CIS600 HW1

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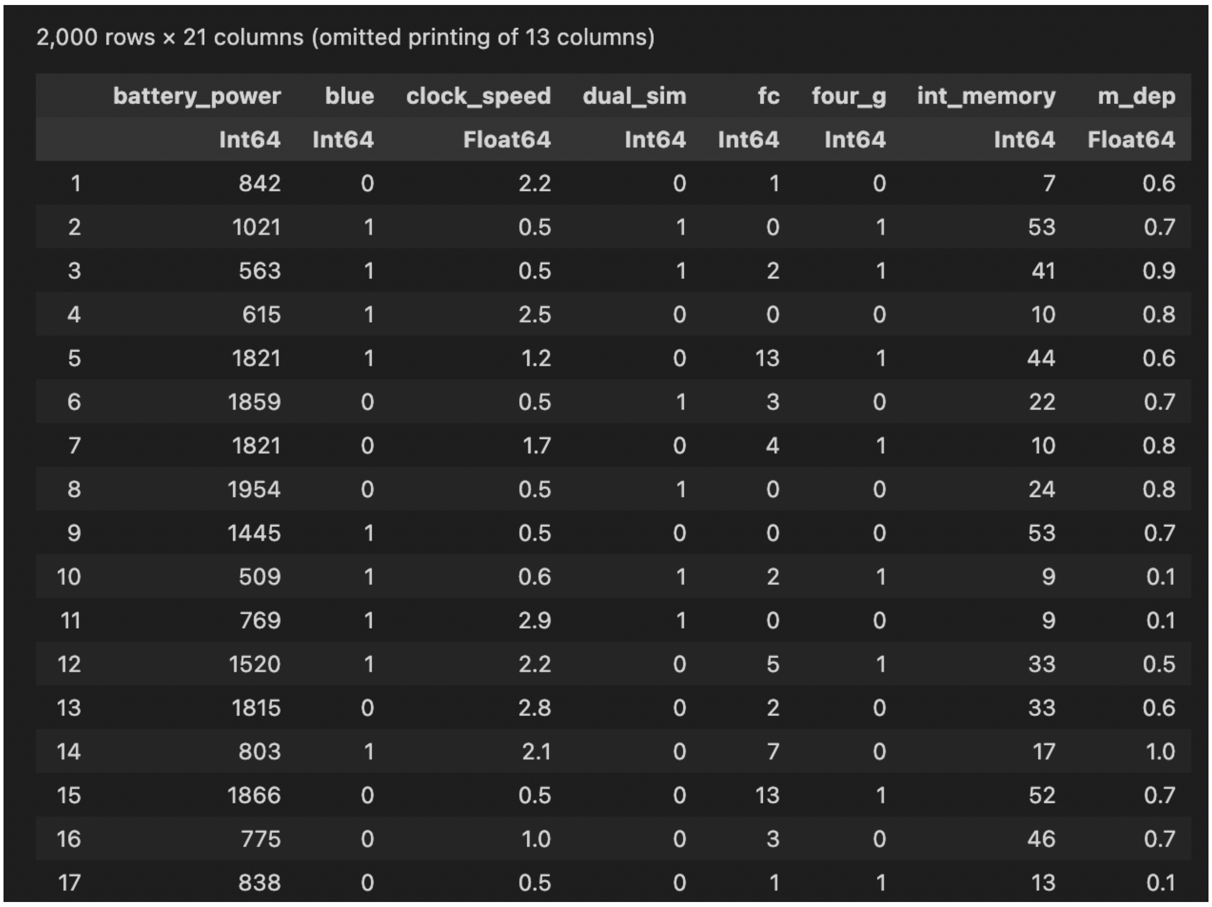
1.Citions

https://fluxml.ai/Flux.jl/stable/
https://docs.juliaplots.org/latest/tutorial/
https://machinelearningmastery.com/simple-genetic-algorithm-from-scratch-in-python/
https://dev.to/dillir07/genetic-algorithm-travelling-salesman-with-julia-477a

