**My algorithm implementation is not perfect but it returns a proper frequent itemset for lengths 1,2, and 3.**

**The Candidate itemset of length 1 is** - ['gene\_1', 'gene\_10', 'gene\_100', 'gene\_11', 'gene\_12', 'gene\_13', 'gene\_14', 'gene\_15', 'gene\_16', 'gene\_17', 'gene\_18', 'gene\_19', 'gene\_2', 'gene\_20', 'gene\_21', 'gene\_22', 'gene\_23', 'gene\_24', 'gene\_25', 'gene\_26', 'gene\_27', 'gene\_28', 'gene\_29', 'gene\_3', 'gene\_30', 'gene\_31', 'gene\_32', 'gene\_33', 'gene\_34', 'gene\_35', 'gene\_36', 'gene\_37', 'gene\_38', 'gene\_39', 'gene\_4', 'gene\_40', 'gene\_41', 'gene\_42', 'gene\_43', 'gene\_44', 'gene\_45', 'gene\_46', 'gene\_47', 'gene\_48', 'gene\_49', 'gene\_5', 'gene\_50', 'gene\_51', 'gene\_52', 'gene\_53', 'gene\_54', 'gene\_55', 'gene\_56', 'gene\_57', 'gene\_58', 'gene\_59', 'gene\_6', 'gene\_60', 'gene\_61', 'gene\_62', 'gene\_63', 'gene\_64', 'gene\_65', 'gene\_66', 'gene\_67', 'gene\_68', 'gene\_69', 'gene\_7', 'gene\_70', 'gene\_71', 'gene\_72', 'gene\_73', 'gene\_74', 'gene\_75', 'gene\_76', 'gene\_77', 'gene\_78', 'gene\_79', 'gene\_8', 'gene\_80', 'gene\_81', 'gene\_82', 'gene\_83', 'gene\_84', 'gene\_85', 'gene\_86', 'gene\_87', 'gene\_88', 'gene\_89', 'gene\_9', 'gene\_90', 'gene\_91', 'gene\_92', 'gene\_93', 'gene\_94', 'gene\_95', 'gene\_96', 'gene\_97', 'gene\_98', 'gene\_99']

**The Frequent itemset of length 1** is - ['gene\_1', 'gene\_12', 'gene\_14', 'gene\_17', 'gene\_21', 'gene\_22', 'gene\_23', 'gene\_25', 'gene\_26', 'gene\_27', 'gene\_3', 'gene\_31', 'gene\_36', 'gene\_37', 'gene\_39', 'gene\_4', 'gene\_43', 'gene\_45', 'gene\_47', 'gene\_48', 'gene\_5', 'gene\_50', 'gene\_53', 'gene\_54', 'gene\_55', 'gene\_56', 'gene\_59', 'gene\_6', 'gene\_60', 'gene\_63', 'gene\_64', 'gene\_66', 'gene\_67', 'gene\_71', 'gene\_72', 'gene\_75', 'gene\_77', 'gene\_78', 'gene\_8', 'gene\_81', 'gene\_83', 'gene\_84', 'gene\_87', 'gene\_89', 'gene\_9', 'gene\_90', 'gene\_91', 'gene\_93', 'gene\_94', 'gene\_98', 'gene\_99']

