

# **Disease Checker Bot – Using Evolutionary Algorithms**

Term Project of Genetic Algorithms



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# Abstract

In this project I have tried to develop a Disease checker bot which is currently being trained on data extracted from SymCat. The bot is being trained through a neural net which is a combination of traditional neural nets and some important steps of evolutionary algorithms like – Selection, Crossover and Mutation. I have presented a detailed approach of all the solutions which I tried and their results have been thoroughly compared.

## Problem Statement

The problem statement consisted of developing a primary healthcare disease checker bot that will try to predict a possible disease based on symptoms shown by the patient. This also includes generating a customizable dataset which can be changed according to the need of the healthcare professionals. The motivation behind this would be that this can be further extended to an Indian demographic specific bot which would be among the first ones in the country.

## Data Set Extraction and Generation

In table 1, all the datasets along with their advantages and disadvantages have been listed.

S. No.	Data Set Name	Advantages	Disadvantages
1	Disease Symptom – Kaggle	1. 24 common diseases with possible combinations of symptoms from among a set of 40 symptoms. 2. Severity associated with symptoms.	1. Very less number of diseases and symptoms included. 2. No description provided for the diseases and symptoms.
2	Health Analytics – Kaggle	1. Has state & district wise distribution data of common health diseases. 2. Demographic distribution present for the same.	1. No symptoms described for the diseases. 2. Description of the diseases very generic.
3	SymCat	1. Has 801 diseases with correlated 474 symptoms. 2. Probability for each symptom in a disease given along with vice-versa. 3. Demographic data (age group, gender, race) available for the diseases & symptoms.	1. No formatted data present. All data has to be scraped from the website. 2. Getting the data ready for a model will also have to be done. 3. Diseases too extensive.

**Table 1 – Various datasets explored during the project along with their advantages and disadvantages.**

Seeing the need of a much more extensive database than the simple – “Disease Symptom – by Kaggle”, further datasets were explored and finally Symcat was chosen as one of the most extensive sources of information which can be converted to a training dataset with feasible labor. It originally has 801 diseases with correlated 474 symptoms along with probability for each symptom in a disease given along with vice-versa along with Demographic data (age group, gender, race) for the diseases & symptoms.

This is very useful when tuning the disease bot checker according to a particular location and expected demographic of the users is already known. Due to time constraints, this tuning based on demographic had not been done.

One of the major disadvantages of Symcat as already mentioned in Table 1 and also visible from Fig. 3 and Fig. 4 are that no formatted data is present. Therefore, to solve this the following methodology was used –

- Data was scraped using a python script from the Symcat website and converted to json file. (Fig. 5)
- Diseases that come under primary healthcare, were shortlisted.
- Data was converted from the JSON file to the standard training.csv (Fig. 6) in the following steps
  - First all possible symptoms of the shortlisted diseases were extracted along with their probabilities. Here the probabilities represent the probability of showing a symptom given you have a particular disease. (Code 1)
  - Now this extracted data was used to generate a larger data set using data augmentation in which probabilities of the symptoms were used and then a dataset was generated which consisted of symptoms as inputs and the expected disease. (Code 2)

< dataset.csv (617.38 KB) Download Icon Fullscreen Icon

Detail **Compact** Column 10 of 18 columns

Disease	Symptom_1	Symptom_2	Symptom_3	Symptom_4	Symptom_5	Symptom_6	Symptom_7
Fungal infection	skin_rash	nodal_skin_erup	tions	dischromic	_patches		
Fungal infection	itching	nodal_skin_erup	tions	dischromic	_patches		
Fungal infection	itching	skin_rash	dischromic	_patches			
Fungal infection	itching	skin_rash	nodal_skin_erup	tions			
Fungal infection	itching	skin_rash	nodal_skin_erup	tions	dischromic	_patches	
Allergy	continuous_snee	zing	shivering	chills	watering_from_e	yes	
Allergy	shivering	chills	watering_from_e	yes			
Allergy	continuous_snee	zing	chills	watering_from_e	yes		
Allergy	continuous_snee	zing	shivering	watering_from_e	yes		

Fig 1 – Sample of data available in the Disease Symptom dataset available on Kaggle.

< Key\_indicator\_districtwise.csv (953.41 KB) Download Icon Fullscreen Icon

Detail **Compact** Column 10 of 644 columns

**About this file**

This file contains the data from 284 districts.

\*Marriage figures are Based on marriages taken place during 2009-2011.

State_Name	State_District_Na...	# AA_Sample_Units...	# AA_Sample_Units...	# AA_Sample_Units...	# AA_Households_T...	# AA_Househol
Uttar Pradesh 25%	284 unique values					
Madhya Pradesh 16%		10 386	8 337	2 234	2802 66.5k	2381
Other (169) 60%						
Assam	Barpeta	53	47	6	13711	12765
Assam	Bongaigaon	89	73	16	17384	14984
Assam	Cachar	105	84	21	27488	24207
Assam	Darrang	26	24	2	5951	5769
Assam	Dhemaji	121	108	13	14481	12619
Assam	Dhubri	42	35	7	11001	9954
Assam	Dibrugarh	91	66	25	21378	16514
Assam	Goalpara	64	56	8	15891	14630
Assam	Golaghat	70	61	9	16021	14183
Assam	Hailakandi	10	8	2	2882	2381

Fig 2 – Sample of data available in the Health Analytics dataset available on Kaggle.

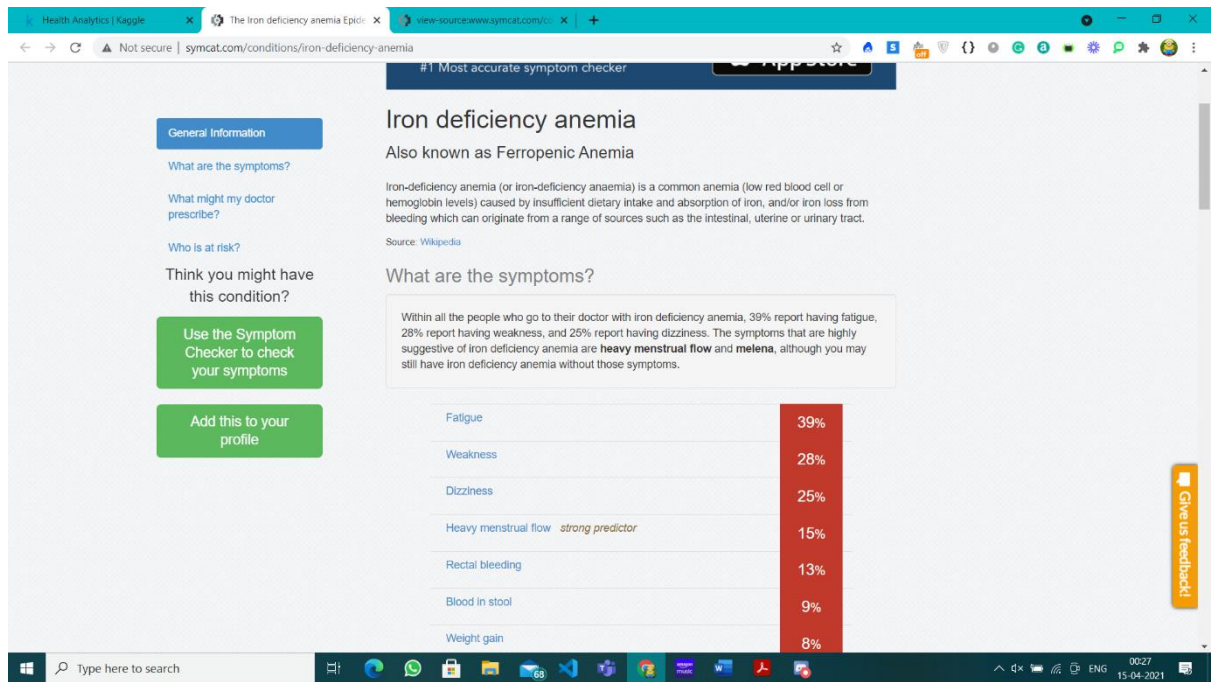


Fig 3 – Sample of data available on the Symcat website. Here we can see a disease (For example - Iron deficiency anemia in the above figure) and its possible symptoms along with their probabilities.