2. Data Set

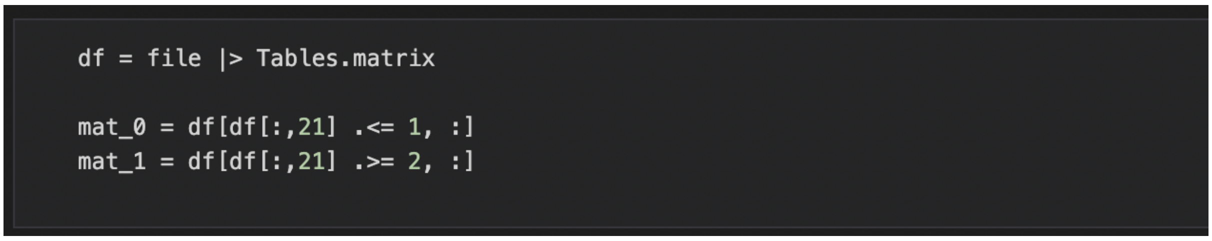
The data set I chose is about sales data of mobile phones of various companies. The data contains battery_power(Total energy a battery can store in one time measured in mAh); blue(Has bluetooth or not); clock_speed(speed at which microprocessor executes instructions); dual_sim(Has dual sim support or not); fc(Front Camera megapixels); four_g(Has 4G or not); int_memory(Internal Memory in Gigabytes); m_dep (Mobile Depth in cm); mobile_wt(Weight of mobile phone) ….. and price_range(This is the target variable with value of 0(low cost), 1(medium cost), 2(high cost) and 3(very high cost))



2,000 rows × 21 columns (omitted printing of 13 columns)

	battery_power	blue	clock_speed	dual_sim	fc	four_g	int_memory	m_dep
	Int64	Int64	Float64	Int64	Int64	Int64	Int64	Float64
1	842	0	2.2	0	1	0	7	0.6
2	1021	1	0.5	1	0	1	53	0.7
3	563	1	0.5	1	2	1	41	0.9
4	615	1	2.5	0	0	0	10	0.8
5	1821	1	1.2	0	13	1	44	0.6
6	1859	0	0.5	1	3	0	22	0.7
7	1821	0	1.7	0	4	1	10	0.8
8	1954	0	0.5	1	0	0	24	0.8
9	1445	1	0.5	0	0	0	53	0.7
10	509	1	0.6	1	2	1	9	0.1
11	769	1	2.9	1	0	0	9	0.1
12	1520	1	2.2	0	5	1	33	0.5
13	1815	0	2.8	0	2	0	33	0.6
14	803	1	2.1	0	7	0	17	1.0
15	1866	0	0.5	0	13	1	52	0.7
16	775	0	1.0	0	3	0	46	0.7
17	838	0	0.5	0	1	1	13	0.1

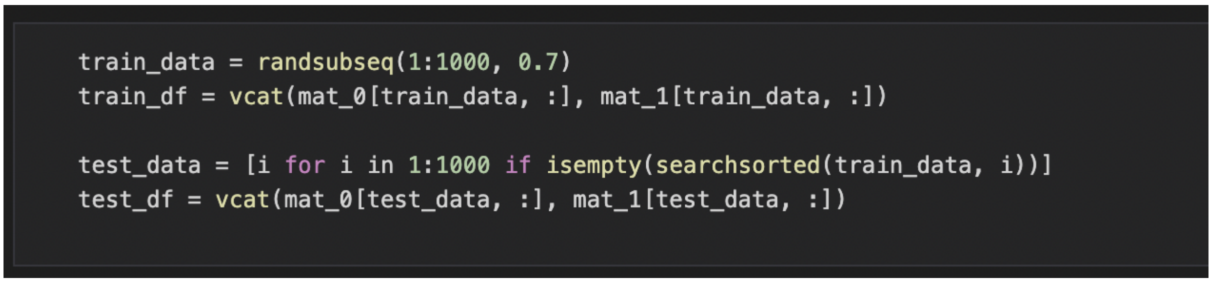
Therefore, the data can be treated as a 2-class classification problem with first class of low to medium price range (0 and 1 price range) and second class of high to very high cost (2 and 3 price range).



```
df = file |> Tables.matrix

mat_0 = df[df[:,21] .<= 1, :]
mat_1 = df[df[:,21] .>= 2, :]
```

