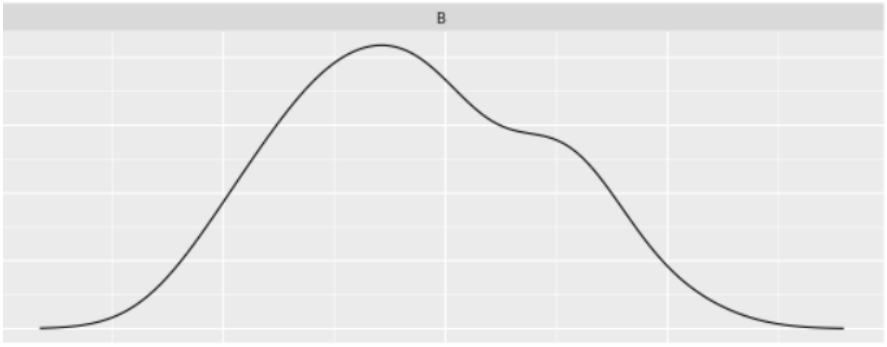
- **0.76: the odds of having large order amongst female is 0.76 times the odds of having large orders among males**
- **If you flip the numerator and denominator, the odds of having large order amongst males is 1.3 times the odds of having large orders amongst females (reciprocal of 0.76) ⇒ meaning is still the same**
- **Note that odds of success = p / (1-p)**

- For example, in simple linear regression with only one predictor, we assume a model of the form

$$y \approx f(x) = \beta_0 + \beta_1 x.$$

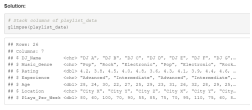
$f(x) = \beta_0 + \beta_1 \cdot x^2$

linear



This is considered unimodal symmetric

Add on pls. OG is from NM2204

THING U WANT TO DO	COMMAND(S)	REMARKS
Import the ***data-set***, `playlist_data.csv` Import .txt file: use read.csv() but include parameters sep = "", header = TRUE	read_csv("playlist_data.csv") read.csv("~/Github/DSA1101 Slayers/datasets/Colleges.txt", sep = "", header = TRUE) Put header = TRUE when the first row is the names of the variables	REQUIRES TIDYVERSE LIBRARY
Assign the ***data-set*** to a variable, `playlist_data`	playlist_data <- read_csv("playlist_data.csv")	REQUIRES TIDYVERSE LIBRARY
Install packages	install.packages() PACKAGESSSSSS with an s	No need re-install if used library before.
Get more information about `read_csv()` command	?read_csv()	
Display all the columns of the variable stacked one below another	glimpse(playlist_data)	
Any type of filtering library(dplyr)	dplyr SPELLING PLEASE	

distinct(): find the unique senders		
Print all lines/specified number of lines	%>% print(***n = length(***playlist_data$DJ_Name))	Filter (%>%) is required
Conjugate strings within a print statement paste0()	paste0("hello", 4) Prints hello4 Note that usage of ",”does not automatically give a space paste0("the equation is: price(hat) = ", M2$coeff[1], " + ", M2$coeff[2], "price + ",M2$coeff[3], "I(NW = 0)")	

Append vector	col = c(og_vector, new_values)
	Eg col = c(col, "light")
	
	OR
	append(og_vector, new_values)
	
	OR for an INDEXED LIST
	(typically with for loops)
	
	skibbidi = c()
	
	for (i in 1:15) {
	  kout = kmeans(standardised.X, centers = i)
	  skibbidi[i] = kout$withinss
	}	

ggplot garbage	ggplot(data = playlist_data, mapping = aes(x=Age,y=Rating)) +
	  geom_point(shape=23, fill = "purple", size=3) +
	  labs(x = "Age", y = "Rating", title = "Scatter graph of Age against Ratings", caption = "My insight is that since there are both high and low ratings for both younger and older DJs, ratings are not dependent on age")
		Refer to documentation: https://ggplot2.tidyverse.org/reference/#plot-basics
		Refer to Challenge 2

Initialize list	student_info <- ***list***(student_names=c("Alice","Bob","Catherine"), scores=c(85L, 92L, 78L), passed=c(TRUE,	Refer to Challenge 3, Q10