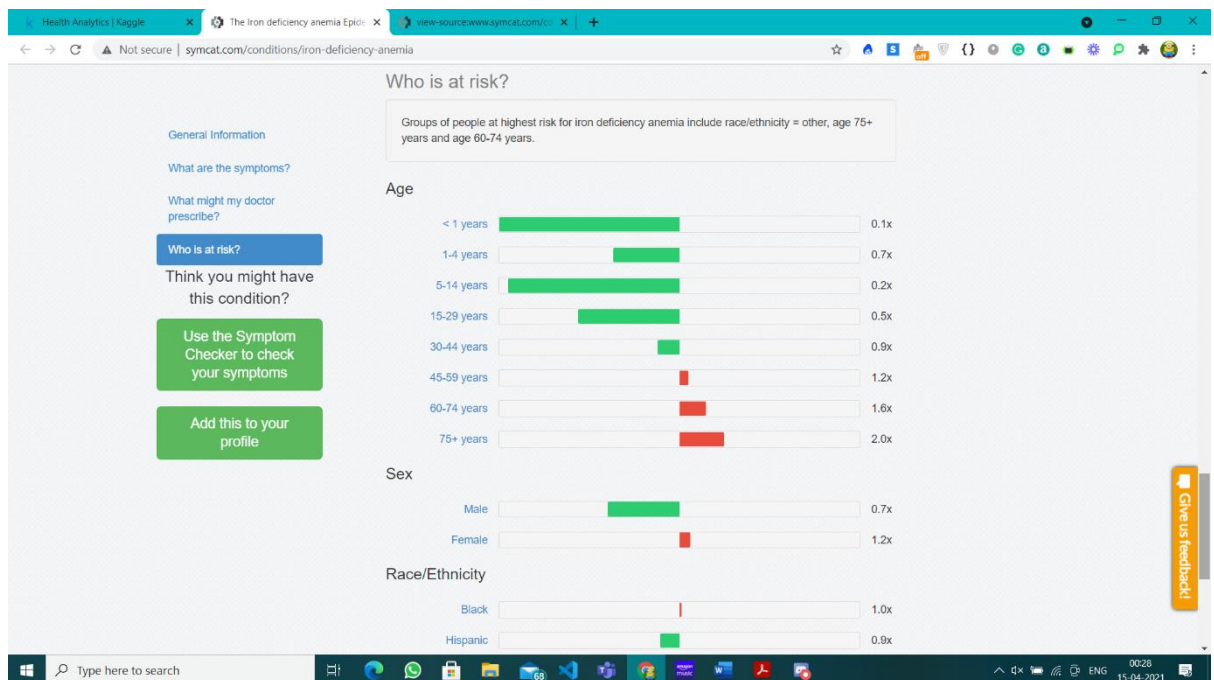


Fig 4 – Sample of data available on the Symcat website. Here we can see a disease (For example - Iron deficiency anemia in the above figure) and its expected demographic distribution.

```

"malaria": {
  "condition_name": "Malaria",
  "condition_slug": "malaria",
  "condition_description": "Malaria is a mosquito-borne infectious disease of humans and other animals caused by protists (a type of microorganism) of the genus Plasmodium. It begins with a bite from an infected female Anopheles mosquito, which introduces the protists through saliva into the circulatory system. In the blood, the protists travel to the liver to mature and reproduce. Malaria causes symptoms that typically include fever and headache, which in severe cases can progress to coma or death. The disease is widespread in tropical and subtropical regions in a broad band around the equator, including much of Sub-Saharan Africa, Asia, and the Americas.",
  "condition_remarks": "Within all the people who go to their doctor with malaria, 94% report having headache, 87% report having fever, and 72% report having fainting. The symptoms that are highly suggestive of malaria are headache, ache all over, weakness, fainting, vulvar sore, excessive growth, knee lump or mass, itchy eyelid, and wrist weakness, although you may still have malaria without those symptoms.",
  "symptoms": {
    "headache": {
      "slug": "headache",
      "probability": 0.94
    },
    "fever": {
      "slug": "fever",
      "probability": 0.87
    },
    "ache-all-over": {
      "slug": "ache-all-over",
      "probability": 0.72
    },
    "fainting": {
      "slug": "fainting",
      "probability": 0.72
    },
    "vulvar-sore": {
      "slug": "vulvar-sore",
      "probability": 0.72
    },
    "excessive-growth": {
      "slug": "excessive-growth",
      "probability": 0.72
    },
    "knee-lump-or-mass": {
      "slug": "knee-lump-or-mass",
      "probability": 0.72
    },
    "itchy-eyelid": {
      "slug": "itchy-eyelid",
      "probability": 0.72
    },
    "wrist-weakness": {
      "slug": "wrist-weakness",
      "probability": 0.72
    }
  }
}

```

Fig 5 – Data scraped from the Symcat website in json format. Here we can see a disease (For example - malaria in the above figure), its description and probable symptoms along with their probabilities.

acne-or-pi	skin-rash	abnormal	skin-moles	skin-swelling	skin-growths	warts	skin-dryness	shortness	difficulty-t	cough	sharp-chest	depressive	fever	wheezing	hurts-to-b	nasal-cong	sore-throat	headache	frontal-her	coryza	prognosis
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	thyroid-dise
0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	allergy
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	thyroid-dise
0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	alcohol-witt
0	1	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	chickenpox
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	mumps
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	astigmatism
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	goiter
0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0	0	flu
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	indigestion
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	goiter
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	epilepsy
0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	0	malaria
0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	liver-disease
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	myopia
0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	alcohol-witt
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	alcoholic-liv
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	thyroid-dise
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	myopia
0	1	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	acne
0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	arrhythmia
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	scurvy
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	myopia
0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	gastritis
0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	scurvy

Fig 6 – Sample of Training.csv which has been generated from the data augmentation step after cleaning of the dataset from the data scraped from the Symcat website.



# Approach

Several approaches to train an artificial neural net using evolutionary algorithms

–

- Using PyGAD - which is an open-source Python 3 library for building the genetic algorithm and optimizing machine learning algorithms.
- Using existing frameworks to build a model along with handwritten selection, crossover and mutation function. Following frameworks were explored –
  - Keras
  - Pytorch

## PyGad

PyGAD is an open-source Python 3 library which is used for building the genetic algorithm and optimizing machine learning algorithms. [PyGAD](#) supports different types of crossover, mutation, and parent selection. [PyGAD](#) allows different types of problems to be optimized using the genetic algorithm by customizing the fitness function.

The pygad.gann module was used which builds and trains neural networks (for either classification or regression) using the genetic algorithm.

The steps to use PyGad for building and training a neural network using the genetic algorithm are as follows:

- Prepare the training data. (Code 3)
- Create an instance of the pygad.gann.GANN class. (Code 4)
  - this is done with the `__init__()` function.
  - The architecture of the created network has the following layers:
    - An input layer with 144 neurons (i.e. inputs (symptoms))
    - A single hidden layer with 200 neurons.
    - An output layer with 48 neurons (i.e. classes (diseases)).
- Fetch the population weights as vectors. (Code 5)



- For the genetic algorithm, the parameters (i.e. genes) of each solution are represented as a single vector.
- Prepare the fitness function. (Code 6)
  - The fitness function for training a neural network uses the `pygad.nn.predict()` function to predict the class labels based on the current solution's weights.
  - Based on such predictions, the classification accuracy is calculated. This accuracy is used as the fitness value of the solution.
- Prepare the generation callback function. (Code 7)
  - After each generation of the genetic algorithm, the fitness function will be called to calculate the fitness value of each solution.
  - This callback function can be used to update the `trained_weights` attribute of layers of each network in the population.
  - Code 7 shows the implementation for a function that updates the `trained_weights` attribute of the layers of the population networks. It works by converting the current population from the vector form to the matrix form using the `pygad.gann.population_as_matrices()` function. It accepts the population as vectors and returns it as matrices.

The population matrices are then passed to the `update_population_trained_weights()` method in the `pygad.gann` module to update the `trained_weights` attribute of all layers for all solutions within the population.

- Create an instance of the `pygad.GA` class. (Code 8)
- Run the created instance of the `pygad.GA` class.

This completes our training step of the population. Now for the results we -

- Plot the Fitness Values
- Retrieve Information about the best solution.
- Make predictions on test set using the trained weights.

- Calculate some statistics.

```
df = pd.read_csv(file_dir + 'Training.csv')

# Random in place shuffling of the original input data before splitting it into train and test set

df = df.sample(frac=1).reset_index(drop=True)

rows = len(df.index)

test_ratio = 0.1
train_ratio = 1-test_ratio
df_train = df.iloc[:int(train_ratio*rows),:]
df_test = df.iloc[int(train_ratio*rows+1):,:]

from sklearn import preprocessing
le = preprocessing.LabelEncoder()
arn = pd.concat([df_train['prognosis'], df_test['prognosis']])
le.fit(arn)

x_train = df_train[df_train.columns.difference(['prognosis'])]
y_train = le.fit_transform(df_train['prognosis'])

x_test = df_test[df_test.columns.difference(['prognosis'])]
y_test = le.fit_transform(df_test['prognosis'])
```

**Code 3 – Prepare the training data by using pandas and preprocessing module from sklearn.**

```
# Reading the input data.
data_inputs = x_train.to_numpy()

# Reading the output data.
data_outputs = y_train

# The length of the input vector for each sample (i.e. number of neurons in the input layer).
num_inputs = data_inputs.shape[1]
# The number of neurons in the output layer (i.e. number of classes).
num_classes = 48

# Creating an initial population of neural networks. The return of the initial_population()
function holds references to the networks, not their weights. Using such references, the weights
of all networks can be fetched.
num_solutions = 20 # A solution or a network can be used interchangeably.
GANN_instance = pygad.gann.GANN(num_solutions=num_solutions,
                                num_neurons_input=num_inputs,
                                num_neurons_hidden_layers=[200],
                                num_neurons_output=num_classes,
                                hidden_activations=["relu"],
                                output_activation="softmax")
```

**Code 4 – Create an instance of the pygad.gann.GANN class with number of neurons in model architecture as [144 , 200, 48].**

```
population_vectors =
pygad.gann.population_as_vectors(population_networks=GANN_instance.population_networks)
```

