Intelligent Neural Network For Bacteria Classification: An Innovation In Artificial Neural Network

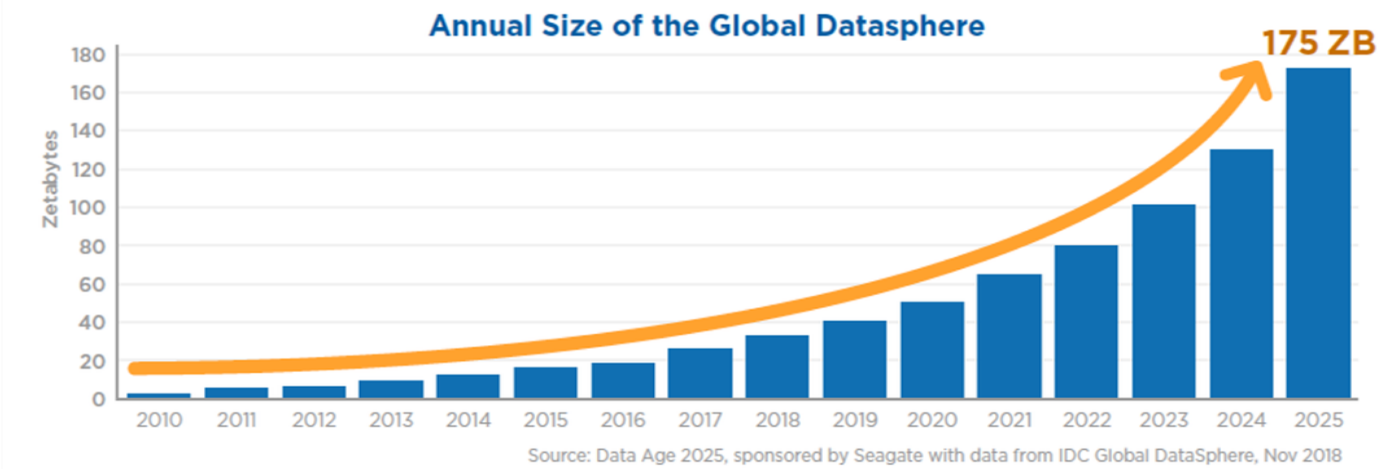
Ananda Khamaru, Sunil Karforma, Soumendranath Chatterjee, Ishita Saha Raktima Bandyopadhyay

Abstract : The work focused on reliable outcome from next generation artificial neural network (ANN). ANN was efficiently used for decision making on labeled and unlabeled data but problem was that it was always generated as a result though the short input data. The conventional ANN model is being used in some financial sectors for prediction and analysis of financial data, but it would not make an outcome due to less applicable data. Our objective is to design a neural network which will have the intelligence by which it can generate most prominent decision. A mathematical model of new generation artificial neural network called Intelligent Neural Network (INN) has been proposed, which would solve that problem and would make the decision like a human. The INN model has been designed with two layers of fully connected neurons, where the first layer neurons has taken input as the features of bacteria and produced input for hidden neurons; and in the second layer the output from hidden neurons provided as input of decision neurons and the output of decision neurons was the expected result. This model was trained by back propagation process by reducing Sum Squared Error(SSE) through Stochastic Gradient Descent(SGD) technique. Prediction accuracy of this model was 97.11% to distinguish medically important bacteria. This study would help to laboratory users to identify medically important bacteria in an easy way.

Index Terms : Medically important bacteria, INN, Cost function, SGD, SSE

1. INTRODUCTION

Adopting machine learning approach in every sector there is a new trend for better decision making and curtailing time. Massive amount of data population from huge Iot devices may increase upto 175 zeta byte by 2025 [1]. We are unable to analyse such large scale data manually, for that reason, we require statistical based computer program. In this paper we propose a robust method named as Intelligent Neural Network (INN) is an innovation in ANN. It will help to the researcher to get actual outcome on decision making or to analyse research outcome based on neural network. The INN provides a clear perception on object classification, data analysis and prediction problem. In this paper our proposed algorithm is used on bacterial classification, where we have taken thirteen organisms along with their six fundamental biochemical properties. The thirteen pathogenic bacteria are Escherichia coli, Enterobacter aerogenes, Klebsiella pneumonia, Shigella dysenteriae, Salmonella typhimurium, Proteus vulgaris, Pseudomonas aeruginosa, Alcaligenes faecalis, Staphylococcus aureus, Lactococcus lactis, Micrococcus luteus, Corynebacterium xerosis, and Bacillus cereus. Pathogenic strains of Escherichia coli are mainly responsible for traveler's diarrhea and urinary tract infection [5]. E.0157 is a harmful bacterial species which can produce toxins; infants and old aged persons may suffer from dehydration, renal diseases , anemia, and organ malfunction [7]. Enterobacter aerogenes is widely prevalent in the environment and generally exist in vegetables, soil, fresh water, human and animal -excreta. E. aerogenes can be found in postoperative wound infections or abscesses. The antimicrobial treatment can heal the patient infected by Enterobacter aerogenes. Klebsiella is a hospital-acquired pathogenic organism causing of urinary tract infections and nosocomial pneumonia [11]. Shigella dysenteriae is found in water and unhygienic food. S.dysenteriae can survive outside of the human body and is