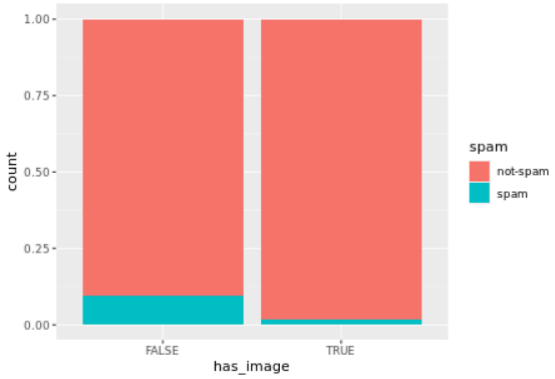
	TRUE, FALSE))	
Explicit coercion (conversion)	prices <- ***as.numeric***(prices)	Refer to Challenge 3, Q12
Implicit coercion (conversion)	nums <- c(5, 10, 15) noms <- c("apple", "banana", "cherry") ***numnoms <- c(nums, noms)*** Combining the numeric and character vectors will implicitly coerce the numeric vector to character. The resulting vector will be character type. R coerces data to a common type when vectors are combined. ***R coerces data to a common type when vectors are combined***	Refer to Challenge 3, Q13
What does unlist() do?	It converts a list to a vector.	
Filter: tl;dr	comm_data %>% ***filter(date == "2/8/2023" & channel == "Twitter")*** %>% select(date, channel, message) common_cyl <- cars %>% filter(ncyl %in% c(4, 6, 8))	The AND(&), OR(|) all apply here https://www.tutorialspoint.com/r/r_operators.htm Datacamp
arrange()	Will arrange rows in ASCENDING ORDER. To reverse order, put desc()	
create a new data frame with summarised data summarise() Summarising based on other variable: eg summarise ave sentiment FOR EACH sender (summarise variable A categorised by variable B)	%>% summarise(total_char = sum(nchar(message))) %>% summarise(avg_sentiment=mean(sentiment)) %>% group_by(sender) %>% summarise(avg_score=mean(sentiment))	https://dplyr.tidyverse.org/reference/summarise.html Challenge 4, Q8 & 12 Challenge 4, Q7
Create dataframe / data frame	df <- data.frame(first_column, second_column)	
Access ONE specific column only OR Access/limit to certain columns	data_frame$column_name For MULTIPLE columns: use %>% select()	

Access vector within list, given vector name	**mixed_data** <- list(**numeric_vector = c(10, 20, 30)**, character_vector = c("red", "green", "blue"), logical_vector = c(TRUE, FALSE, TRUE)) mean_numeric <- mean(***mixed_data$numeric_vector***)	Challenge 3, Q16
Access a vector inside of a list, given the name of the vector Eg uk bob = "tire", you want to find "tire" and uk bob	**score_bob <-** **student_info$scores[student_info$names == "Bob"]**	Challenge 3, Q10
Find and ***print the indices of all occurrences of the word*** "apple."	words <- c("apple", "banana", "cherry", "apple") **indices <-** ***which(words == "apple")*** print(indices)	Challenge 3, Q19
Create frequency table	**table(row, column)** **For all categorical variables data**	Topic 2 Video 8
Create contingency table Create a table where all the rows OR columns add to 1	**prop.table(name_of_freq_table)** **prop.table(name_of_freq_table, "name_of_row/column")** **Eg tab = prop.table(table, "gender")#proportion by gender** Remember if using a single variable, don't use the variable directly ie must do: prop.table(table(Churned)) Instead of prop.table(Churned) **For all categorical variables data** **NOTE: prop.table(name_of_freq_table)with NO ADDITIONAL PARAMETERS will make the WHOLE TABLE TO ADD TO 1.** **i.e.** **[,1] [,2] [,3]** **[1,] 1 3 5** **[2,] 2 4 6** **will become**	Topic 2 Video 8