**Code 5 - Fetch the population weights as vectors.**

```

def fitness_func(solution, sol_idx):
    global GANN_instance, data_inputs, data_outputs

    predictions =
pygad.nn.predict(last_layer=GANN_instance.population_networks[sol_idx],
                  data_inputs=data_inputs)
    correct_predictions = numpy.where(predictions ==
data_outputs)[0].size
    solution_fitness =
    (correct_predictions/data_outputs.size)*100

    return solution_fitness

```

**Code 6 - Fitness function.**

```

def callback_generation(ga_instance):
    global GANN_instance

    population_matrices =
pygad.gann.population_as_matrices(population_networks=GANN_instance.population_networks,
population_vectors=ga_instance.population)

    GANN_instance.update_population_trained_weights(population_trained_weights=population_matrices)

    print("Generation =
{generation}".format(generation=ga_instance.generations_completed))

    print("Fitness =
{fitness}".format(fitness=ga_instance.best_solution()[1]))

```

**Code 7 – Callback function which is called at the end of every generation. Major component of this function includes the weight update step which is similar to back propagation in simple artificial neural nets.**

```

initial_population = population_vectors.copy()

num_parents_mating = 4

num_generations = 500

mutation_percent_genes = 5

parent_selection_type = "sss"

crossover_type = "single_point"

mutation_type = "random"

keep_parents = 1

ga_instance = pygad.GA(num_generations=num_generations,
                       num_parents_mating=num_parents_mating,
                       initial_population=initial_population,
                       fitness_func=fitness_func,
                       mutation_percent_genes = mutation_percent_genes,

```

```
parent_selection_type = parent_selection_type,
                        crossover_type=crossover_type,
                        mutation_type=mutation_type,
                        keep_parents=keep_parents,
                        on_generation=callback_generation)
```

**Code 8 – Initializing a random initial population and then initializing an instance of pygad.ga class. This instance acts as a bundle for all the population along with various fitness and callback functions.**

```
ga_instance.run()
```

**Code 9 – starts to train the population**

```
ga_instance.plot_result()
```

**Code 10 – plots the best\_fitness\_in\_generation vs number of generation graph**

```
solution, solution_fitness, solution_idx =
ga_instance.best_solution()
print("Parameters of the best solution :
{solution}".format(solution=solution))
print("Fitness value of the best solution =
{solution_fitness}".format(solution_fitness=solution_fitness))
print("Index of the best solution :
{solution_idx}".format(solution_idx=solution_idx))
```

**Code 11 – Information about the best solution is retrieved from the ga\_instance.**

```
predictions =
pygad.nn.predict(last_layer=GANN_instance.population_networks[sol
ution_idx], data_inputs=data_inputs)
print("Predictions of the trained network :
{predictions}".format(predictions=predictions))
```

**Code 12 – Prediction step on the training or test data according to the need of the user.**

## Simple ANN model + Steps of Evolutionary Algorithms written from Scratch

On seeing the low performance of PyGad, I decided to manually build a model and then evolve it using both the standard mathematical gradient descent along with evolutionary algorithms supporting convergence of the population. The following steps were applied in sequential order –

- Step 1 – Preparing the data. This involved converting numpy arrays to tensors for faster processing on GPU
- Step 2 - An artificial neural net (ANN) was built. In case of PyTorch , a separate function for training of the ANN was also required.
- Step 3 - Hyperparameters were initialised
- Step 4 - Selection, crossover and mutation functions were defined

- Step 5 - Random initial population was initialised
- Step 6 - For each generation, the following steps are being performed
  - Step 6.1 - Each member of the population undergoes usual neural network training. But the difference from normal neural net training is that for a single generation, the members are only trained for a very small number of epochs (this is controlled by the hyperparameter - `epochs_per_nn` )
  - Step 6.2 - Fitness is calculated on the basis of classification accuracy
  - Step 6.3 - Some parents from previous generation are added to the pool to maintain sustainability of parents.
  - Step 6.4 - Population is sorted in decreasing order of their fitness values and then the population is resized to the original population size.
  - Step 6.5 - The best member among the population at the current generation is considered and compared with the so far best member which has been produced.
  - Step 6.6 - Selection function is called which returns a list of parents among the current population which will undergo crossover to produce children.
  - Step 6.7 - Crossover is applied on parents
  - Step 6.8 - The resultant children of crossover undergo mutation.
  - Step 6.9 - After this the children networks are added to the population and then next generation starts.
- Step 7 - After all the generations are over, we get the best model from the variable - `best_model` . This is used as the final model in predictions and calculating the accuracies.

The following types of selection, crossover and mutations were used

- Selection –

- Fittest\_selection – members in decreasing order of their fitness are selected as parents, i.e. fitter the member more is its possibility to be a parent.
- Crossover –
  - Uniform Crossover – In this crossover two parents result in a single child. Here each parent has an equal probability ( $p_{\text{cross}} = 0.5$ ) to contribute to the weights of each layer of the resulting child.
- Mutation –
  - Bitwise Mutation – Each layer individually can go under mutation depending on  $p_{\text{mut}}$ .

Now each of these steps were applied for two different neural network frameworks – Keras and PyTorch. While Keras was preferred for its ease of access of layer weights which are the main subject for crossover and mutation, along with a more readable code, PyTorch helped in using GPU in a much more efficient way by transferring all the data stored in tensors along with the whole population of models being transferred to and trained on the GPU device side using CUDA. This resulted in an exponential decrease in amount of training time. Hence this allowed me to do perform much more experimentation with the hyperparameters, and types of selection, crossover and mutation functions.

Now the two implementations are provided –

## ***Keras with Steps of Evolutionary Algorithms***

### **Step 1 –**

```
symp_train_data = tf.convert_to_tensor(x_train.values,
dtype=tf.int64)
train_outputs = tf.convert_to_tensor(y_train)

symp_test_data = tf.convert_to_tensor(x_test.values,
dtype=tf.int64)
test_outputs = tf.convert_to_tensor(y_test)
```

### **Step 2 –**

```
class ANN(Sequential):

    def __init__(self, child_weights=None):
        super().__init__()
```

```

        self.fitness = 0
        if child_weights is None:
            layer1 = Dense(200, input_shape=(144,),
activation='relu')
            layer2 = Dense(48, activation=None)
            self.add(layer1)
            self.add(layer2)

    def forward_propagation(self, train_feature, train_label):
        predict_label = self.predict(train_feature)

```

### Step 3 –

```

p_cross = 0.5
p_mut = 0.3
num_parents = 10
population = 30
epochs = 50
epochs_per_nn = 1

```

### Step 4 - selection not defined

```

def selection (pool):
    global num_parents

    #choosing te fittest num_parent members of te population
    parents = copy.deepcopy(pool[:num_parents])
    return parents

def crossover(nn1, nn2):
    global p_cross , symp_train_data , train_outputs
    nn1_weights = []
    nn2_weights = []
    child_weights = []

    for layer in nn1.layers:
        nn1_weights.append(layer.get_weights()[0])
        # print(len(nn1_weights[1]))
    for layer in nn2.layers:
        nn2_weights.append(layer.get_weights()[0])

    for i in range(len(nn1_weights)):
        for j in range(len(np.shape(nn1_weights[i]))):
            cross = random.random() #uniform crossover
            if cross<p_cross:
                nn1_weights[i][j] = nn2_weights[i][j];

        child_weights.append(nn1_weights[i])

    mutation(child_weights)
    final_child_weights=nn1.get_weights()

    final_child_weights[0] = child_weights[0]
    final_child_weights[2] = child_weights[1]

    child = ANN()
    child.set_weights(final_child_weights)

```



```

predict_label = child.predict(symp_train_data)
preds_classes = np.argmax(predict_label, axis=-1)
child.fitness = accuracy_score(train_outputs, preds_classes)
print("Fitness of the child is ",str(child.fitness))
return child

```

```

def mutation(child_weights):
    global p_mut
    for i in range(len(child_weights)):
        # selection = random.randint(0, len(child_weights)-1)
        mut = random.random()
        if mut <= p_mut:
            child_weights[i] *= random.uniform(0.8,1.2)
        else:
            pass

```

### Step 5 -

```

# store all active ANNs
networks = []
pool = []
# Generation counter
generation = 0

# Initial Population
for i in range(population):
    pool.append(ANN())

# Track Max Fitness
max_fitness = 0
next_gen_confirmed = []
fitness_per_generation = []

best_model = ANN()

```

### Step 6 -

```

# Evolution Loop
for i in range(epochs):
    generation += 1
    logging.debug("Generation: " + str(generation) + "\r\n")
    networks = []
    for ann in pool:
        # Propagate to calculate fitness score
        # Step 6.1
        ann.compile(optimizer=optimizers.Adam(),
        loss=keras.losses.SparseCategoricalCrossentropy(from_logits=True),
        metrics=[keras.metrics.SparseCategoricalAccuracy()])
        ann.fit(x=symp_train_data, y = train_outputs , epochs =
        epochs_per_nn, verbose=0)
        # Step 6.2
        predict_label = ann.predict(symp_train_data,)
        preds_classes = np.argmax(predict_label, axis=-1)
        ann.fitness = accuracy_score(train_outputs,
        preds_classes)

        # Add to pool after calculating fitness
        networks.append(ann)