I use 70% of the data to train the model and use the rest to do the test.

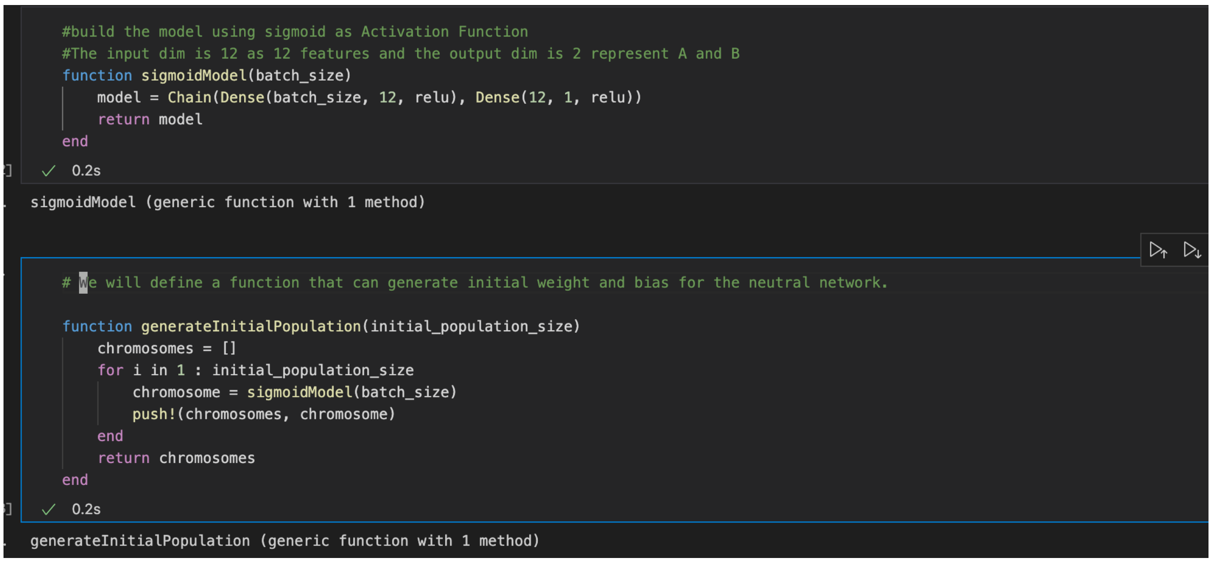


```
train_data = randsubseq(1:1000, 0.7)
train_df = vcat(mat_0[train_data, :], mat_1[train_data, :])

test_data = [i for i in 1:1000 if isempty(searchsorted(train_data, i))]
test_df = vcat(mat_0[test_data, :], mat_1[test_data, :])
```

3. Neural Network

3.1 Generating initial population



```
#build the model using sigmoid as Activation Function
#The input dim is 12 as 12 features and the output dim is 2 represent A and B
function sigmoidModel(batch_size)
    model = Chain(Dense(batch_size, 12, relu), Dense(12, 1, relu))
    return model
end
```

```
✓ 0.2s
sigmoidModel (generic function with 1 method)
```