	[,1] [,2] [,3] **[1,] 0.04761905 0.1428571 0.2380952** **[2,] 0.09523810 0.1904762 0.2857143** **Where total = 1+2+3+4+5+6 = 21** **[1,1] = 1/21 = 0.04761905** **[2,1] = 2/21 = 0.09523810** **To get proportions by row, try** q = table(Churned) q = q/rowSums(q) Same goes for colSums() if columns need to be added. [OR do **q = prop.table(q, "gender")**#proportion by gender **but i dont trust you to do this**]	
Create bar plot No library needed	**barplot()** barplot(max.temp, main = "Maximum Temperatures in a Week", xlab = "Degree Celsius", ylab = "Day", names.arg = c("Sun", "Mon", "Tue", "Wed", "Thu", "Fri", "Sat"), col = "darkred", horiz = TRUE)	
Create a Boxplot Find outlier values of boxplot (without ggplot)	**boxplot(total, xlab = "variable", col = "blue")** **Outlier = boxplot(column_variable)$out** **Eg** **outtie = boxplot(fev_var, xlab = "FEV", col = "blue")$out ; outtie**	
Comment on boxplot outliers		
Find the position of the outliers, ie the index of outliers	**index = which(FEV %in% c(out))** **Note FEV is the name of the variable/column, not the entire db** **FEV %in% c(out) gives you a logical list of TRUEs and FALSEs ⇒ which() will isolate the TRUEs and return the indexes of the outliers**	

Get number of rows/columns dim()	**Returns no. rows (obs) and columns (variables)** **Stands for dimensions** **dim(db)**	
Directly copy dataset into Rstudio, by implicitly defining the variables based on column names attach() Note spelling!	**attach(db_name)** **Now the name of the dataset is fev** **Can reference the variables/column directly eg.** **Forced_Expiratory_Volume <- read.csv("~/GitHub/DSA1101 Slayers/datasets/FEV.csv")** **attach(Forced_Expiratory_Volume)** **hist(FEV, col = 10, freq = FALSE)** **#where FEV is the name of the variable from the Forced_Expiratory_Volume db**	Tutorial 2
Is the sample of (variable) normally distributed?	**USE QQPLOT. IF QN DOESNT ASK, INITIATE IT YOURSELF** **qqnorm(fev_var, pch = 10)** **qqline(fev_var, col = "red")**	Tutorial 2
predict()	**predict(model_fit, newdata = , type = "prob")** **type = "class" will just give u the most likely category.** **Note that if categorical value, keep the factor = c("3") or factor = c("1") yada yada** **Note if new data has multiple predictors/catagories, put the, in a data frame eg new_data = data.frame(width = 5, length = "yes")** **NEW DATA IS LIKE ALL THE PREDICTORS, DO NOT PUT UR RESPONSE VARIABLE AS UR NEW DATA** **Someone tell me why the FUCK new.data and newdata are 2 DIFFERENT BUT COMPLETELY VALID INPUT VARIABLES** **USE newdata**	

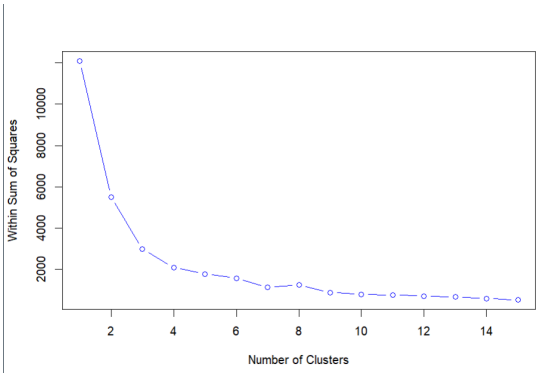
lm(price ~ area)$coeff	**Linear regression** **M1 = lm()** **summary(M1)**	

geom_bar usage
 	
How to get bar chart to go of proportions (like percentage, in a piechart, but in bar from)
	email %>%
	  mutate(has_image = image>0) %>%
	  ggplot(aes(x = has_image, fill = spam)) +
	  geom_bar(position = "fill")
	
	 
	
		Datacamp

correlation cor(heighty, fev_var)	cor(1st_var, 2st_var) #does NOT matter which variable goes first #idt it works for categorical variables	

Create a decision tree
 	
Libraries:
- rpart
- rpart.plot
 	
Relevant functions:
- rpart()
- rpart.control()
	fit <- rpart(subscribed ~ job + marital + education + default + housing + loan + contact + poutcome,
	  method = "class",
	  data = bankdata,
	  control = rpart.control(minsplit = 1),
	  parms = list(split = "information"))
	
	method = "class", #tells R to return the category of response (yes or no)[DSA1101 will only use method = "class", no "anova" or "poision"]
	