```

```

pool = networks
# Sort the population by fitness
# Step 6.3
pool+= next_gen_confirmed

# Step 6.4
pool = sorted(pool, key=lambda x: x.fitness)
pool.reverse()
pool = pool[:population]
next_gen_confirmed = pool[:3]
fitness_per_generation.append(pool[0].fitness)
logging.debug("Max Fitness of generation : " +
str(pool[0].fitness) + "\r\n")

# Step 6.5
if pool[0].fitness > max_fitness:
    max_fitness = pool[0].fitness
    logging.debug("Max Fitness: " + str(max_fitness) +
"\r\n")
    best_model = pool[0]

# Step 6.6
parents = selection(pool)

# Step 6.7 and step 6.8 (Mutation function is called inside the crossover function)
for i in range(len(parents)):
    target = (i+1) % num_parents
    child = crossover(parents[i], parents[target])

# Step 6.9
pool.append(child)

```

## ***PyTorch with Steps of Evolutionary Algorithms***

### **Step 1 –**

```

device = "cuda" if torch.cuda.is_available() else "cpu"

symp_train_data = torch.tensor(x_train.values,
dtype=torch.int64).to(device)
train_outputs = torch.tensor(y_train).to(device)

symp_test_data = torch.tensor(x_test.values,
dtype=torch.int64).to(device)
test_outputs = torch.tensor(y_test).to(device)

categorical_column_sizes = [2 for column in
df.columns.difference(['prognosis'])]
categorical_embedding_sizes = [(2, min(50, (2+1)//2)) for column in
df.columns.difference(['prognosis'])]

```

## Step 2 –

```
class Model(nn.Module):

    def __init__(self, embedding_size, output_size = 48, layers =
[200], p=0.1):
        self.fitness = 0
        super().__init__()
        self.all_embeddings = nn.ModuleList([nn.Embedding(ni, nf)
for ni, nf in embedding_size])
        self.embedding_dropout = nn.Dropout(p)

        all_layers = []
        num_categorical_cols = sum((nf for ni, nf in
embedding_size))
        input_size = num_categorical_cols

        for i in layers:
            all_layers.append(nn.Linear(input_size, i))
            all_layers.append(nn.ReLU(inplace=True))
            all_layers.append(nn.BatchNorm1d(i))
            all_layers.append(nn.Dropout(p))
            input_size = i

        all_layers.append(nn.Linear(layers[-1], output_size))

        self.layers = nn.Sequential(*all_layers)

    def forward(self, x_categorical):
        embeddings = []
        for i,e in enumerate(self.all_embeddings):
            embeddings.append(e(x_categorical[:,i]))
        x = torch.cat(embeddings, 1)

        x = self.embedding_dropout(x)
        x = self.layers(x)

        return x

def train(model, epochs):
    optimizer = torch.optim.Adam(model.parameters(), lr=0.001)
    loss_function = nn.CrossEntropyLoss()

    for i in range(epochs):
        y_pred = model(symp_train_data)

        single_loss = loss_function(y_pred, train_outputs)

        optimizer.zero_grad()
        single_loss.backward()
        optimizer.step()
```

## Step 3 –

```
p_cross = 0.5
p_mut = 0.3
```

```

num_parents = 10
population = 30
epochs = 50
epochs_per_nn = 1

```

#### Step 4 –

```

def selection (pool):
    global num_parents

    #choosing te fittest num_parent members of te population
    parents = copy.deepcopy(pool[:num_parents])
    return parents

def crossover(nn1, nn2):
    global p_cross
    child = Model(categorical_embedding_sizes).to(device)

    for i in range(len(nn1.all_embeddings)):
        if hasattr(nn1.all_embeddings[i], 'weight'):
            for j in range(len(nn1.all_embeddings[i].weight)):
                cross = random.random() #uniform crossover
                if cross < p_cross:
                    child.all_embeddings[i].weight.data[j] =
nn2.all_embeddings[i].weight.data[j];
                else:
                    child.all_embeddings[i].weight.data[j] =
nn1.all_embeddings[i].weight.data[j];

    for i in range(len(nn1.layers)):
        if hasattr(nn1.layers[i], 'weight'):
            for j in range(len(nn1.layers[i].weight)):
                cross = random.random() #uniform crossover
                if cross < p_cross:
                    child.layers[i].weight.data[j] =
nn2.layers[i].weight.data[j];
                else:
                    child.layers[i].weight.data[j] =
nn1.layers[i].weight.data[j];

    child = mutation(child)

    return child

def mutation(child):
    global p_mut
    for i in range(len(child.all_embeddings)):
        if hasattr(child.all_embeddings[i], 'weight'):
            for j in range(len(child.all_embeddings[i].weight)):
                mut = random.random()
                if mut <= p_mut:
                    child.all_embeddings[i].weight.data[j] *=
random.uniform(0.8,1.2)
                else:

```

```

        pass
    for i in range(len(child.layers)):
        if hasattr(child.layers[i], 'weight'):
            for j in range(len(child.layers[i].weight)):
                mut = random.random()
                if mut <= p_mut:
                    child.layers[i].weight.data[j] *=
random.uniform(0.7,1.3)
                else:
                    pass

    return child

```

## Step 5 –

```

# store all active ANNs
networks = []
pool = []
# Generation counter
generation = 0

# Initial Population
for i in range(population):
    pool.append(Model(categorical_embedding_sizes).to(device))
# Track Max Fitness
max_fitness = 0
next_gen_confirmed = []
fitness_per_generation = []

best_model = Model(categorical_embedding_sizes).to(device)

```

## Step 6 –

```

for i in range(epochs):
    generation += 1
    logging.debug("Generation: " + str(generation) + "\r\n")
    networks = []
    for ann in pool:
        # Propagate to calculate fitness score
        #Step 6.1
        train(ann, epochs_per_nn

        #Step 6.2
        predict_label =
ann(symp_train_data).detach().cpu().numpy()
        predict_label = np.argmax(predict_label, axis=-1)
        ann.fitness = accuracy_score(train_outputs.cpu(),
predict_label)
        # Add to pool after calculating fitness
        networks.append(ann)

    pool = networks

    # Step 6.3
    pool+= next_gen_confirmed

```

```

# Step 6.4
pool = sorted(pool, key=lambda x: x.fitness)
pool.reverse()
pool = pool[:population]
next_gen_confirmed = copy.deepcopy(pool[:3])
fitness_per_generation.append(pool[0].fitness)
logging.debug("Max Fitness of generation : " +
str(pool[0].fitness) + "\r\n")

# Step 6.5
if pool[0].fitness > max_fitness:
    max_fitness = pool[0].fitness
    logging.debug("Max Fitness: " + str(max_fitness) +
"\r\n")
    best_model = pool[0]
# Step 6.6
parents = selection(pool)

# Step 6.7 and step 6.8 (Mutation function is called inside the crossover function)
for i in range(len(parents)):
    target = (i+1) % num_parents
    child = crossover(parents[i], parents[target])

# Step 6.9
pool.append(child)

```

# Observations

## CLASSIFIER ACCURACY

- Naïve bayes
  - Train Accuracy – 55.48%
  - Test Accuracy – 53.75%

### On Training Data

Accuracy: 0.5548007246376812				
	precision	recall	f1-score	support
acne	0.79	1.00	0.88	184
acute-respiratory-distress-syndrome-ards	0.47	0.93	0.63	184
acute-sinusitis	0.42	0.83	0.56	184
alcoholic-liver-disease	0.68	0.98	0.81	184
alcohol-withdrawal	0.98	0.99	0.99	184
allergy	0.90	0.98	0.94	184
anemia	0.50	0.92	0.65	184
appendicitis	0.26	1.00	0.42	184
arrhythmia	0.73	0.84	0.78	184
asthma	0.54	0.86	0.67	184
astigmatism	0.50	1.00	0.67	184
bladder-obstruction	1.00	1.00	1.00	184
cerebral-palsy	0.75	1.00	0.86	184
chickenpox	0.91	0.93	0.92	184
cirrhosis	0.98	0.98	0.98	184
common-cold	0.23	0.72	0.35	184
conjunctivitis	0.99	0.99	0.99	184
contact-dermatitis	0.51	0.91	0.66	184
dengue-fever	0.59	0.93	0.72	184
stroke	0.00	0.00	0.00	184
thyroid-disease	0.00	0.00	0.00	184
protein-deficiency	0.00	0.00	0.00	184
rabies	0.00	0.00	0.00	184
scurvy	0.00	0.00	0.00	184
sickle-cell-anemia	0.00	0.00	0.00	184
sinus-bradycardia	0.00	0.00	0.00	184
iron-deficiency-anemia	0.00	0.00	0.00	184
liver-disease	0.68	1.00	0.81	184
malaria	0.55	0.97	0.70	184
mumps	0.00	0.00	0.00	184
myopia	0.00	0.00	0.00	184
flu	0.00	0.00	0.00	184
fungal-infection-of-the-skin	0.00	0.00	0.00	184
gallstone	0.00	0.00	0.00	184
gastritis	0.81	1.00	0.89	184
goiter	0.63	0.90	0.74	184
heat-stroke	0.52	1.00	0.68	184
indigestion	0.32	1.00	0.48	184
osteoarthritis	0.68	0.97	0.80	184
pneumonia	0.51	1.00	0.68	184
tuberculosis	0.36	1.00	0.53	184
typhoid-fever	0.00	0.00	0.00	184
vitamin-a-deficiency	0.00	0.00	0.00	184
vitamin-b12-deficiency	0.00	0.00	0.00	184
vitamin-b-deficiency	0.00	0.00	0.00	184
vitamin-d-deficiency	0.00	0.00	0.00	184
whooping-cough	0.00	0.00	0.00	184
epilepsy	0.00	0.00	0.00	184
accuracy			0.55	8832
macro avg	0.37	0.55	0.43	8832
weighted avg	0.37	0.55	0.43	8832