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transmitted from one person to another through fecal-oral contact or mechanical transmitter like houseflies.. It is liable for abdominal pain, bloody diarrhoea, stomach cramps, and fever in human beings [12, 13]. Salmonella typhimurium is the causative agent of acute intestinal inflammation, fever, and diarrhea. S.typhimurium is also accountable for typhoid fever in humans [16]. Proteus vulgaris is non-spore forming motile bacterial species with various modes of transmission [17, 19] Pseudomonas aeruginosa is responsible for chronic infections in skin (burn or surgical wounds), urinary tract, and respiratory tract of humans [20]. P.aeruginosa is widely ubiquitous in nature and showed its optimum growth in between 25^0C to 37^0C temperature [21]. Alcaligenes faecalis is acquired from moist items such as nebulizers, respirators, and lavage of fluids [23]. Staphylococcus aureus is a group of bacteria liable for several infections in tissues of the body. S.aureus is causative agent of infections in lactating women, newborn babies , and people having chronic diseases like vascular disease, lung disease, cancer, and diabetes [26]. Lactococcus lactis was first screened from green plants and showed the ability to grow on various sugars. L.lactis bacteria can boost the immune system to recover allergies, hypertension, and show beneficial effects on the skin, and IBD [27]. L.lactis is well known probiotic for human health. Micrococcus luteus is present in the respiratory tract and mucosal linings of the upper pharynx of humans and can survive in an environment with high salt concentration or little water at a 37^0C temperature [28, 29]. Corynebacterium xerosis is well known virulent species and causes peritonitis, septicemia, pleura pneumonia, endo carditic, osteomyelitis, meningitis, septic arthritis and ventriculitis especially in surgical patients or immunocompromised patients [30]. Bacillus cereus is commonly found in soil and variety of foods. B.cereus is the causative agent of diarrhea, vomiting, and nausea due to its toxin production [31]. These genera are more imperative in medical science and biochemical characterizations are generally done to identify these medically important pathogenic bacteria. Now Bacterial taxonomy is based on the polyphasic methods i.e. phenotypic, biochemical, serotypic and molecular methods. Soft-computing is a new area in the field of bacterial identification. Neural network has been exoploted as a soft-computing based classifier for the taxonomy of pathogenic bacteria. An Intelligent Neural Network has been considered as a mathematical model for information processing.[32]. INN(Intelligent Neural Network) has become a new branch of a technological revolution for sharp and concrete decision making in the field of taxonomy of organism. In the digital universe most of the complex operations are being done through programmable intelligent electronic devices. The neural network extensively have been widely used in many research fields such as voice recognition, face recognition, pattern matching, data analytics, and smart pathological equipment development and so on. During the present study, intelligent neural network has been applied as a soft-computing based classifier in the taxonomy of medically important pathogenic bacteria. Results of the present piece of work has been discussed in section 2 and the next generation Intelligent Neural Network method and its various important parts have been discussed in section 3 and finally concluded in section 4.

2 Literature Review

In this section, we discussed some relevant research works which have been done by the application of Artificial Neural Network (ANN).Larsen et al. in 2015 [2] found and analysed some ecologically important microbial communities. . The authors focused on the prediction of microbial community structure by using Artificial Neural Network (ANN) and revealed a Microbial Assembled Prediction (MAP) model which could work on environmental parameters. In this study the ANN based model basically was used to determine bacterial community structure fluctuation with the changes of environment. Shen and Bax in 2015 [3] developed a neural network based robust TALOS-N computer program for protein structural study by NMR spectroscopy. Through this, study TALOS-N was found to be a useful tool to get torsion angles by analyzing chemical shifts of its backbone and also to calculate the NMR protein structure.The application of of neural network method in TALOS-N program it was possible to predict the side-chain $\chi 1$ torsion angles and if maximum outcome probability did not satisfy the cutoff value, then outcome was shown as not predicted otherwise predicted. Here cutoff value was a barrier for prediction.

In[41] Zieliński et al. delineated their texture model, which used deep neural network for the classification of bacteria by their texture of colony images. In the context of deep learning architecture, the CNNs (Convolution Neural Network) have been used to classify the species by the variations of Random Forest algorithm and SVM. However, the texture model has encountered a demand of recognizing species with asymmetrical formations.Huang et al.[42] utilized machine learning methods for the characterization and classification of eighteen bacterial species. All the bacterial species were disease-causing agents in human and subhuman primates. Based on the colony morphology, the authors used three different algorithms to classify the species. The Convolution Neural Network (CNN) and Auto encoder have been used to implement supervised and unsupervised methods respectively, for the classification of bacterial species. This model was successful up to 90% in the accuracy of identifying bacterial species . In the above related works, the authors have not clarified actual outcome on decision and prediction related problem when short input has applied in the trained neural network. During our study, we focused on actual possible outcome regarding input in the INN. Use of this model in laboratory, the user would not be confused about the species and prediction accuracy would be more than the previous works as explained in this section.