	METHOD IS A STRING VARIABLE HOR ie method = "class"
		Topic 5 Pre-lect vid 3

	control = rpart.control(minsplit = 1), #tells R how to split the node; minsplit = 1 means a branch is created when there is at least 1 observation in that branch => ***tells R how big we want the tree to be*** (how many branches we want) parms = list(split = "information")) # what criteria to use to choose the root node & internal nodes; either info gained or gini index; default val is gini **TO PRINT THE TREE:** rpart.plot(fit, type = 4, extra = 2, clip.right.labs = FALSE)	
standardise all the predictors (the x es)	Lag1 = scale(Lag1)	
Get the inverse of a matrix Transpose the matrix Multiply matrix by matrix	solve(matrix_name) t(matrix_name) matrix_name %*% matrix_name	
Create a matrix	cbind(1st_desired_col, 2nd_desired_col) Eg cbind(1, SAT) #SAT is variable name returns SAT [1,] 1 1315 [2,] 1 1310 [3,] 1 1336 [4,] 1 1300 [5,] 1 1250 [6,] 1 1320 [7,] 1 1290 Or can do cbind(c(1,2), c(3,4)) [,1] [,2] [1,] 1 3 [2,] 2 4	
Create scatterplot (Without ggplot)	plot(x, y, pch = 20) #notice its x then y please	

	#pch is just the shape of the points, can ignore For this type (type = "b"), plot(1:K, wss, col = "blue", type="b", xlab="Number of Clusters", ylab="Within Sum of Squares")  	
Get R square value / R^2 / R2 Get adjusted R square	M1 = lm(price ~ size) summary(M1) # take from here OR summary(hdb.model)$r.squared adjusted R square: summary(M1)**$adj.r.squared**	
Form equation of Linear Model M2$coeff	M2$coeff ## (Intercept) size NW1 ## -15257.51385 77.98513 30569.08729 M2$coeff[1]: β0 M2$coeff[2]: β1 M2$coeff[2]: β2	

knn()	Requires library(class) knn.pred = knn(train.x, test.x, train.y, k = 1)	Documented in Topic 4 my own code
Create histogram (without ggplot)	hist(Temperature, main = "Maximum daily temperature at La Guardia Airport", xlab = "Temperature in degrees Fahrenheit", xlim = c(50,100), col = "darkmagenta", freq = FALSE)	
Overlay density plot line over histogram	lines(density(data$x), col = "red")	
Sample data randomly sample(values, size_of_subsample)	sample(my_vec, size = 3) sample(1:10, size = 3) Will randomly give 3 numbers from 1 to 10	
standardised features scale(all_relavent_predictors)	standardized.X = scale(caravan[,-86]) # scaling all the data set, except the last column	
Forming Naive Bayes Classifier Requires library(e1071)	model <- naiveBayes(Enrolls ~ Age+Income+JobSatisfaction+Desire, traindata)#, laplace=0)	

	model <- naiveBayes(response_var ~ predictor1 + predictor2, traindata) Then use: results <- predict(model,testdata,"raw"); results results[2]/results[1]	

Create ROC / Find AUC
 	
Requires library(ROCR)
	Drop unnecessary columns first.
	
	Idea: use testing data, see how well the model does. So split the test set into predictors and response.
	
	#prelude (still using predict)
	nb_prediction = predict(nb_model,
	newdata = banktest[,-ncol(banktest)],
	type = 'raw')
	NOTE its banktest[,-ncol(banktest)] WITH THE NEGATIVE SIGN SO ITS EVERYTHING **BUT** THE LAST COLUMN => ***REMOVES THE RESPONSE VARIABLE***
	
	type = 'raw' will give raw probabilities
	If type = "response" doesnt work than idk just change to "class" or "raw" instead
	
	library(ROCR)
	
	score <- nb_prediction[,c("yes")]
	#this will return all the probabilities that each outcome will be positive (or 'yes').
	#so if the prediction of 'yes' is 0.9, it's very likely to be yes,, if the prediction
		Tutorial 8 and 9

	of 'yes' is 0.001 then its very likely to be no actual_class <- banktest$subscribed == 'yes' #this converts all to TRUE and FALSE which will be treated as 1 or 1 (due to how the method works) pred <- prediction(score , actual_class) #this formats the input so 'score' and 'actual_class' match with each other perf <- performance(pred , "tpr", "fpr") #now we can plot the figure plot(perf, lwd = 2) #lwd specifies how thick the curve is abline(a = 0, b = 1, col = "blue", lty = -3) #create diagonal curve that slices square into half by its diagonal	