### On Test Data

Accuracy: 0.5375				
	precision	recall	f1-score	support
acne	0.80	1.00	0.89	20
acute-respiratory-distress-syndrome-ards	0.51	0.90	0.65	20
acute-sinusitis	0.37	0.75	0.49	20
alcoholic-liver-disease	0.70	0.95	0.81	20
alcohol-withdrawal	0.95	1.00	0.98	20
allergy	1.00	0.95	0.97	20
anemia	0.55	0.90	0.68	20
appendicitis	0.26	1.00	0.41	20
arrhythmia	0.70	0.80	0.74	20
asthma	0.44	0.75	0.56	20
astigmatism	0.50	1.00	0.67	20
bladder-obstruction	1.00	1.00	1.00	20
cerebral-palsy	0.71	1.00	0.83	20
chickenpox	0.86	0.90	0.88	20
cirrhosis	0.95	0.95	0.95	20
common-cold	0.15	0.45	0.23	20
conjunctivitis	0.95	1.00	0.98	20
contact-dermatitis	0.46	0.85	0.60	20
dengue-fever	0.61	0.95	0.75	20
stroke	0.00	0.00	0.00	20
thyroid-disease	0.00	0.00	0.00	20
protein-deficiency	0.00	0.00	0.00	20
rabies	0.00	0.00	0.00	20
scurvy	0.00	0.00	0.00	20
sickle-cell-anemia	0.00	0.00	0.00	20
sinus-bradycardia	0.00	0.00	0.00	20
iron-deficiency-anemia	0.00	0.00	0.00	20
liver-disease	0.62	1.00	0.77	20
malaria	0.57	1.00	0.73	20
mumps	0.00	0.00	0.00	20
myopia	0.00	0.00	0.00	20
flu	0.00	0.00	0.00	20
fungal-infection-of-the-skin	0.00	0.00	0.00	20
gallstone	0.00	0.00	0.00	20
gastritis	0.68	0.95	0.79	20
goiter	0.59	0.85	0.69	20
heat-stroke	0.53	1.00	0.69	20
indigestion	0.33	1.00	0.49	20
osteoarthritis	0.60	0.90	0.72	20
pneumonia	0.57	1.00	0.73	20
tuberculosis	0.34	1.00	0.51	20
typhoid-fever	0.00	0.00	0.00	20
vitamin-a-deficiency	0.00	0.00	0.00	20
vitamin-b12-deficiency	0.00	0.00	0.00	20
vitamin-b-deficiency	0.00	0.00	0.00	20
vitamin-d-deficiency	0.00	0.00	0.00	20
whooping-cough	0.00	0.00	0.00	20
epilepsy	0.00	0.00	0.00	20
accuracy			0.54	960
macro avg	0.36	0.54	0.42	960
weighted avg	0.36	0.54	0.42	960

- Normal NN
  - Train Accuracy – 83.45%
  - Test Accuracy – 82.12%



## On Training Data

Accuracy: 0.8345438039037676

	precision	recall	f1-score	support
acne	0.93	0.94	0.93	191
acute-respiratory-distress-syndrome-ards	0.91	0.76	0.83	180
acute-sinusitis	0.69	0.67	0.68	184
alcohol-withdrawal	0.96	0.94	0.95	179
alcoholic-liver-disease	0.95	0.96	0.95	186
allergy	0.94	0.93	0.93	180
anemia	0.90	0.92	0.91	179
appendicitis	0.75	0.86	0.80	182
arrhythmia	0.80	0.84	0.82	187
asthma	0.59	0.69	0.64	183
astigmatism	0.48	0.49	0.49	187
bladder-obstruction	0.97	0.98	0.98	188
cerebral-palsy	0.98	0.98	0.98	179
chickenpox	0.72	0.86	0.79	183
cirrhosis	0.91	0.93	0.92	179
common-cold	0.62	0.54	0.58	186
conjunctivitis	0.91	0.92	0.92	187
contact-dermatitis	0.86	0.79	0.82	177
dengue-fever	0.74	0.68	0.71	184
epilepsy	0.98	0.95	0.96	186
flu	0.68	0.71	0.69	179
fungal-infection-of-the-skin	0.84	0.85	0.85	184
gallstone	0.74	0.81	0.77	187
gastritis	0.65	0.55	0.60	181
goiter	0.87	0.90	0.89	176
heat-stroke	0.97	0.97	0.97	178
indigestion	0.72	0.63	0.67	184
iron-deficiency-anemia	0.92	0.94	0.93	190
liver-disease	0.96	0.91	0.93	186
malaria	0.86	0.87	0.87	182
mumps	1.00	0.96	0.98	184
myopia	0.50	0.48	0.49	188
osteoarthritis	0.97	0.98	0.98	180
pneumonia	0.76	0.72	0.73	186
protein-deficiency	0.90	0.90	0.90	185
rabies	0.73	0.66	0.69	185
scurvy	0.91	0.95	0.93	180
sickle-cell-anemia	0.87	0.94	0.91	189
sinus-bradycardia	0.89	0.79	0.84	184
stroke	0.90	0.91	0.91	183
thyroid-disease	0.93	0.93	0.93	186
tuberculosis	0.96	0.96	0.96	183
typhoid-fever	0.55	0.65	0.60	188
vitamin-a-deficiency	0.95	0.89	0.92	184
vitamin-b-deficiency	0.90	0.91	0.91	177
vitamin-b12-deficiency	0.96	0.96	0.96	188
vitamin-d-deficiency	0.94	0.94	0.94	184
whooping-cough	0.74	0.77	0.75	184
accuracy			0.83	8812
macro avg	0.84	0.83	0.83	8812
weighted avg	0.84	0.83	0.83	8812

## On Test Data

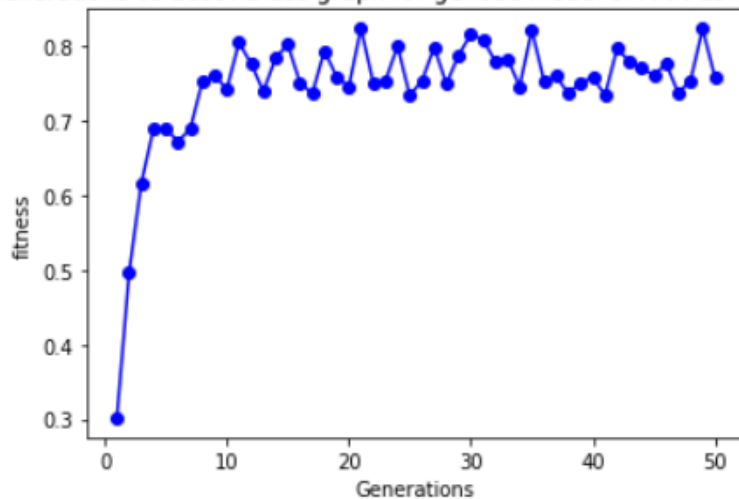
Accuracy: 0.8212461695607763

	precision	recall	f1-score	support
acne	0.80	0.92	0.86	13
acute-respiratory-distress-syndrome-ards	1.00	0.75	0.86	24
acute-sinusitis	0.67	0.50	0.57	20
alcohol-withdrawal	0.96	0.92	0.94	25
alcoholic-liver-disease	1.00	1.00	1.00	18
allergy	0.92	1.00	0.96	24
anemia	0.95	0.76	0.84	25
appendicitis	0.67	0.73	0.70	22
arrhythmia	0.57	0.76	0.65	17
asthma	0.73	0.76	0.74	21
astigmatism	0.41	0.41	0.41	17
bladder-obstruction	1.00	1.00	1.00	16
cerebral-palsy	0.96	0.96	0.96	25
chickenpox	0.76	0.90	0.83	21
cirrhosis	0.89	1.00	0.94	25
common-cold	0.47	0.44	0.46	18
conjunctivitis	0.75	0.88	0.81	17
contact-dermatitis	0.83	0.74	0.78	27
dengue-fever	0.62	0.40	0.48	20
epilepsy	1.00	1.00	1.00	18
flu	0.70	0.84	0.76	25
fungal-infection-of-the-skin	0.85	0.85	0.85	20
gallstone	0.60	0.75	0.67	16
gastritis	0.69	0.48	0.56	23
goiter	1.00	0.89	0.94	28
heat-stroke	0.96	1.00	0.98	26
indigestion	0.74	0.70	0.72	20
iron-deficiency-anemia	0.87	0.93	0.90	14
liver-disease	1.00	0.89	0.94	18
malaria	0.84	0.95	0.89	22
mumps	1.00	0.80	0.89	20
myopia	0.33	0.31	0.32	16
osteoarthritis	1.00	0.96	0.98	24
pneumonia	0.79	0.61	0.69	18
protein-deficiency	0.75	0.95	0.84	19
rabies	0.81	0.68	0.74	19
scurvy	0.96	0.96	0.96	24
sickle-cell-anemia	0.88	0.93	0.90	15
sinus-bradycardia	0.70	0.70	0.70	20
stroke	0.95	0.95	0.95	21
thyroid-disease	0.90	1.00	0.95	18
tuberculosis	0.95	0.90	0.93	21
typhoid-fever	0.50	0.81	0.62	16
vitamin-a-deficiency	0.95	0.90	0.92	20
vitamin-b-deficiency	1.00	0.85	0.92	27
vitamin-b12-deficiency	0.89	1.00	0.94	16
vitamin-d-deficiency	0.95	0.95	0.95	20
whooping-cough	0.70	0.80	0.74	20
accuracy			0.82	979
macro avg	0.82	0.82	0.81	979
weighted avg	0.83	0.82	0.82	979