3 Methodology

3.1 Design of INN

In this section, we proposed a robust Intelligent Neural Network (INN) method, an innovation of next generation ANN. The INN provides a clear perception on decision making, prediction and classification related problem based on the satisfactory constant which would be fixed by the minimum possible value from training outcome. In this study we proposed a two layered INN to train and predict the thirteen medically important disease causing bacteria, where entire training has been accomplished through forward and backward propagation. These two propagation criteria have been divided into two separate ways for training to the INN. In

the first propagation the input features have been applied to the initial nodes and computed output has been forwarded to the next level nodes as input; computed output has been forwarded to the next level to generate a set of outputs. A mathematical function with fixed synaptic weights of neurons has been used in the forward propagation, and the signal has been computed for each neuron [37, 38]. The function produced yield for neuron j as

$$y_j(n) = \Psi(\vartheta_j(n) + Bias\ ) \quad (1.1)$$

Where, n is the number of repetition and $\vartheta_j(n)$ is the measured yield at the local field of neuron j, defined as

$$\vartheta_j(n) = \sum_{i=1}^{m} w_{ji}(n)\, y_i(n) \quad (1.2)$$

In the equation (1.2), m implies a total number of input signals from neuron i to neuron j with $w_{ji}(n)$ conjunctive synaptic weights and $y_i(n)$ is the output of neuron i to the input in neuron j. For the first hidden neuron in the network, for m=1 and $y_j(n) = x_i(n)$ where i refers to the first input terminal of the network. The activation function in equation (1.1) is a Logistic function defined as:

$$\Psi_j(\vartheta_j(n) + Bias\ ) = \frac{1}{1 + \exp(-(\vartheta_j(n) + Bias\ ))}$$

$$\forall\ -\infty < (\vartheta_j(n) + Bias\ ) < \infty \quad (1.3)$$

This is a sigmoidal nonlinearity function generate an output on the induced local field of neuron j and Bias. The output amplitude of neuron j lies inside the range $0 \le y_j \le 1$ for non linearity activation function [36]. This function has been used at each level in all neurons with the identical bias to figure out the output. Backward pass is the next phase of this method, where the output from last neuron j is compared with actual coveted output and measures the amount of error signal produced by neuron j at iteration n define as

$$e_j(n) = d_j(n) - y_j(n) \quad (2.1)$$

Where $d_j(n)$ is coveted output and $y_j(n)$ is the actual output from neuron j at iteration n.

Cost function-The universal cost function depends on error energy produced by the network model at each level of result. The error energy measured for neuron j is $\frac{1}{2}e_j^2(n)$ and the entire error energy comes from all neurons in the output layer of the network as $\xi(n)$ [36,37] formed by

$$\xi(n) = \frac{1}{2}\sum_{j \in C} e_j^2(n) \quad (2.2)$$

In the equation (2.2) C adverted to the set of all neurons in the last layer of the network. In this study thirteen patterns of bacterial species has been used to trained this network model, so the average squared error energy will calculate by addition of all error energy obtain in the equation (2.2) and then it is divided by the number of patterns used in the network [38], which is defined as

$$\xi_{av} = \frac{1}{N}\sum_{n=1}^{N} \xi(n) \quad (2.3)$$

Where N implies the number of patterns which is13in this work and ξ_{av} is the cost function used to measure the learning performance.

Now we need to reduce the error obtain from each neuron's outcome and it is possible by updating weight vectors through the backward pass in each time of iteration. Weight vectors in this intelligent neural network model have updated by stochastic gradient descent (SGD) technique [36]. The small correction in synaptic weight vector $w_{ji}(n)$ by $\Delta w_{ji}(n)$ defined as

$$\Delta w_{ji}(n) = -\eta \frac{\partial \xi(n)}{\partial w_{ji}(n)} \quad (2.4)$$

Where η, the learning-rate was assigned in this network and was unchanged throughout the training process of fixed no. of epochs. Back-propagation technique uses the partial derivative to correct weight vectors at all layers in the network and it happens through chain rule of calculus, shown as

$$\frac{\partial \xi(n)}{\partial w_{ji}(n)} = \frac{\partial \xi(n)}{\partial e_j(n)} \frac{\partial e_j(n)}{\partial y_j(n)} \frac{\partial y_j(n)}{\partial v_j(n)} \frac{\partial v_j(n)}{\partial w_{ji}(n)} \quad (2.5)$$

Forward and backward propagation techniques which were used through two layered network to train the INN model and saved the weight vectors in database. The same input vectors applied in the trained INN and saved the minimum outcome value into database. Less input vectors applied into trained INN model and compared the maximum possible outcome (Ƭ) with and minimum saved outcome (f) and if Ƭ >=f then it would be predicted exact possible outcome otherwise nothing would be predicted.