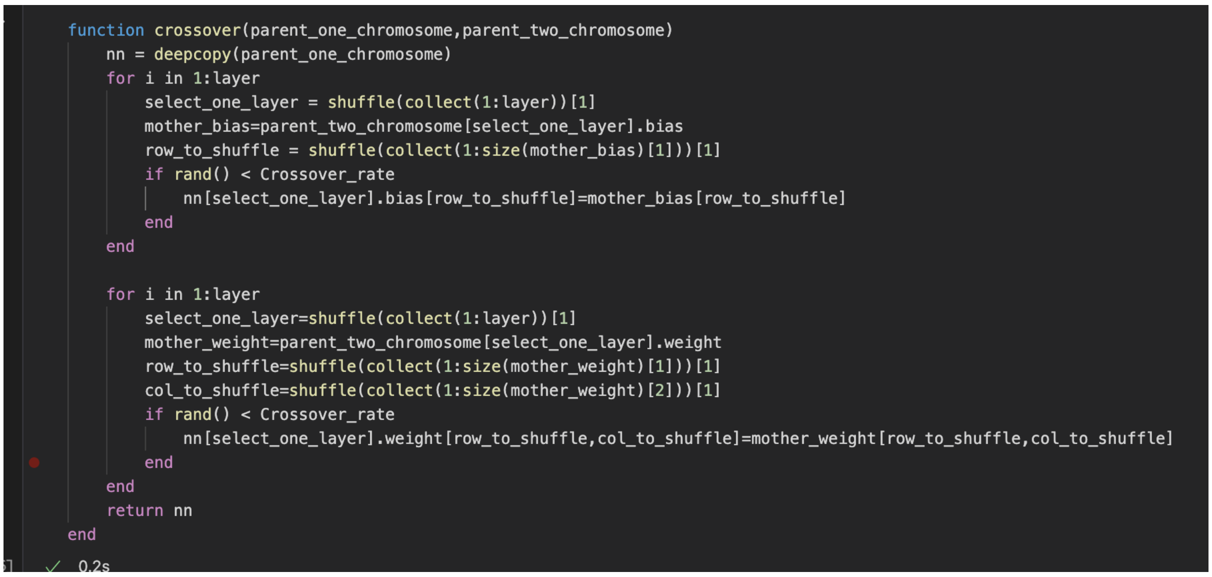
```
# We will define a function that can generate initial weight and bias for the neutral network.

function generateInitialPopulation(initial_population_size)
    chromosomes = []
    for i in 1 : initial_population_size
        chromosome = sigmoidModel(batch_size)
        push!(chromosomes, chromosome)
    end
    return chromosomes
end
```

```
✓ 0.2s
generateInitialPopulation (generic function with 1 method)
```

We define a function that can generate models with initial weights and bias for the neutral network.
The models use sigmoidal node functions as the activation function.