- PyGad

- Train Accuracy – 81.75%
- Test Accuracy – 78.33%

Generations vs best fitness graph for genetic model of ANN using PyGad



## On Training Data

Accuracy: 0.8175951086956522

	precision	recall	f1-score	support
acne	0.95	0.98	0.97	184
acute-respiratory-distress-syndrome-ards	0.93	0.88	0.91	184
acute-sinusitis	0.63	0.82	0.71	184
alcohol-withdrawal	0.72	0.98	0.83	184
alcoholic-liver-disease	0.98	0.99	0.99	184
allergy	0.90	0.98	0.94	184
anemia	1.00	0.92	0.96	184
appendicitis	0.88	0.82	0.85	184
arrhythmia	0.96	0.84	0.90	184
asthma	0.75	0.78	0.77	184
astigmatism	0.52	0.54	0.53	184
bladder-obstruction	1.00	1.00	1.00	184
cerebral-palsy	0.87	1.00	0.93	184
chickenpox	0.97	0.92	0.94	184
cirrhosis	0.99	0.98	0.98	184
common-cold	0.44	0.70	0.54	184
conjunctivitis	0.99	0.99	0.99	184
contact-dermatitis	0.83	0.83	0.83	184
dengue-fever	0.85	0.63	0.72	184
epilepsy	0.00	0.00	0.00	184
flu	0.71	0.82	0.76	184
fungal-infection-of-the-skin	0.88	0.89	0.88	184
gallstone	0.75	0.86	0.80	184
gastritis	0.60	0.66	0.67	184
goiter	0.62	0.92	0.74	184
heat-stroke	0.99	1.00	1.00	184
indigestion	0.68	0.73	0.71	184
iron-deficiency-anemia	0.93	1.00	0.96	184
liver-disease	0.97	0.96	0.97	184
malaria	0.94	0.99	0.97	184
mumps	1.00	0.99	0.99	184
myopia	0.52	0.49	0.51	184
osteoarthritis	1.00	0.99	1.00	184
pneumonia	0.73	0.92	0.81	184
protein-deficiency	0.98	1.00	0.99	184
rabies	0.78	0.83	0.81	184
scurvy	0.96	0.99	0.97	184
sickle-cell-anemia	0.94	1.00	0.97	184
sinus-bradycardia	0.83	0.96	0.89	184
stroke	0.59	1.00	0.74	184
thyroid-disease	0.93	0.99	0.96	184
tuberculosis	1.00	1.00	1.00	184
typhoid-fever	0.58	0.69	0.63	184
vitamin-a-deficiency	0.99	0.96	0.97	184
vitamin-b-deficiency	0.00	0.00	0.00	184
vitamin-b12-deficiency	0.61	0.99	0.75	184
vitamin-d-deficiency	0.00	0.00	0.00	184
whooping-cough	0.00	0.00	0.00	184
accuracy			0.82	8832
macro avg	0.77	0.82	0.79	8832
weighted avg	0.77	0.82	0.79	8832

## On Test Data

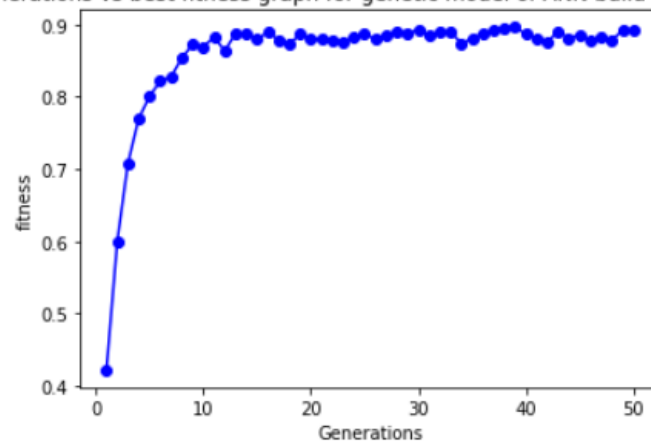
Accuracy: 0.7833333333333333

	precision	recall	f1-score	support
acne	0.95	0.95	0.95	20
acute-respiratory-distress-syndrome-ards	0.79	0.75	0.77	20
acute-sinusitis	0.47	0.75	0.58	20
alcohol-withdrawal	0.73	0.95	0.83	20
alcoholic-liver-disease	0.95	1.00	0.98	20
allergy	1.00	0.95	0.97	20
anemia	1.00	0.90	0.95	20
appendicitis	0.81	0.65	0.72	20
arrhythmia	0.89	0.80	0.84	20
asthma	0.67	0.60	0.63	20
astigmatism	0.48	0.50	0.49	20
bladder-obstruction	1.00	1.00	1.00	20
cerebral-palsy	0.83	1.00	0.91	20
chickenpox	0.95	0.90	0.92	20
cirrhosis	0.95	0.95	0.95	20
common-cold	0.30	0.35	0.33	20
conjunctivitis	1.00	1.00	1.00	20
contact-dermatitis	0.89	0.80	0.84	20
dengue-fever	1.00	0.60	0.75	20
epilepsy	0.00	0.00	0.00	20
flu	0.62	0.75	0.68	20
fungal-infection-of-the-skin	0.79	0.95	0.86	20
gallstone	0.61	0.85	0.71	20
gastritis	0.64	0.45	0.53	20
goiter	0.62	1.00	0.77	20
heat-stroke	1.00	1.00	1.00	20
indigestion	0.59	0.85	0.69	20
iron-deficiency-anemia	0.87	1.00	0.93	20
liver-disease	1.00	0.90	0.95	20
malaria	0.95	0.90	0.92	20
mumps	1.00	1.00	1.00	20
myopia	0.47	0.45	0.46	20
osteoarthritis	1.00	1.00	1.00	20
pneumonia	0.62	0.90	0.73	20
protein-deficiency	0.90	0.95	0.93	20
rabies	0.71	0.75	0.73	20
scurvy	0.95	1.00	0.98	20
sickle-cell-anemia	0.91	1.00	0.95	20
sinus-bradycardia	0.75	0.90	0.82	20
stroke	0.65	1.00	0.78	20
thyroid-disease	1.00	1.00	1.00	20
tuberculosis	1.00	0.95	0.97	20
typhoid-fever	0.52	0.70	0.60	20
vitamin-a-deficiency	1.00	0.95	0.97	20
vitamin-b-deficiency	0.00	0.00	0.00	20
vitamin-b12-deficiency	0.62	1.00	0.77	20
vitamin-d-deficiency	0.00	0.00	0.00	20
whooping-cough	0.00	0.00	0.00	20
accuracy			0.78	960
macro avg	0.74	0.78	0.75	960
weighted avg	0.74	0.78	0.75	960

### • Keras with Steps of Evolutionary Algorithms

- Training Time – 15 min 43 sec
- Train Accuracy – 89.66%
- Test Accuracy – 85.45%

Generations vs best fitness graph for genetic model of ANN build using Keras



## On Training Data

Accuracy: 0.8966259057971014

	precision	recall	f1-score	support
acne	0.98	0.95	0.97	184
acute-respiratory-distress-syndrome-ards	0.95	0.88	0.91	184
acute-sinusitis	0.91	0.62	0.74	184
alcohol-withdrawal	0.99	0.99	0.99	184
alcoholic-liver-disease	0.98	0.99	0.99	184
allergy	1.00	0.96	0.98	184
anemia	0.99	0.91	0.95	184
appendicitis	1.00	0.74	0.85	184
arrhythmia	0.99	0.81	0.89	184
asthma	0.93	0.71	0.80	184
astigmatism	0.57	0.54	0.56	184
bladder-obstruction	1.00	1.00	1.00	184
cerebral-palsy	1.00	1.00	1.00	184
chickenpox	0.91	0.96	0.93	184
cirrhosis	0.99	0.98	0.99	184
common-cold	0.58	0.86	0.69	184
conjunctivitis	0.99	0.99	0.99	184
contact-dermatitis	0.84	0.89	0.86	184
dengue-fever	0.73	0.77	0.75	184
epilepsy	1.00	1.00	1.00	184
flu	0.95	0.80	0.87	184
fungal-infection-of-the-skin	0.90	0.87	0.89	184
gallstone	0.88	0.83	0.85	184
gastritis	0.57	0.85	0.68	184
goiter	0.96	0.95	0.96	184
heat-stroke	1.00	0.99	1.00	184
indigestion	0.80	0.67	0.73	184
iron-deficiency-anemia	0.94	0.99	0.97	184
liver-disease	0.98	0.95	0.96	184
malaria	0.95	0.99	0.97	184
mumps	1.00	0.99	0.99	184
myopia	0.56	0.59	0.57	184
osteoarthritis	1.00	0.99	1.00	184
pneumonia	0.66	0.99	0.79	184
protein-deficiency	1.00	0.94	0.97	184
rabies	0.78	0.84	0.81	184
scurvy	0.97	0.98	0.98	184
sickle-cell-anemia	0.99	1.00	1.00	184
sinus-bradycardia	0.84	0.97	0.90	184
stroke	1.00	0.99	0.99	184
thyroid-disease	0.96	0.96	0.96	184
tuberculosis	1.00	1.00	1.00	184
typhoid-fever	0.67	0.58	0.62	184
vitamin-a-deficiency	0.98	0.97	0.98	184
vitamin-b-deficiency	0.99	0.98	0.99	184
vitamin-b12-deficiency	0.99	1.00	1.00	184
vitamin-d-deficiency	0.99	1.00	1.00	184
whooping-cough	0.85	0.80	0.83	184
accuracy			0.90	8832
macro avg	0.91	0.90	0.90	8832
weighted avg	0.91	0.90	0.90	8832