3.3 Data Representation

The features of unknown organisms were extracted from Bergey's manual and encoded by binary value 0 and 1 (0=Negative and 1= Positive). In this study, only four features of bacteria were collected from Bergey's manual [40] which have been shown in the table-2. These features were encoded into binary values for preparing an input vector for training the proposed INN in table-3.

3.2 Flowchart

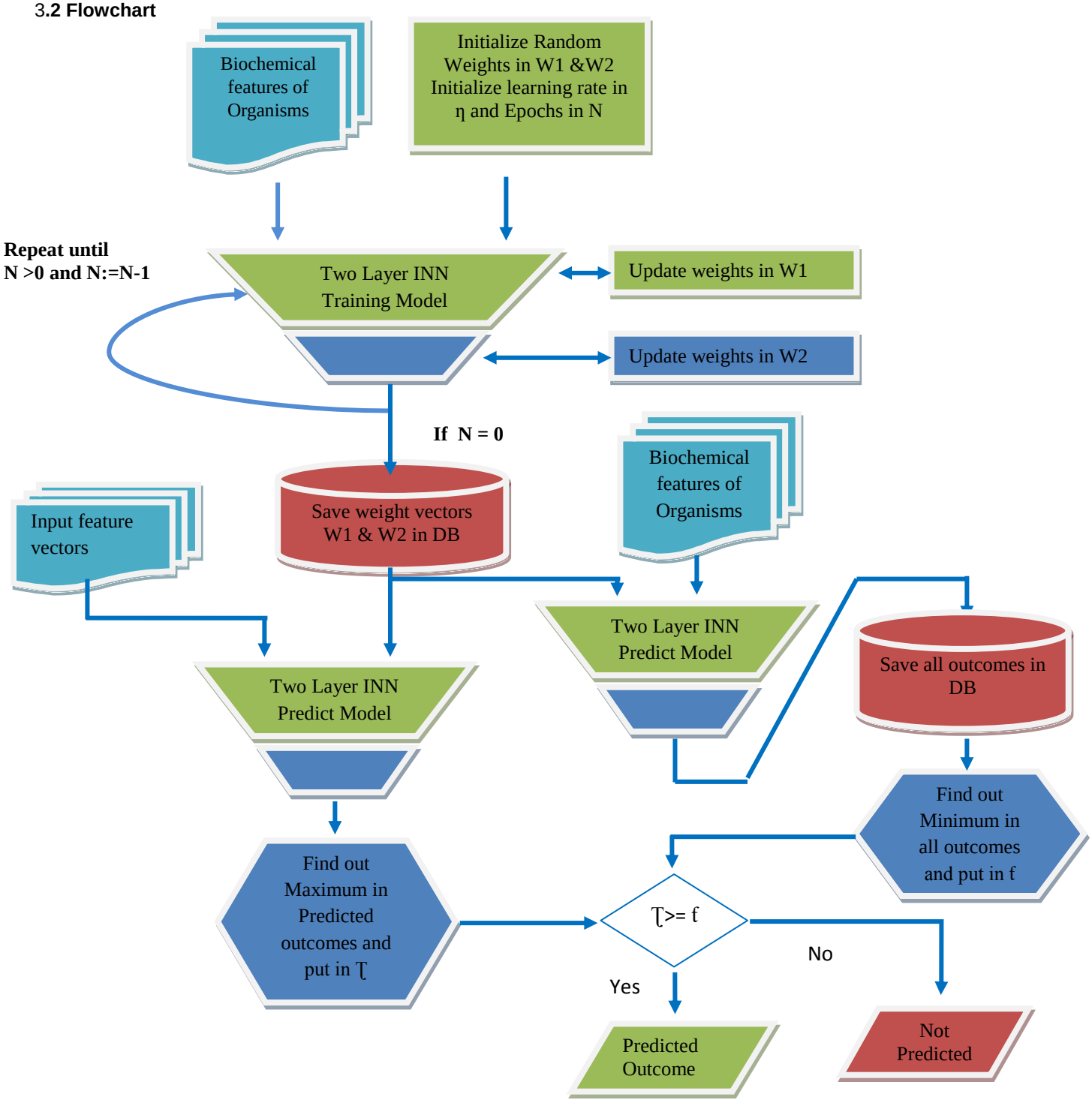

Table-1: *An overview of thirteen disease causing organism and their cultural characteristics noticed in incubate for 24 to 72 hours at 37°C [Source: Cappuccino and Sherman, 2009].*

