A Development of Snake Bite Identification System (N'viteR) using NEURO-GA

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Abstract- **It is crucial to differentiate between venomous and non-venomous snake whereby an immediate and effective medical care can be instituted to the victims. However, early identification is not easy. We developed a snake bite identification system (N'viteR) to differentiate the snake using Neuro-GA technique. Based on 200 cases, this work had revealed that Neuro-GA has yield a high accuracy in identifying the snake. A number of experiments have been done which based on number of epoch, momentum, learning rate, number of generation, population and chromosome. This hybrid technique has achieved 97.6% of accuracy which enables early identification of snake and immediate specific anti-venom can be administered. Hence, reduces the rate of morbidity and mortality.**

Keywords- snake identification, snake identification system, Back Propagation Neural Network, Genetic Algorithm, Neuro-GA, identification accuracy.

I. INTRODUCTION

Globally, it is estimated that 5·4–5·5 million people are bitten by snakes each year resulting in about 400 000 amputations, 2.5 million envenoming and between 20 000 and 125 000 lost their life from snake bites [1,2,3]. There are about 45,000 snake bites, of which 7000 to 8000 are venomous, occur annually in the United States. In Malaysia, snake bites are not uncommon. WHO (1999) reported that it is especially common in northwest peninsular Malaysia but the mortality caused by snakebite is low (0.3 per 100000 populations) [4].

Most snakes in Malaysia are non-venomous and are relatively harmless to human. In Malaysia and its coastal waters, there are at least 40 species of front fanged poisonous snakes, of which 18 are land snakes and more than 22 are sea snakes [5]. The land snakes include the two subfamilies Crotalinae (represented by the *alloselasma* and *Trimeresurus*) and Elapinae (represented by the five genera *Naja, Bungarus, Ophiophagus, Maticora* and *Calliophis*); whereas the sea snakes include three subfamilies: Laticaudinae, (represented by the genus *Laticauda*); Hydrophiini (represented by the six genera *Enhydrina, Kerilia, Hydrophis,Thalassophis,Pelamis and Kolpophis*) and Ephalophiini (represented by the only genus *Aipysurus*) [5].

Snake venom is classified into four groups according to its effect on the victim's body. Haemotoxic group causes disruption of normal coagulation process leading to active bleeding from almost everywhere in the body, both externally and internally. Extensive intra and extravascular haemolysis and its sequelae follow in terms of acute renal shutdown and haemolytic jaundice. Neurotoxic group either leads to a synaptic block at neuromuscular junction by blocking acetylcholoine or causes a post receptor block. Paralysis of striated muscles is the clinical expression. Acute myocarditis, dysrhythmias and vasodilatation are the clinical expression of cardiotoxicity. Local toxic group leads to severe local inflammation necrosis [6,7].

Not all snake bites result in envenomation. In the case of cobras, the percentage of blank bites may be quite high, 45% in one series of 47 cases from Malaysia [8]. The symptoms and signs of envenomation may occur immediately or delay. For example; the primary local clinical findings after most pit viper bites emerge within 30 to 60 minutes and may delay up to 12 hours. In fact, some of the cases the envenomation may occur within 2 weeks after being bitten [9].

Based on the above facts, it is crucial to differentiate between venomous and venomous snake so that appropriate and cost effective medical care can be instituted to the patients. Accurate identification or differentiation can be made by examining the captured snake whether it is alive or dead. Accurate description of the anatomy of the bitten snake by the victims or relative may assist the physician to make a proper diagnosis and the exact species of the bitten snake can be identified. Unfortunately, many victims do not recognized, do not visualized or having difficulty in describing the structure of the bitten snake.

The main focus of this project was to produce an output that able to differentiate between venomous and non-venomous snake bite. The produced output was based on the patient's symptoms or chief complaint. The target user of this system was the medical officers and the students who may

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use the system for medical purposes. We hypothesized that the implementation of these systems avoids future medical negligence and it will be more cost effective.