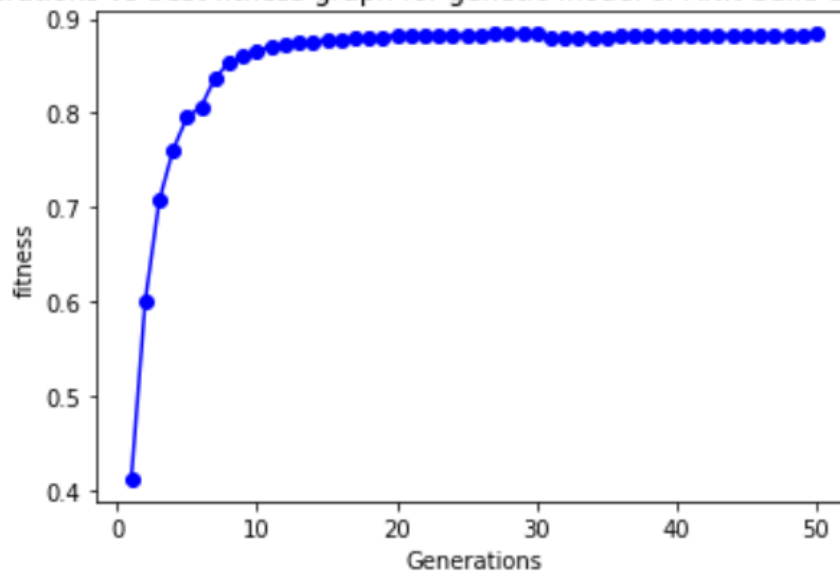
## On Test Data

Accuracy: 0.8545063405797102

	precision	recall	f1-score
acne	0.96	0.97	0.97
acute-respiratory-distress-syndrome-ards	0.95	0.88	0.91
acute-sinusitis	0.87	0.64	0.74
alcohol-withdrawal	0.71	0.98	0.82
alcoholic-liver-disease	0.98	0.99	0.99
allergy	0.98	0.97	0.98
anemia	1.00	0.91	0.95
appendicitis	1.00	0.74	0.85
arrhythmia	1.00	0.80	0.89
asthma	0.76	0.76	0.76
astigmatism	0.57	0.58	0.57
bladder-obstruction	1.00	1.00	1.00
cerebral-palsy	0.81	1.00	0.90
chickenpox	0.87	0.98	0.92
cirrhosis	0.99	0.98	0.99
common-cold	0.45	0.89	0.60
conjunctivitis	0.99	0.99	0.99
contact-dermatitis	0.92	0.80	0.85
dengue-fever	0.74	0.76	0.75
epilepsy	0.00	0.00	0.00
flu	0.93	0.80	0.86
fungal-infection-of-the-skin	0.89	0.90	0.89
gallstone	0.93	0.80	0.86
gastritis	0.60	0.74	0.67
goiter	0.95	0.97	0.96
heat-stroke	1.00	0.99	1.00
indigestion	0.64	0.83	0.72
iron-deficiency-anemia	0.94	0.99	0.96
liver-disease	0.98	0.95	0.96
malaria	0.96	0.99	0.97
mumps	1.00	0.99	0.99
myopia	0.57	0.55	0.56
osteoarthritis	1.00	0.99	1.00
pneumonia	0.52	1.00	0.69
protein-deficiency	1.00	0.93	0.96
rabies	0.77	0.80	0.79
scurvy	0.97	0.98	0.98
sickle-cell-anemia	0.99	1.00	1.00
sinus-bradycardia	0.84	0.98	0.90
stroke	1.00	0.99	0.99
thyroid-disease	0.98	0.95	0.96
tuberculosis	1.00	1.00	1.00
typhoid-fever	0.67	0.62	0.65
vitamin-a-deficiency	0.98	0.97	0.98
vitamin-b-deficiency	0.98	0.98	0.98
vitamin-b12-deficiency	0.75	0.99	0.85
vitamin-d-deficiency	1.00	0.70	0.82
whooping-cough	0.00	0.00	0.00
accuracy			0.85
macro avg	0.84	0.85	0.84
weighted avg	0.84	0.85	0.84

- PyTorch with Steps of Evolutionary Algorithms
  - Training Time – 2 min 7 sec (more than **7 times speedup when compared to Keras Model**. This is due to the fact that in PyTorch model, **we can transfer the data tensors along with model to the device side i.e. the GPU side and thus increasing the efficiency of GPU** and hence exponentially decreasing the training time)
  - Train Accuracy – 89.71%
  - Test Accuracy – 83.69%

Generations vs best fitness graph for genetic model of ANN build using PyTorch



On Training Data

Accuracy: 0.8971920289855072

	precision	recall	f1-score	support
acne	0.98	0.96	0.97	184
acute-respiratory-distress-syndrome-ards	0.96	0.86	0.91	184
acute-sinusitis	0.91	0.62	0.74	184
alcohol-withdrawal	0.99	0.99	0.99	184
alcoholic-liver-disease	0.99	0.98	0.99	184
allergy	0.99	0.97	0.98	184
anemia	0.99	0.91	0.95	184
appendicitis	0.98	0.76	0.85	184
arrhythmia	0.98	0.82	0.89	184
asthma	0.91	0.72	0.81	184
astigmatism	0.57	0.52	0.55	184
bladder-obstruction	1.00	1.00	1.00	184
cerebral-palsy	1.00	1.00	1.00	184
chickenpox	0.89	0.97	0.93	184
cirrhosis	0.98	0.99	0.99	184
common-cold	0.62	0.76	0.68	184
conjunctivitis	0.99	0.99	0.99	184
contact-dermatitis	0.85	0.86	0.86	184
dengue-fever	0.74	0.76	0.75	184
epilepsy	1.00	1.00	1.00	184
flu	0.95	0.80	0.87	184
fungal-infection-of-the-skin	0.92	0.86	0.89	184
gallstone	0.80	0.90	0.84	184
gastritis	0.62	0.74	0.68	184
goiter	0.95	0.97	0.96	184
heat-stroke	1.00	0.99	1.00	184
indigestion	0.74	0.72	0.73	184
iron-deficiency-anemia	0.94	0.99	0.97	184
liver-disease	0.99	0.93	0.96	184
malaria	0.96	0.99	0.98	184
mumps	1.00	0.99	0.99	184
myopia	0.56	0.61	0.58	184
osteoarthritis	1.00	0.99	1.00	184
pneumonia	0.68	0.98	0.80	184
protein-deficiency	1.00	0.95	0.97	184
rabies	0.79	0.79	0.79	184
scurvy	0.95	1.00	0.98	184
sickle-cell-anemia	0.99	1.00	1.00	184
sinus-bradycardia	0.85	0.96	0.90	184
stroke	0.99	0.99	0.99	184
thyroid-disease	0.97	0.95	0.96	184
tuberculosis	1.00	1.00	1.00	184
typhoid-fever	0.65	0.64	0.64	184
vitamin-a-deficiency	1.00	0.95	0.97	184
vitamin-b-deficiency	1.00	0.98	0.99	184
vitamin-b12-deficiency	0.99	1.00	1.00	184
vitamin-d-deficiency	1.00	0.99	1.00	184
whooping-cough	0.74	0.92	0.82	184
accuracy			0.90	8832
macro avg	0.90	0.90	0.90	8832
weighted avg	0.90	0.90	0.90	8832