Bacterial Species	Shape/Gram Stain(+ / -)	Agar Slant Cultural features	Responsible for
E.coli	Rod/-	White, moist, glistening growth	Infection in the urinary tract, traveler's diarrhea, renal failure, anemia, dehydration; organ failure, and mental disequilibrium
E. aerogenes	Rod/-	Abundant, thick, white, glistening growth	Nosocomial infections and meningitis
K.pneumoniae	Rod/ -	Slimy, white, somewhat translucent, raised growth	Pneumonia, liver abscess, and meningitis
S.dysenteriae	Rod/ -	Thin, even, grayish growth	Shigellosis, diarrhea, fever, abdominal pain, and stomach cramps
S.typhimurium	Rod/-	Thin, even, grayish growth	Fever, acute intestinal inflammation, and diarrhea
P.vulgaris	Rod/-	Thin, blue-gray, spreading growth	Hospital-acquired infections
P.aeruginosa	Rod/-	Abundant, thin, white growth, with medium turning green	Hospital acquired severe infections
A. faecalis	Rod*/ -	Thin, white, spreading, viscous growth	Corneal ulcer in human eye
S.aureus	Cocci/ +	Abundant, opaque, golden growth	Vascular disease, cancer, lung disease, and diabetes
L.lactis	Cocci/+	Thin, even growth	Infective endocarditis in adults and in children
M.luteus	Cocci /+	Soft, smooth, yellow growth	Impaired resistance in patients and colonizing the surface of heart valves
C.xerosis	Rod/ +	Grayish, granular, limited growth	Septicemia, peritonitis, endocarditis, pleura pneumonia, osteomyelitis, septic arthritis, meningitis
B.cereus	Rod /+	Abundant, opaque, white waxy growth	Diarrhea, nausea, and vomiting

Table-2: *Disease causing organisms and their biochemical reactions [Source: Cappuccino and Sherman 2014].*

Bacterial Species	Shape/Gram Stain(+ / -)	Litmus Milk Reaction	Sucrose	H_2S Production
E.coli	Rod /-	Acid, curd±, reduction±	A±	-
E. aerogenes	Rod /-	Acid	AG±	-
K.pneumoniae	Rod/ -	Acid, gas, curd±	AG	-
S.dysenteriae	Rod/ -	Alkaline	A±	-
S.typhimurium	Rod /-	Alkaline	A±	+
P.vulgaris	Rod /-	Alkaline	AG±	+
P.aeruginosa	Rod /-	Rapid peptonization	-	-
A.faecalis	Rod*/ -	Alkaline	-	-
S.aureus	Cocci/ +	Acid, reduction ±	A	-
L.lactis	Cocci/+	Acid, rapid reduction with curd	A	-
M.luteus	Cocci /+	Alkaline	-	-
C.xerosis	Rod/ +	Alkaline	A±	-
B.cereus	Rod /+	Peptonization	A	-

Table-3: *Input vector of binary value [1= positive, 0=negative] for training to the proposed INN model of thirteen pathogenic bacteria.*

Bacterial Species	Shape/ Gram Stain				Litmus Milk Reaction									Sucrose					H_2S Production	
	Rod/-	Rod/+	Rod*/-	Cocci/+	Acid	curd±	gas±	Alkaline	Rapid peptonization	Rapid reduction with curd	gas	reduction±	Peptonization	AG	AG±	A	A±	-	+	-
E.coli	1	0	0	0	1	1	1	0	0	0	0	1	0	0	0	0	1	0	0	1
E. aerogenes	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
K.pneumoniae	1	0	0	0	1	1	0	0	0	0	1	0	0	1	0	0	0	0	0	1
S.dysenteriae	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1
S.typhimurium	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	1	0
P.vulgaris	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0	0	1	0
P.aeruginosa	1	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	1
A.faecalis	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1
S.aureus	0	0	0	1	1	0	0	0	0	0	0	1	0	0	0	1	0	0	0	1
L.lactis	0	0	0	1	1	0	0	0	0	1	0	0	0	0	0	1	0	0	0	1
M.luteus	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	1
C.xerosis	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	1
B.cereus	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	1

3.5 Experiment and Analysis

The proposed INN model has been used to classify thirteen unknown organisms based on their essential features and the outcome generated by the model has been analyzed in this section. This paper mainly focused on the realistic decision making by neural network; when the number of inputs is less than the trained inputs. The INN was trained four times by changing learning rate and epochs for getting prominent decision in bacteria classification. In this study, features of thirteen unknown organisms were collected from Bergey's manual [40] and their essential features such as: Gram Stain, Litmus Milk Reaction, Sucrose, and H_2S Production were collected and were prepared as input vectors for training to the INN. The proposed model leveraged to distinguish thirteen unknown organisms separately and if applied inputs are less in respect to the trained inputs then it makes a decision like human. Entire experiment was done through measuring the Sum Squared Error(SSE) and followed its magnitude gradually drop down by varying learning rate and epochs in the same proposed model.

$$SSE = \left(\sum_{pn=1}^{N} \sum_{q=1}^{L} \left(D_q - f_{q,k} \right)^2 \right)$$

Here N is indicated for thirteen medically important bacteria which play a key role in human health and L is number layers which is two. All the observational data at the training time of INN has been stored in the Table-4.