3.2 Crossover Function

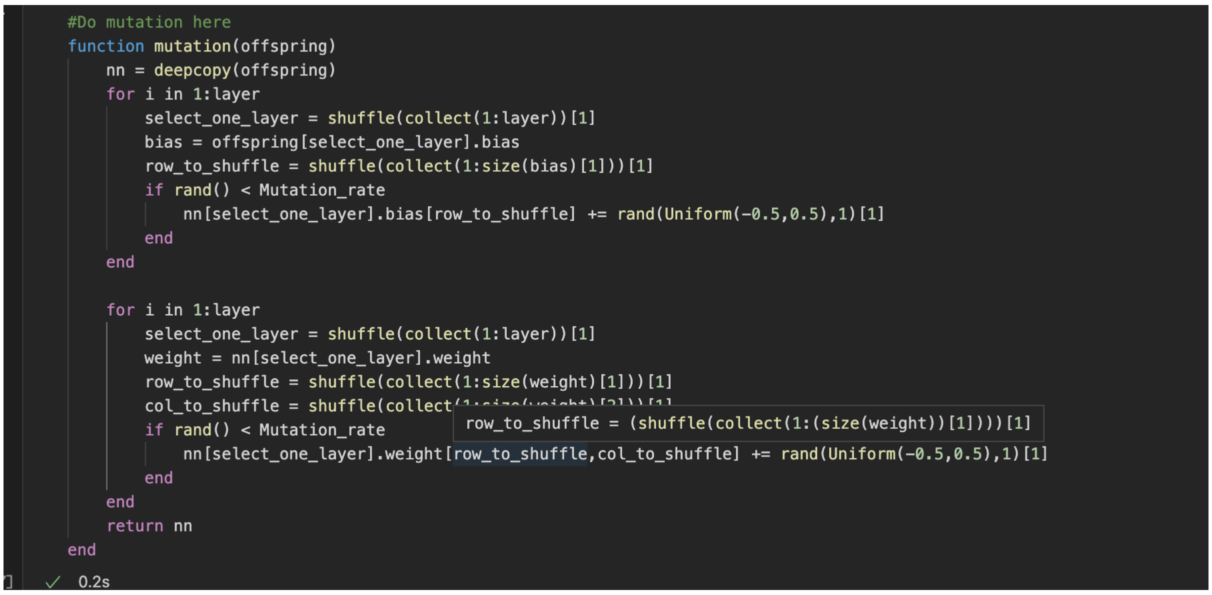


```
function crossover(parent_one_chromosome,parent_two_chromosome)
    nn = deepcopy(parent_one_chromosome)
    for i in 1:layer
        select_one_layer = shuffle(collect(1:layer))[1]
        mother_bias=parent_two_chromosome[select_one_layer].bias
        row_to_shuffle = shuffle(collect(1:size(mother_bias)[1]))[1]
        if rand() < Crossover_rate
            nn[select_one_layer].bias[row_to_shuffle]=mother_bias[row_to_shuffle]
        end
    end

    for i in 1:layer
        select_one_layer=shuffle(collect(1:layer))[1]
        mother_weight=parent_two_chromosome[select_one_layer].weight
        row_to_shuffle=shuffle(collect(1:size(mother_weight)[1]))[1]
        col_to_shuffle=shuffle(collect(1:size(mother_weight)[2]))[1]
        if rand() < Crossover_rate
            nn[select_one_layer].weight[row_to_shuffle,col_to_shuffle]=mother_weight[row_to_shuffle,col_to_shuffle]
        end
    end
    return nn
end
✓ 0.2s
```

Create a new model using two parent models by clone a parent model, then change some of its features(bias and weights) as another parent's feature

3.3 Mutation Function

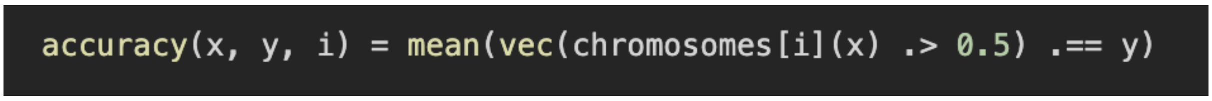


```
#Do mutation here
function mutation(offspring)
    nn = deepcopy(offspring)
    for i in 1:layer
        select_one_layer = shuffle(collect(1:layer))[1]
        bias = offspring[select_one_layer].bias
        row_to_shuffle = shuffle(collect(1:size(bias)[1]))[1]
        if rand() < Mutation_rate
            nn[select_one_layer].bias[row_to_shuffle] += rand(Uniform(-0.5,0.5),1)[1]
        end
    end

    for i in 1:layer
        select_one_layer = shuffle(collect(1:layer))[1]
        weight = nn[select_one_layer].weight
        row_to_shuffle = shuffle(collect(1:size(weight)[1]))[1]
        col_to_shuffle = shuffle(collect(1:size(weight)[2]))[1]
                         row_to_shuffle = (shuffle(collect(1:(size(weight))[1])))[1]
        if rand() < Mutation_rate
            nn[select_one_layer].weight[row_to_shuffle,col_to_shuffle] += rand(Uniform(-0.5,0.5),1)[1]
        end
    end
    return nn
end
✓ 0.2s
```

Mutation is made by making a random change in the chromosome model.