On Test Data

Accuracy: 0.8369565217391305

	precision	recall	f1-score	support
acne	0.98	0.96	0.97	184
acute-respiratory-distress-syndrome-ards	0.97	0.85	0.91	184
acute-sinusitis	0.86	0.65	0.74	184
alcohol-withdrawal	0.74	0.99	0.85	184
alcoholic-liver-disease	0.98	0.99	0.99	184
allergy	1.00	0.96	0.98	184
anemia	0.99	0.92	0.95	184
appendicitis	0.99	0.75	0.85	184
arrhythmia	1.00	0.80	0.89	184
asthma	0.78	0.78	0.78	184
astigmatism	0.57	0.59	0.58	184
bladder-obstruction	1.00	1.00	1.00	184
cerebral-palsy	0.81	1.00	0.90	184
chickenpox	0.88	0.98	0.93	184
cirrhosis	0.99	0.98	0.99	184
common-cold	0.47	0.82	0.60	184
conjunctivitis	0.99	0.99	0.99	184
contact-dermatitis	0.85	0.86	0.86	184
dengue-fever	0.75	0.76	0.75	184
epilepsy	0.00	0.00	0.00	184
flu	0.77	0.85	0.81	184
fungal-infection-of-the-skin	0.92	0.86	0.89	184
gallstone	0.88	0.84	0.86	184
gastritis	0.60	0.80	0.69	184
goiter	0.59	0.97	0.73	184
heat-stroke	1.00	0.99	1.00	184
indigestion	0.71	0.73	0.72	184
iron-deficiency-anemia	0.94	0.99	0.97	184
liver-disease	0.99	0.95	0.97	184
malaria	0.91	0.99	0.95	184
mumps	1.00	0.99	0.99	184
myopia	0.57	0.54	0.56	184
osteoarthritis	1.00	0.99	1.00	184
pneumonia	0.53	1.00	0.70	184
protein-deficiency	1.00	0.95	0.97	184
rabies	0.78	0.80	0.79	184
scurvy	0.97	0.98	0.98	184
sickle-cell-anemia	0.79	0.99	0.88	184
sinus-bradycardia	0.84	0.98	0.90	184
stroke	0.99	0.98	0.99	184
thyroid-disease	0.98	0.95	0.96	184
tuberculosis	1.00	1.00	1.00	184
typhoid-fever	0.66	0.63	0.64	184
vitamin-a-deficiency	0.98	0.97	0.98	184
vitamin-b-deficiency	1.00	0.79	0.88	184
vitamin-b12-deficiency	0.70	1.00	0.83	184
vitamin-d-deficiency	0.00	0.00	0.00	184
whooping-cough	0.00	0.00	0.00	184
accuracy			0.84	8832
macro avg	0.81	0.84	0.82	8832
weighted avg	0.81	0.84	0.82	8832

- Random Forest Classifier
  - Train Accuracy – 86.08%
  - Test Accuracy – 78.43%

### On Training Data

Accuracy: 0.8608469202898551

	precision	recall	f1-score	support
acne	0.97	0.96	0.97	184
acute-respiratory-distress-syndrome-ards	0.95	0.87	0.91	184
acute-sinusitis	0.96	0.58	0.72	184
alcoholic-liver-disease	0.75	0.98	0.85	184
alcohol-withdrawal	0.99	0.98	0.99	184
allergy	0.99	0.97	0.98	184
anemia	0.99	0.92	0.95	184
appendicitis	0.99	0.74	0.85	184
arrhythmia	0.99	0.81	0.89	184
asthma	0.79	0.75	0.77	184
astigmatism	0.57	0.55	0.56	184
bladder-obstruction	1.00	1.00	1.00	184
cerebral-palsy	0.83	1.00	0.91	184
chickenpox	0.89	0.97	0.93	184
cirrhosis	0.98	0.99	0.99	184
common-cold	0.44	0.92	0.59	184
conjunctivitis	0.99	0.99	0.99	184
contact-dermatitis	0.86	0.86	0.86	184
dengue-fever	0.73	0.77	0.75	184
stroke	0.00	0.00	0.00	184
thyroid-disease	0.88	0.82	0.85	184
protein-deficiency	0.92	0.86	0.89	184
rabies	0.86	0.85	0.85	184
scurvy	0.62	0.72	0.67	184
sickle-cell-anemia	0.93	0.98	0.96	184
sinus-bradycardia	1.00	0.99	1.00	184
iron-deficiency-anemia	0.67	0.80	0.73	184
liver-disease	0.95	0.98	0.97	184
malaria	0.98	0.95	0.96	184
mumps	0.97	0.99	0.98	184
myopia	1.00	0.99	0.99	184
flu	0.56	0.58	0.57	184
fungal-infection-of-the-skin	1.00	0.99	1.00	184
gallstone	0.62	1.00	0.77	184
gastritis	1.00	0.95	0.97	184
goiter	0.76	0.84	0.80	184
heat-stroke	0.97	0.98	0.98	184
indigestion	0.99	1.00	1.00	184
osteoarthritis	0.84	0.97	0.90	184
pneumonia	1.00	0.98	0.99	184
tuberculosis	0.99	0.93	0.96	184
typhoid-fever	1.00	1.00	1.00	184
vitamin-a-deficiency	0.69	0.59	0.63	184
vitamin-b12-deficiency	0.98	0.97	0.98	184
vitamin-b-deficiency	0.98	0.99	0.98	184
vitamin-d-deficiency	0.69	1.00	0.82	184
whooping-cough	1.00	0.99	1.00	184
epilepsy	0.00	0.00	0.00	184
accuracy			0.86	8832
macro avg	0.84	0.86	0.85	8832
weighted avg	0.84	0.86	0.85	8832

### On Test Data

Accuracy: 0.784375

	precision	recall	f1-score	support
acne	0.95	0.90	0.92	20
acute-respiratory-distress-syndrome-ards	0.74	0.70	0.72	20
acute-sinusitis	0.63	0.60	0.62	20
alcoholic-liver-disease	0.76	0.95	0.84	20
alcohol-withdrawal	0.95	1.00	0.98	20
allergy	1.00	0.95	0.97	20
anemia	0.95	0.90	0.92	20
appendicitis	1.00	0.65	0.79	20
arrhythmia	0.89	0.80	0.84	20
asthma	0.56	0.50	0.53	20
astigmatism	0.05	0.05	0.05	20
bladder-obstruction	1.00	1.00	1.00	20
cerebral-palsy	0.83	1.00	0.91	20
chickenpox	0.86	0.90	0.88	20
cirrhosis	1.00	0.90	0.95	20
common-cold	0.36	0.60	0.45	20
conjunctivitis	1.00	1.00	1.00	20
contact-dermatitis	0.79	0.75	0.77	20
dengue-fever	0.57	0.60	0.59	20
stroke	0.00	0.00	0.00	20
thyroid-disease	0.94	0.75	0.83	20
protein-deficiency	0.77	0.85	0.81	20
rabies	0.62	0.75	0.68	20
scurvy	0.47	0.45	0.46	20
sickle-cell-anemia	0.95	1.00	0.98	20
sinus-bradycardia	1.00	1.00	1.00	20
iron-deficiency-anemia	0.43	0.60	0.50	20
liver-disease	0.90	0.95	0.93	20
malaria	1.00	0.85	0.92	20
mumps	0.95	0.95	0.95	20
myopia	1.00	1.00	1.00	20
flu	0.10	0.10	0.10	20
fungal-infection-of-the-skin	1.00	1.00	1.00	20
gallstone	0.51	1.00	0.68	20
gastritis	1.00	0.95	0.97	20
goiter	0.63	0.60	0.62	20
heat-stroke	0.95	0.95	0.95	20
indigestion	0.95	1.00	0.98	20
osteoarthritis	0.81	0.85	0.83	20
pneumonia	1.00	1.00	1.00	20
tuberculosis	1.00	0.95	0.97	20
typhoid-fever	1.00	0.90	0.95	20
vitamin-a-deficiency	0.50	0.50	0.50	20
vitamin-b12-deficiency	0.95	0.95	0.95	20
vitamin-b-deficiency	1.00	1.00	1.00	20
vitamin-d-deficiency	0.67	1.00	0.80	20
whooping-cough	1.00	1.00	1.00	20
epilepsy	0.00	0.00	0.00	20
accuracy			0.78	960
macro avg	0.77	0.78	0.77	960
weighted avg	0.77	0.78	0.77	960

# Conclusion

All the above results can be summarised as -

S. No.	Approach	Train Accuracy	Test Accuracy
1	Naïve Bayes Classifier	55.48%	53.75
2	Simple Artificial Neural Net Classifier using Keras	83.45%	82.12%
3	PyGad	81.75%	78.33%
4	ANN Model using Keras + manual evolutionary algorithm's steps	89.66%	85.45%
5	ANN Model using PyTorch + manual evolutionary algorithm's steps	89.71%	83.69%
6	Random Forest Classifier	86.08%	78.43%

From the above table we can see that –

- While a simple ANN can outperform naïve bayes by a large margin, it is still behind the Random Forest Classifier in terms of accuracy.
- On applying PyGad, a decrease in performance was observed and on further reasearch it was found that t is still a package still under development. Due to this they have yet not been able to provide proper benefit of Evolutionary Algorithms
- We can also see that while PyTorch and Keras Models give similar accuracies, there is a large difference in terms of their training time for same hyperparameters.
- We can see that on writing functions for selection, crossover and mutation from scratch and using them along with the ANN has lead to a significant increase in performance and the resulting model is now even better than the Random Forest Classifier.

So from all the above points we can safely conclude that **ANN Model using PyTorch along with manual evolutionary algorithm's steps** have outperformed all the other models.

# References and Regards

- PyGAD documentation: <https://pygad.readthedocs.io/en/latest/>
- Application of GA in ANN: <https://medium.com/swlh/genetic-algorithm-in-artificial-neural-network-5f5b9c9467d0>
- Building models with Keras and PyTorch: <https://medium.com/deep-learning-with-keras/which-activation-loss-functions-in-multi-class-clasification-4cd599e4e61f>