Table-4: Comparison of four training processes through INN model by varying learning rate and epochs to get less SSE for best identification of bacteria in Table-1.

In the above table it was noticed that the SSE was decreasing by increased of learning rate up to 0.02 for fixed epoch 10000 but SSE was raised when we applied learning rate 0.05 by that epoch. On the other side the proposed INN fixed epoch 100000 and increased the same learning rate as previous the SSE was decreased up to 0.002056. In the comparison of both epochs 10000 and 100000 respectively on learning rate 0.05 with the SSE 0.330504 and 0.002056 respectively, so the value 0.002056 was less than the other one. The proposed INN provides the prominent result on the training of learning value was about to 0.011. In figure 2 Series1 is drawn when learning rate was 0.015 and epochs was of 10000 and in that figure series 2 was drawn for same learning rate and of 100000 epochs. Considering both the curves, it was decided that SSE was being saturated in series 2 and value was about to 0.006. In figure 3, Series1 was drawn when learning rate was of 0.02 and epochs was of 10000 and in that figure series 2 was drawn for same learning rate and of 100000 epochs. Considering both the curves, it was decided that SSE was being saturated in series 2 and value was about to

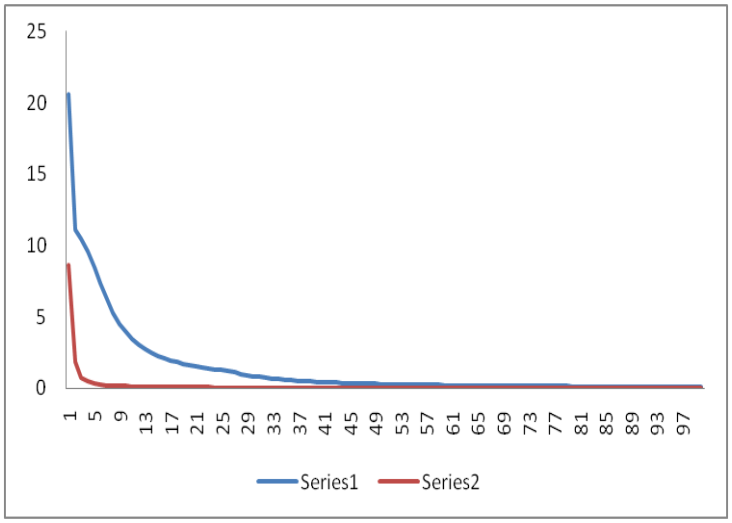

Figure 1: SSE plotted for 10000 and 100000 epochs by Series1 and Series2 respectively; where learning rate 0.01