Hence, this paper proposed the snake bite identification systems (N'viteR) based on the combination of two Artificial Intelligence (AI) techniques; Back Propagation Neural Network (BPNN) and Genetic Algorithm (GA), which is Neuro-GA.

In order to develop N'viteR, the following objectives were derived: (i) to collect snake bite cases and identify the clinical effects of snake bites, (ii) to design and develop N'viteR using Neuro-GA, (iii) to evaluate N'viteR based on number of epoch, values of momentum and value of learning rate.

This paper was organized as follows: Section II briefly discussed some related work on AI technique for identification process and Section III described the theoretical and empirical studies. Section IV illustrated the system design and development processes. Section V elaborated the system evaluation and finally Section VI provide the conclusion.

II. SOME RELATED WORK

Several researches have been done specifically to study the ability of AI techniques for identification process. A study by Yusoff et. al (2011) shown that, the adaption of BPNN to identify a flies used for maggot therapy had yield a 94.4% of accuracy [10]. A Neural network-based symptomatic species identification system which use a symptom vector as an input has yield the most probable result in identifying the venomous species in India including the envenomation severity. The result from the system could help to determine anti-venom dosage and also for species-specific prognosis [11].

On the order hand, Halim et. al (2011) conducted a comparison study of two Neural Network techniques; Resilient Propagation and standard BPNN for snake identification. The study shown that the Resilient Propagation give a higher percentage of accuracy compared to the BPNN with 90% and 88.3%, respectively [12].

III.THEORETICALAND EMPIRICAL STUDIES

A. Theoretical study

In Malaysia, 17 out of 105 land snakes are venomous and dangerous to humans. Based on research done by Lim, the venomous and non-venomous can be distinguished by four criteria; shape of head, pupil, fang and anal region. However, the identification of the snake normally can only be done by getting verbally description by the victims or the person who accompanied them. False description, unable to see clearly and unable to describe are the most common problems. Therefore, it will be easy if the captured snakes can be identified by the person who has an experience or ability to recognize the snakes. However, this will gives an effect to the ecology and the captured snakes may still alive and give harm to other person. As a result, 60% of the snake bite cases are unidentified which risks the wrong administration of anti-venom [13].

Jamaiah et. al (2006) reveal that there are many clinical features of snake bites which can help to distinguish between venomous and non-venomous snakes. The symptom of envenomation may take quite some time for the post-bite symptom to occur but from research done, it shows that there are common symptoms in most patients. Table 1 shows clinical features of confirmed snake bites symptoms on patients.

Snake bite often resulting in puncture wounds inflicted by the snake fangs which may contain the venom. Snake venoms are the most complex of all animal toxins which contain up to 20 biologically active proteins and polypeptides [14]. It can be divided into three groups; (i) Haemototoxin or cardiovascular toxins, (ii) Neurotoxins, and (iii) Myotoxins [15].

Every snake may have different kind of venoms. Therefore, different bites may show different clinical symptoms. It is crucial for the snake bite patients being fully inspected by doctors. This is because the patients may show symptoms identical to non-venomous snake bite but they actually bitten by a venomous species, or vice versa [16]. Once admitted to the hospital, the snake bite identification should be carried out to determine the type of snake in order to administer anti-venom and provide a proper treatment.

TABLE 1: SYMPTOMS OF SNAKE BITE

Pain at bite site	Fever
Swelling / Oedema	Redness
Progressive swelling	Bleeding
Vomiting	Conscious
Skin discoloration	Hematuria
Bruising	Ptosis
Necrosis	Blurred of vision
Numbness	Drowsiness
Acute renal failure	Hypersalivation
Shock (hypovolemia)	Blister
Short of breath	Bleeding tendency
Chest pain	Myoglobinuria
Chest discomfort	Muscle pain
Palpitation	Weakness
Nausea	Bite mark present
Dizziness	Giddiness

B. Empirical study

The snake bite cases from year 2006 to 2009 were collected from Emergency Department, Hospital Universiti Sains Malaysia (HUSM), Malaysia. 200 cases have been chosen based on venomous and non-venomous cases. The cases will be analyzed according to the symptoms (Table 1) and those with presented symptoms will be represented as 1, otherwise 0. Next, the data will be clean before being tabulated and manage into two different sets of data; 180 cases for training and 20 cases for testing. Table 2*a* and 2*b* show unprocessed and reprocessed data.