Predict for ROC / AUC
Ie using ROCR to predict
 	
This is the main bits, repeated from previous row.
 	
prediction() followed by performance(), then plot()
	#TO FORMAT THE INPUT
	pred <- prediction(score , actual_class)
	
	perf <- performance(pred , "tpr", "fpr")
	
	plot(perf, lwd =2)	

	abline(a=0, b=1, col ="blue", lty =3)	

Determine AUC value	AUC value determines what is the best threshold for a negative to become a positive (usually delta)
	
	threshold <-
	round(as.numeric(unlist(perf@alpha.values))
	)
	
	fpr <-
	round(as.numeric(unlist(perf@x.values)), 4)
	
	tpr <-
	round(as.numeric(unlist(perf@y.values)), 4)
	
	#adjust margins and plot TPR and FPR
	par(mar = c(5,5,2,5))
	
	#the plotting stuff: just copy paste LMAO
	plot(alpha ,tpr , xlab ="Threshold", xlim
	=c(0 ,1) ,
	ylab = "True positive rate ", type
	="l", col = "blue")
	par(new ="True")
	plot(alpha ,fpr , xlab ="", ylab ="", axes
	=F, xlim =c(0 ,1) , type ="l", col = "red"
	)
	axis(side =4) # to create an axis at the
	4th side
	mtext(side =4, line =3, "False positive
	rate")
	text(0.18 ,0.18 , "FPR")
	text(0.58 ,0.58 , "TPR")
		https://sets.netlify.app/module/65d9a044a1d9248bb0c34963/topic/65d9a076a1d9248bb0c34b55/6619fd77da66393bf2be69e8 not relavent

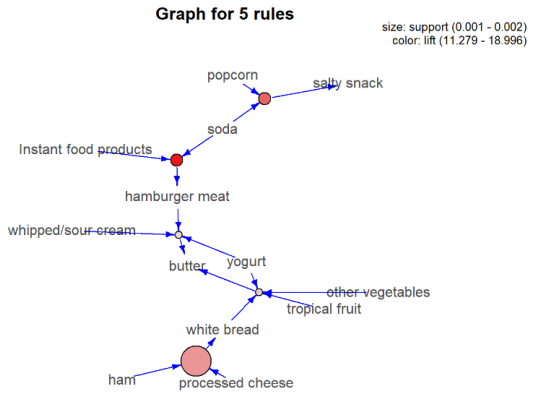
Final code for ROC / AUC for KNN	pred.knn = knn(train.X, test.X, cl = train.Y, k = 30) # "prob = TRUE" is NOT added --> to get the class labels
	pred.knn.prob= knn(train.X, test.X, cl = train.Y, k = 30, prob = TRUE) # --> to get the probabilities of winning labels
	winning.prob = attr(pred.knn.prob, "prob") # to extract the winning probabilities
	
	n = length(test.Y)
	prob = numeric(length = 0) # n is the length of "test.y" used in knn() above
	for (i in 1:n) {
	prob[i] = ifelse(pred.knn[i] == "yes", winning.prob[i], 1 - winning.prob[i])
	}
	helppain = prediction(prob, test.Y)
	rocObjKNN = performance(helppain, measure = "tpr", x.measure = "fpr")
	plot(rocObjKNN, lwd =2)
	abline(a=0, b=1, col ="blue", lty =3)
		Refer to statistical assignment (and below this document)

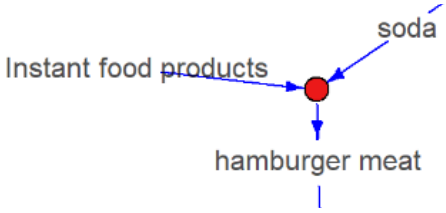
Logistic regression Generalised Linear Regression (GLM)	M1 <- glm(Churned ~ . , # . is all columns except the response col data = churn, family = binomial(link = "logit")) #logit is default tho Note: Churned must be equal to 0 and 1, it can be as.factor(), but the category names MUST be 0 or 1. Ironically it doesn't matter if you converted to factor, for glm.	