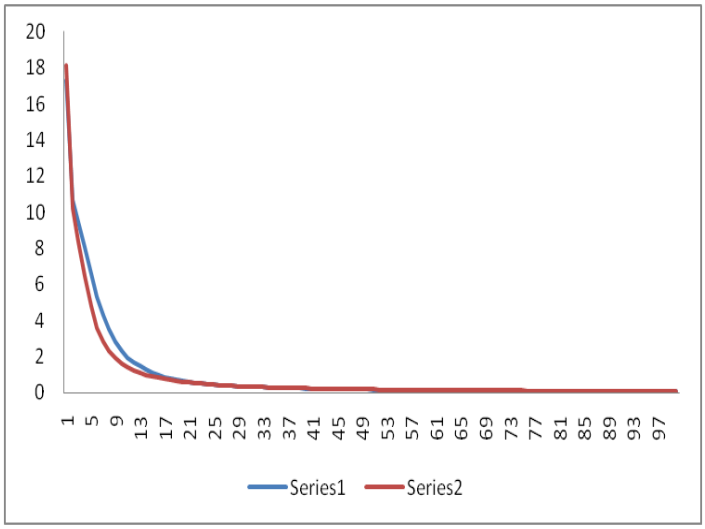

***Figure 2:** SSE plotted for 10000 and 100000 epochs by Series1 and Series2 respectively; where learning rate 0.015*

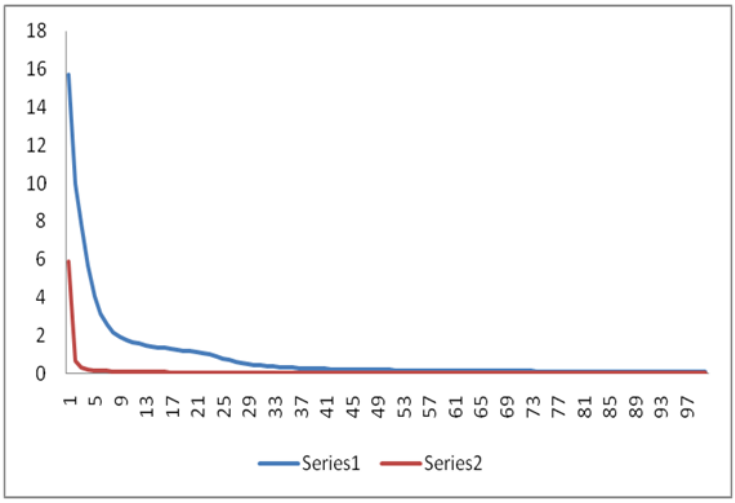

Figure 3: SSE plotted for 10000 and 100000 epochs by Series1 and Series2 respectively; where learning rate 0.02

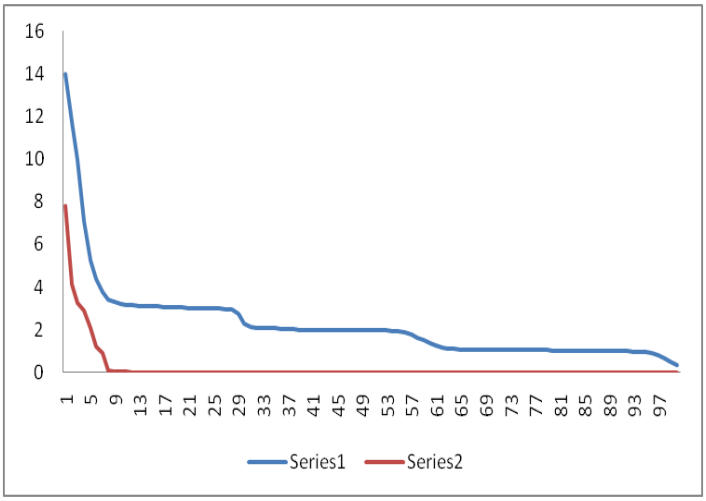

***Figure 4:** SSE plotted for 10000 and 100000 epochs by Series1 and Series2 respectively; where learning rate 0.05*

rate of 0.05 and epochs of 10000. Few more seconds were taken in 100000 epochs than the epochs of 10000 in training to the INN with 0.05 but the prediction accuracy almost best in 100000 epochs. Comparison of SSE for both epochs have been shown in Figure 1 to 4; where two different color curves depicted the downfall of SSE in training. In figure 1, Series1 is drawn when learning rate was 0.01 and epochs was of 10000 and in that figure, series 2 was drawn for same learning rate and of 100000 epochs; considering both the curves, it has been decided that SSE is being saturated in series 2 and 0.004. In figure 4 Series 1 was drawn when learning rate was 0.05 and epochs was of 10000 and in that figure series 2 was drawn for same learning rate and of 100000 epochs. Considering both the curves, it was decided that SSE was being saturated in series 2 and value is about to 0.002. Comparing all these figures, the SSE value was about to zero for the learning rate of 0.05 by applied epochs of 100000, it has been taken as final training for the INN to classify the bacteria prominently.

The confusion matrix has been shown in Table-5 for all the bacterial classes and their classification accuracy. To calculate the prediction accuracy by the relation of the matrix as

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN}$$

Where TP and TN refers true positive and true negative respectively; on the other side FP and FN refers false positive and false negative respectively in the above accuracy to calculate equation. Overall accuracy has been calculated on the confusion matrix (Table-5) and gets the approximate value of 97.11%, which is considered as best prediction result.

***Table-5**: Confusion matrix of classified bacteria by INN when it was trained by 0.05 learning rate with 100000 epochs*