IV. SYSTEM DESIGN

The Neuro-GA technique is proposed in N'viteR since it has an element of learning and optimization. The learning

element owned by BPNN will possible the system to learn the data (cases) while the GA will help to chose the best (optimum) weight of cases to be tested with. The Neuro-GA algorithm for N'viteR are as follows:

Step 1: Initialize population and random weight
Step 2: Back propagation training of the weight
Step 3: Fitness function -where selection the lowest Mean Square Error (MSE) from the population of chromosome
Step 4: Crossover the chromosome that been choose
Step 5: Mutation the chromosome
Step 6: Replacement the parents with new offspring
Step 7: Stopping condition until reach ***n***–generation

A. Back Propagation Neural Network (BPNN)

Fig. 1 shows the architecture of BPNN which consists of 32 input nodes (symptoms of snake bite) and five hidden nodes that have been adjusted to produce a better result. The output node represents venomous and non-venomous snakes.

TABLE 2*a* : UNPROCESSED DATA

1	1	0	1	1	1	1	1
0	0	1	1	1	1	0	1
0	0	0	0	1		0	0
0	0	0	0	0		0	0
0	0	0	0	0		0	0
0	0	0	0	0		0	0
0	0	0	0	0		0	0
0	1	0	0	0		1	1
0	0	0	0	0		0	0
0	0	0	0	0		0	0
N	**U**	N	N	Vi		N	C

TABLE 2*b* : PREPROCESSED DATA

1	1	0	1	1	1	1	1
0	0	1	1	1	1	0	1
0	0	0	0	1	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
0	1	0	0	0	0	1	1
0	0	0	0	0	0	0	0
0	0	0	0	0	0	0	0
N	**N**	N	N	Vi	N	N	C

B. N'viteR architecture

Fig. 2 shows the architecture of N'viteR. The input will be processed based on weight initialized by GA. The weight will be passed to BPNN where the training process will be done until it reaches the ***n*** epoch (condition). From a training process, the value of MSE of each chromosome will be guided to select the fittest chromosome. The chosen chromosome will then be crossover and mutated. The new offspring from crossover and mutation will replace the parents. The point of crossover is 0.07 while the point of mutation is 0.05.The process will be executed until it reaches ***n***–generation. Finally all new weights will be tested to find the best weight. Fig. 3 shows the flow of N'viteR which combine BPNN and GA.