**The Candidate itemset of length 2 is** - [['gene\_1', 'gene\_12'], ['gene\_1', 'gene\_14'], ['gene\_1', 'gene\_17'], ['gene\_1', 'gene\_21'], ['gene\_1', 'gene\_22'], ['gene\_1', 'gene\_23'], ['gene\_1', 'gene\_25'], ['gene\_1', 'gene\_26'], ['gene\_1', 'gene\_27'], ['gene\_1', 'gene\_3'], ['gene\_1', 'gene\_31'], ['gene\_1', 'gene\_36'], ['gene\_1', 'gene\_37'], ['gene\_1', 'gene\_39'], ['gene\_1', 'gene\_4'], ['gene\_1', 'gene\_43'], ['gene\_1', 'gene\_45'], ['gene\_1', 'gene\_47'], ['gene\_1', 'gene\_48'], ['gene\_1', 'gene\_5'], ['gene\_1', 'gene\_50'], ['gene\_1', 'gene\_53'], ['gene\_1', 'gene\_54'], ['gene\_1', 'gene\_55'], ['gene\_1', 'gene\_56'], ['gene\_1', 'gene\_59'], ['gene\_1', 'gene\_6'], ['gene\_1', 'gene\_60'], ['gene\_1', 'gene\_63'], ['gene\_1', 'gene\_64'], ['gene\_1', 'gene\_66'], ['gene\_1', 'gene\_67'], ['gene\_1', 'gene\_71'], ['gene\_1', 'gene\_72'], ['gene\_1', 'gene\_75'], ['gene\_1', 'gene\_77'], ['gene\_1', 'gene\_78'], ['gene\_1', 'gene\_8'], ['gene\_1', 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**The Frequent itemset of length 3 is** - [['gene\_1', 'gene\_3', 'gene\_5'], ['gene\_1', 'gene\_59', 'gene\_72']]

**Python Code for the apriori algorithm:**

The algorithm manages to find the correct number of Candidate itemsets for length 1 and 2. However I found it easier to simply generate all possible 3-tuples from the frequent itemset of length 1 and iterate through that checking if the item was frequent or not.

I use the defined python function “combinations” from the **itertools** library to generate the 2-tuples and 3-tuple candidate itemsets.

import csv, operator, numpy, collections, itertools

def all\_combinations(any\_list, i):

return itertools.chain.from\_iterable(

itertools.combinations(any\_list, i))

#Function to see if the items are present in length 2 itemset

def stringstonum(s1, s2):

j = 0

for i in range(0, len(s1)):

if ((s1[i] == '1') and (s2[i] == '1')):

j += 1

return j

#Function to see if the items are present in length 3 itemset

def stringstonum3(s1, s2, s3):

j = 0

for i in range(0, len(s1)):

if ((s1[i] == '1') and (s2[i] == '1') and (s3[i] == '1')):

j += 1

return j

dictof1 = dict()

with open('gene\_data\_transaction.txt','rb') as market:

transactionreader = csv.reader(market, delimiter = ',')

for row in transactionreader:

for i in row:

i = i.replace(" ", "")

if i in dictof1:

dictof1[i] += 1

else:

dictof1[i] = 1

listof1 = sorted(dictof1)

index = []

with open('gene\_data\_binary.txt', 'rb') as bina:

for line in bina:

index.append(line.split())

binstrings = ["" for i in range(0,99)]

for i in range(0,99):

for j in range(0,99):

binstrings[i] += str(index[j][i])

finlist1 = []

for i in range(1,100):

finlist1.append('gene\_' + str(i))

bindict = {}

for i in range(0,99):

bindict[finlist1[i]] = binstrings[i]

finaldict = {key: value for key, value in dictof1.items() if value >= 50}

freqlist1 = sorted(finaldict)

listof2 = [list(l) for l in itertools.combinations(freqlist1,2)]

fin2 = []

for i in range(0, len(listof2)):

if (stringstonum(bindict[listof2[i][0]], bindict[listof2[i][1]]) >= 50):

fin2.append(listof2[i])

listof3 = [list(l) for l in itertools.combinations(freqlist1,3)]

fin3 = []

for i in range(0, len(listof3)):

if (stringstonum3(bindict[listof3[i][0]], bindict[listof3[i][1]], bindict[listof3[i][2]]) >= 50):

fin3.append(listof3[i])

with open("itemset.txt","w+") as item:

item.write("The Candidate itemset of length 1 is - " + str(listof1) + '\n')

item.write("The Frequent itemset of length 1 is - " + str(freqlist1) + '\n')

item.write("The Candidate itemset of length 2 is - " + str(listof2) + '\n')

item.write("The Frequent itemset of length 2 is - " + str(fin2) + '\n')

item.write("The Candidate itemset of length 3 is - " + str(listof3) + '\n')

item.write("The Frequent itemset of length 3 is - " + str(fin3) + '\n')