Bacterial Species	1	2	3	4	5	6	7	8	9	10	11	12	13
1	0.9998	0.0006	0.0020	0.0000	0.0074	0.0000	0.0036	0.0002	0.0034	0.0006	0.0008	0.0006	0.0032
2	0.0001	0.9997	0.0030	0.0030	0.0000	0.0056	0.0048	0.0041	0.0025	0.0010	0.0004	0.0000	0.0050
3	0.0017	0.0056	0.9998	0.0103	0.0000	0.0000	0.0008	0.0072	0.0024	0.0032	0.0015	0.0000	0.0010
4	0.0031	0.0005	0.0006	0.9988	0.0103	0.0002	0.0059	0.0014	0.0006	0.0013	0.0002	0.0091	0.0010
5	0.0059	0.0001	0.0016	0.0112	0.9995	0.0035	0.0031	0.0002	0.0002	0.0033	0.0008	0.0000	0.0036
6	0.0000	0.0087	0.0012	0.0003	0.0089	0.9997	0.0000	0.0004	0.0048	0.0011	0.0072	0.0001	0.0020
7	0.0041	0.0048	0.0004	0.0114	0.0031	0.0000	0.9998	0.0042	0.0008	0.0013	0.0051	0.0000	0.0007
8	0.0002	0.0015	0.0033	0.0004	0.0000	0.0010	0.0054	0.9998	0.0018	0.0028	0.0016	0.0002	0.0032
9	0.0053	0.0043	0.0006	0.0025	0.0000	0.0001	0.0002	0.0032	0.9998	0.0077	0.0011	0.0002	0.0015
10	0.0008	0.0004	0.0028	0.0000	0.0005	0.0004	0.0004	0.0010	0.0018	0.9997	0.0036	0.0018	0.0049
11	0.0002	0.0003	0.0025	0.0000	0.0000	0.0093	0.0024	0.0006	0.0013	0.0039	0.9998	0.0018	0.0047
12	0.0029	0.0004	0.0016	0.0150	0.0001	0.0001	0.0002	0.0008	0.0005	0.0041	0.0039	0.9997	0.0041
13	0.0005	0.0061	0.0019	0.0000	0.0004	0.0003	0.0004	0.0015	0.0008	0.0053	0.0031	0.0052	0.9998

In the Table-5 numeric label has been considered in the place of bacterial species are as 1) Escherichia coli, 2) Enterobacter aerogenes, 3) Klebsiella pneumonia, 4) Shigella dysenteriae, 5) Salmonella typhimurium, 6)Proteus vulgaris, 7)Pseudomonas aeruginosa, 8)Alcaligenes faecalis, 9)Staphylococcus aureus, 10)Lactococcus lactis, 11)Micrococcus luteus, 12)Corynebacterium xerosis, and 13)Bacillus cereus.

The performance of INN was finally compared with the conventional ANN having same set of features of the bacterial species taken into consideration in this research work. The conventional ANN was trained as the same way as INN was trained and its weight vectors were saved in database. Performance was compared on the basis of prediction accuracy and the time consumed to prepare the final outcome which was shown in Table-6. The same set of input features has been applied on both trained models to observe the outcome. The conventional ANN was prepared as a whole set of bacterial species with their percentage of prediction as well; but the INN was generated only one result. The INN always has taken less time in comparison with conventional ANN for decision making. The conventional ANN model was shown all bacterial species with their percentage of prediction for applying biochemical features: Rod/-, Acid and AG. Another set of inputs [Rod/-, Acid, Curd+/- and Gas+/-] were applied to both trained models, conventional ANN showed all bacterial species with their percentage of prediction, where Escherichia coli was predicted by 99.37% and the same prediction made by INN has taken less time in respect to ANN.

***Table-6:** Comparison of the predicted outcome between two models by using same features of bacterial species*

Trained Features	Applied features for prediction	Model	Result	Time (Sec)
Gram Stain, Litmus Milk Reaction, Sucrose, and H_2S Production	Rod/-, Acid, AG	Conventional ANN	Escherichia coil =0.0040% Entrobacter aerogens =54.160% Klebbsiella pneumoniae =82.450% shigella dysenteriae =0.0003% Salmonella typhimurium =0.0360% Proteus vulgaris =0.0552% Pseudomonas aeruginosa =0.0020% Alcaligenes faecalis =0.6031% Staphylococcus areus =0.0173% Lactococcus lactis =2.7760% Micrococcus luteus =0.0296% Coryne-bacterium xerosis =0.0155% Bacillus cereus =0.0372%	0.51
	Rod/-, Acid, AG	INN	Not Predicted	0.39
	Rod/-, Acid, Curd+/-, Gas+/-	Conventional ANN	Escherichia coil =99.370% Entrobacter aerogenes =0.0065% Klebbsiella pneumoniae =0.1532% shigella dysenteriae =0.0001% Salmonella typhimurium =2.6230% Proteus vulgaris =0.0003% Pseudomonas aeruginosa =6.9670% Alcaligenes faecalis =0.0675% Staphylococcus areus =47.410% Lactococcus lactis =0.0115% Micrococcus luteus =0.0019% Coryne-bacterium xerosis =0.0000% Bacillus cereus =0.0076%	0.47
	Rod/-, Acid, Curd+/-, Gas+/-	INN	Escherichia coil = 99.370%	0.37

4. CONCLUSION

INN revealed a new dimension over conventional artificial neural network in object classification. It was bit confusing to the user to get decision on prediction, when less feature vectors were applied in trained ANN. The proposed INN is robust in decision making on paucity of input features applied to trained network. It would always show prominent outcome without confusing the user. In multiobjects classification, this neural network perform a key role by generating only one decision; whether it would predict exactly what would be the object or display a message if not likely possible. In this paper, INN has been used in the classification of medically important bacteria, where as prediction accuracy was upto 97.11%. It would help to the laboratory user to identify exact bacterial species by the fundamental biochemical properties of medically important bacterial species..

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