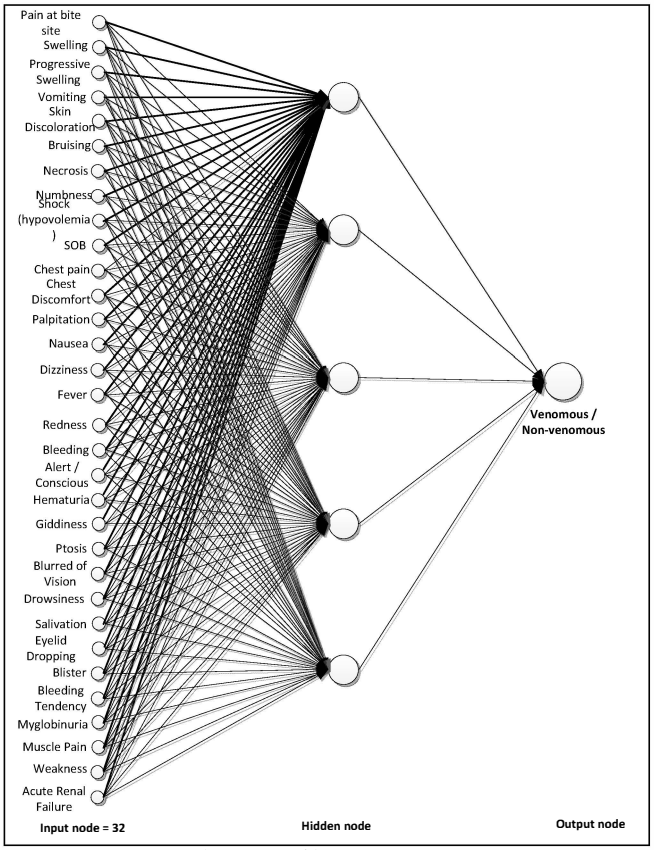

Figure 1: Architecture of BPNN

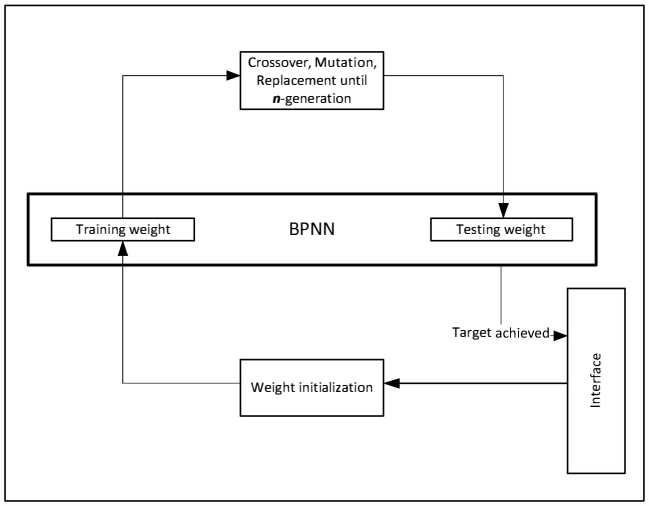

Figure 2: Architecture of N'viteR

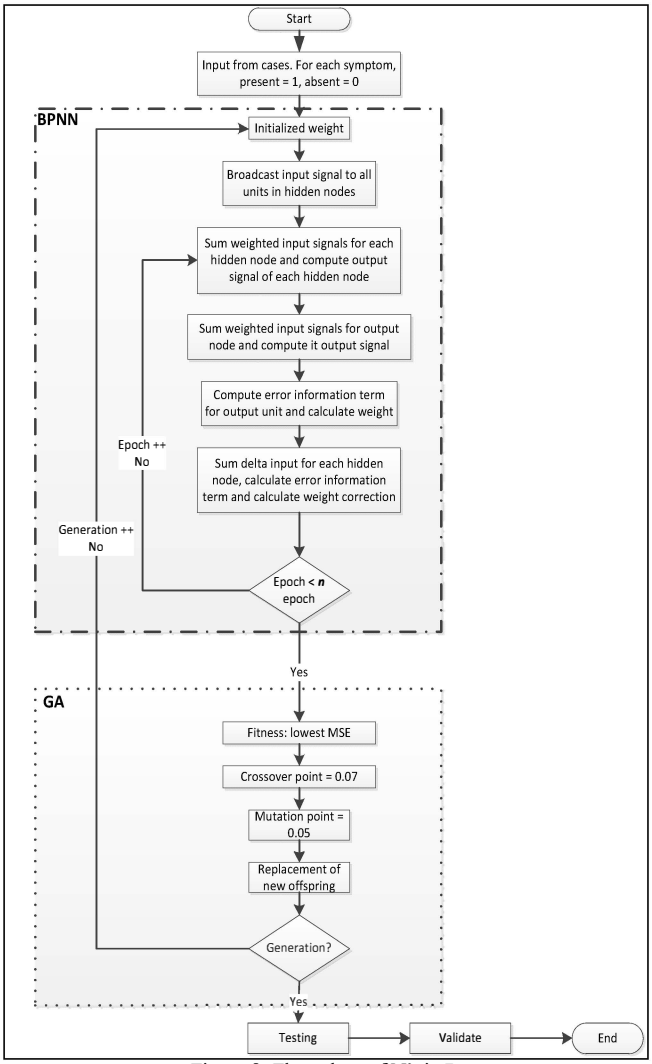

Figure 3: Flow chart of N'viteR

V. SYSTEM EVALUATION

The N'viteR has been experimented according to; i) Number of epoch, ii) Momentum, and iii) Learning Rate. The result of each experiment will be shown through the accuracy percentage based on the following mathematical calculation:

$$\text{Accuracy Percentage} = (\text{Number of correct predictions} / \text{total data tested}) \times 100 \quad (1)$$

A. Experiment 1: Number of epoch

The stopping condition for this experiment is based on number of epoch; 2000 and 4000 epoch.