	REMEMBER ur LHS will be log(p/(1-p)), the log odds of having disease or wtvr. So the next step is finding p itself.	
k-means clusters No external library needed	kout = kmeans(hdb[,c("floor_area_sqm", "amenities")], centers = 2) #centers = nummber of clusters #note kmeans data only accepts dataframes **Plot the clusters** plot(floor_area_sqm, hdb$amenities, col = kout$cluster) #col is colours, so colours differentiate the 2 clusters **Centroids of the clusters** kout$centers #a matrix of cluster centers # floor_area_sqm amenities # 1 69.46017 7.448739 # 2 65.40782 37.279330 # so these are the coordinates of the 2 centroids (of the 2 clusters) **Size of each cluster** kout$size #the number of pts in each cluster # [1] 595 179 **Within Sum of Squares** kout$withinss	STANDARDISE THE INPUTS before starting K-means - Use scale() If doing manually, ie given all the indiv plot points, USE plot() TO DETERMINE WHERE ALL THE PLOTS ARE REMEMBER K-MEANS IS VERY SCATTERPLOT BASED

	#sum of squares of all the different clusters added together kout$tot.withinss	
Association Rules	library(arules) library(arulesViz) Groceries@itemInfo[1:10,] #all columns Groceries@data[,100:110] #all rows #note the 2nd one will give u the sparse matrix (unreadable dot and slash)	
Return the actual itemsets (instead of the general data / summary)	inspect() inspect(sort(itemset.1, by = "support"))	
Attain itemsets that fit a certain support level	itemset.1 = apriori(Groceries, parameter = list(minlen = 1, maxlen = 1, support = 0.02, target = "frequent itemsets")) #so here itemsets that hit the minimum support of 0.02 (2%) are considered frequent itemsets #bc minlen = 1 and maxlen = 1, all returned itemsets only have 1 item (each itemset has a length of 1) summary(itemset.1)	As support increases, number of returned itemsets decreases
Attain and plot all the rules	rules = apriori(Groceries, parameter = list(support = 0.001, confidence = 0.6, target = "rules")) plot(rules)	

	`#limit to only 100 dots / rules with the highest lift`
	`plot(rules, measure = c("support", "confidence"), shading = "lift", col = "black", limit = 100)`
	
	Attain the top few rules
	`inspect(head(sort(rules, by = "lift"), 3))`
	`#note that 3 is a parameter for head() ie head() controls how many outputs come out`
	
	Plot the 5 rules with the highest lift
	`highLiftRules = head(sort(rules, by = "lift"), 5)`
	`plot(highLiftRules, method = "graph"`
	`(refer below for a plot that is more easily readable)`	

Interpreting the weirdass association rules plot	`highLiftRules = head(sort(rules, by = "lift"), 5)`
	`plot(highLiftRules, method = "graph", engine = "igraph", edgeCol = "blue", alpha = 1)`
	
	 	

	As size increases, support increases As colour darkens, lift increases  Those who buy instant food products AND soda, also tend to buy hamburger meat	
Inspect / List the first 6 transactions	inspect(head(data)) #gives first 6 itemsets inspect(head(data, 10))	requires arules library
Add text to a plot Manually add a point to a scatter plot	text(xcord, ycord, "text to insert") points(xcord, ycord, pch = 20, col = "green")	points() WITH AN S ITS PLURAL!!!

Within Sum of Squares (WSS)	K = 15
	wss <- numeric(K)#this creates an empty vector of 15 0s
	
	for (k in 1:K) {
	  wss[k] <- sum(kmeans(scale(data[,c("floor_area_sqm","resale_price")]), centers=k)$withinss)
	}
	
	plot(1:K, wss, col = "blue", type="b", xlab="Number of Clusters", ylab="Within Sum of Squares")
		By default just plot everything first to get a sense of the data
		
		Remember to scale the data before doing kmeans()!

	My own attempt is this:
	
	kdata = scale(sendhelp[,
	c("floor_area_sqm","resale_price")])
	wss = numeric(15)
	
	for (i in 1:15) {
	  wss[i] = sum(kmeans(kdata, centers =
	i)$withinss)
	}
	
	plot(1:15, wss, type = "b")	

Convert sparse matrix into readable itemset	apply(Groceries@data[,100:105], 2, function(r) paste(Groceries@itemInfo[r, "labels"], collapse = ", "))	

NOTES FROM MIDTERM:

1) **Remember to as.factor() EVERYTHING. Not sure? CHECK IF ANY CATEGORICAL VAR NEEDS TO BE CONVERTED FROM INT TO CAT. AS.FACTOR() EVERYTHING**
    a) **If attaching dataframe,**
        i) **breastdata$survival.status = as.factor(breastdata$survival.status) use the dollar signs first!!!**
        ii) **THEN attach, after converting to factor**
        iii) **CHECK AGAIN using glimpse or head**
        iv) **breastdata$survival.status = as.factor(breastdata$survival.status)**
        attach(breastdata)
        glimpse(breastdata)
2) **Removing specific columns: DO NOT**
   breastdata = breastdata[,1] + breastdata[,3] + breastdata[,4]
    a) **INSTEAD: breastdata = breastdata[,c(1,3,4)]**
    b) **OR to remove ID column / first column:**
       breastdata = breastdata[,-1]

3) **Type 1 error: False Positive Rate (FPR)**
   Type 2 Error: False Negative Rate (FNR)
4) **3 sf please!!**

INCLUDING PICTURES IN R MARKDOWN:

```
```{r,eval=TRUE, echo=FALSE}
knitr::include_graphics("~/GitHub/DSA1101 Slayers/Pictures/Confusion Matrix Pic.jpg")
knitr::include_graphics("~/GitHub/DSA1101 Slayers/Pictures/CM spam emails.jpg")
```
```

Hi Bryan, this is Dawn from DSA1101 T3, I wanted to ask about a mistake from assignment 2 (statistical report). I don't understand this comment: "Wrong KNN ROC code (should use 1-attr)"

Hi,
Sorry to reply your question late. I'm stuffed with full schedule these days. :(((

Let's try to understand how ROC curve is plotted, then we can know the difference:
(1) the ROC curve uses the probability of response = yes, Pr (Y = 1) from model.
(2) for each value of threshold delta, like delta = 0.1, compare Pr(Y = 1) vs delta, if a data point has Pr(Y= 1) > delta then that point is predicted as "Yes" or "1"; otherwise that point will be classified as "No" or "0".
(3) With the classification as in (2) be applied to all the data points for each value of delta, the value of TPR and FPR are calculated for each delta value.
(4) With a series of delta from 0 to 1 (where R will generate this series on its own), the values of TPR and FPR will be calculates for each delta in this series.
(5) ROC curve is plotted.
That's how the ROC curve is generated.

Now, back to KNN: when we use function knn() and do not specify "prob = TRUE", the output we get are the labels ("0" and "1") for each point.
When we use as.numeric() to transform the labels "0" and "1" into numeric, we get 0 and 1.
After that, we use those 0 and 1 to plot the ROC curve. Then, at the step 1 above, R will treat 0 and 1 as the probabilities Pr(Y = 1) for data points. That means, for all the data points given, each of them has probability Pr(Y = 1) is either 0 or 1, no other values.
That's why the curve has only 1 bend for this case.

When we run knn() with "prob = TRUE", we will be able to get the probability of response variable equal to the WINNING category.
For example, Y has two category: Yes and No, then the output of
pred.knn = knn(... , prob = TRUE)
winning.prob = attr(pred.knn, "prob")
is a series of winning probabilities which are: the probability that Y = "Yes" if the point is classified as Yes and probability that Y = "No" is the point is classified as No.

To get the probability of Yes for every data point in this case, you might want to run (here, I'm assuming the response has "yes" and "no"):

```
pred.knn =  knn(train.X, test.X, cl = train.Y, k = 30)  # "prob = TRUE" is NOT added --> to get the class labels
pred.knn.prob= knn(train.X, test.X, cl = train.Y, k = 30, prob = TRUE) #  --> to get the probabilities of winning labels
winning.prob = attr(pred.knn.prob, "prob") # to extract the winning probabilities

n = length(test.Y)
prob = numeric(length = 0) # n is the length of "test.y" used in knn() above
for (i in 1:n) {
  prob[i] = ifelse(pred.knn[i] == "yes", winning.prob[i], 1 - winning.prob[i])
}
```

Then, "prob" will be the probabilities of response be "Yes" for every point in the test set.

With this vector "prob", you can use to plot the ROC curve and calculate its AUC values.

```
helppain = prediction(prob, test.Y)
rocObjKNN = performance(helppain, measure = "tpr", x.measure = "fpr")
plot(rocObjKNN, lwd =2)
abline(a=0, b=1, col ="blue", lty =3)
```