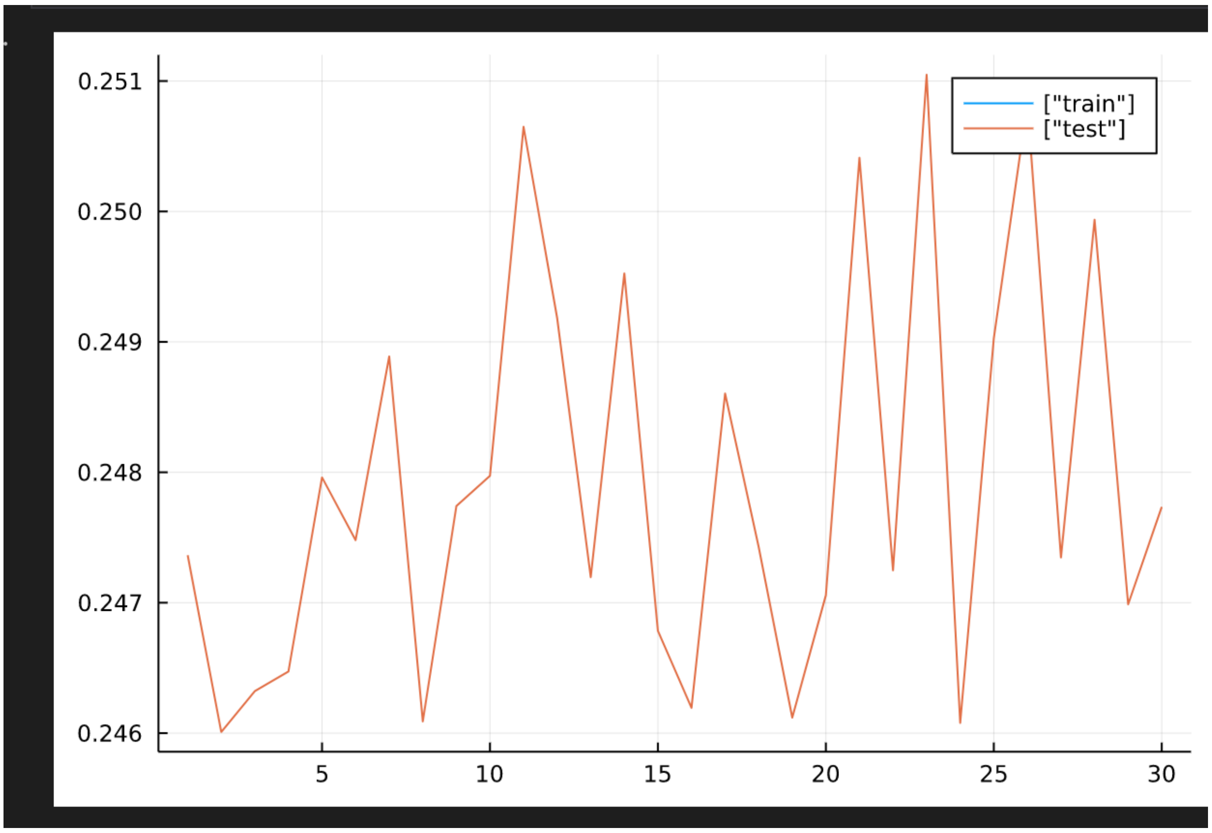
3.4 Fitness Function



```
accuracy(x, y, i) = mean(vec(chromosomes[i](x) .> 0.5) .== y)
```

The fitness is used to check how accuracy the model can make a prediction on a dataset x

4 Outcome



Not ideal, I need to find the problem.
We are not getting an ideal model as the model accuracy we get at the end is still pretty low, and actually lower than some of the chromosomes.

5 Confusion Matrix

```
...   confusion matrix:
      True True Result: 104,  True False Result: 518
      False False Result: 104,   False True Result: FT
```