The default values for Experiment 1*a* are:

- Learning rate = 0.9
- Momentum = 0.9
- Number of generation = 3
- Number of population = 6
- Number of chromosome = 528

Table 3 shows that a high accuracy achieved with arithmetic crossover at 4000 epoch.

TABLE 3: RESULT OF EXPERIMENT 1*a*

Epoch	Types of cross over		
	Arithmetic	One point cross over	Two point crossover
2000	93.8%	82.8%	94%
4000	97%	96.3%	96.2%

The default values for Experiment 1*b* are:

- Learning rate = 0.9
- Momentum = 0.9
- Number of generation = 5
- Number of population = 6
- Number of chromosome = 528

Table 4 shows that a high accuracy achieved with two point crossover at 4000 epoch.

TABLE 4: RESULT OF EXPERIMENT 1*b*

Epoch	Types of cross over		
	Arithmetic	One point cross over	Two point crossover
2000	82.8%	97.73%	91.9%
4000	96.2%	96.3%	97.74%

The default values for Experiment 1*c* are:

- Learning rate = 0.9
- Momentum = 0.9
- Number of generation = 10
- Number of population = 6
- Number of chromosome = 528

Table 5 shows that a high accuracy achieved with one point crossover at 4000 epoch.

TABLE 5: RESULT OF EXPERIMENT 1*c*

Epoch	Types of cross over		
	Arithmetic	One point cross over	Two point crossover
2000	96.9%	82.8%	95.5%
4000	97.7%	98%	97.7%

B. Experiment 2: Momentum and Learning rate

The stopping condition for this experiment is based on number of epoch; 4000 epoch.

The default values for Experiment 2*a*, 2*b* and 2*c* are:

- Number of generation = 4
- Number of population = 6
- Number of chromosome = 528

Table 6 shows that a high accuracy achieved with learning rate = 0.9 and momentum at 0.1. Table 7 shows that a high accuracy achieved with momentum rate = 0.5 and learning rate at 0.1. Table 8 shows that a high accuracy achieved with learning rate and momentum at 0.9.

TABLE 6: RESULT OF EXPERIMENT 2*a*

Generation	Learning rate (at Momentum = 0.1)	
	0.5	0.9
1	97.2%	94.8%
2	96.1%	93.7%
3	93.6%	94.8%
4	95.6%	95.9%
Average	93.7%	94.8%

TABLE 7: RESULT OF EXPERIMENT 2*b*

Generation	Momentum rate (at Learning rate = 0.1)	
	0.5	0.9
1	96%	94.7%
2	95%	94.5%
3	94.3%	93.3%
4	95.7%	93.8%
Average	95.2%	93.6%

TABLE 8: RESULT OF EXPERIMENT 2*c*

Generation	Learning rate = Momentum rate		
	0.1	0.5	0.9
1	95.6%	96.7%	97.2%
2	94.7%	95.6%	97.7%
3	94.7%	94.7%	96.7%
4	96%	94.9%	96%
Average	95.6%	95%	97.6%

V. CONCLUSION

Based on the experiments, it shows that epoch 4000 give a high accuracy with Number of generation = 4, Number of population = 6, Number of chromosome = 528 and Learning rate = Momentum rate = 0.9.

Even though BPNN is the best-known method to deal with classification problem through learning process, a combination with GA yields a high accuracy to identify a venomous and non-venomous snake based on cases provided. This hybrid technique may give higher accuracy if it involves large number of data (cases), generation and populations even it will take a longer time to finish the training process.

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