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Quest for Prevalence Rate of Hepatitis-B Virus Infection in the Nigeria: Comparative Study of Supervised Versus Unsupervised Models

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Abstract Vaccination against Hepatitis-B virus (HBV) and its infection in Nigeria, is lower than many other sub-Saharan African countries. HBV currently in Nigeria, is reported to be the most common cause of many chronic liver disease. Many studies have ensued to ascertain the extent of HBV exposure amongst Nigerians, owing to facts that its average risk is unknown. In this study, we seek to predict estimated HBV prevalence rate in Niger Delta, and within the sub-groups. We use 30,000 HBV-registered cases as predicted using supervised models below. Result shows a hyper-endemic HBV prevalence rate of infection in the Niger Delta region as trend for the highest chronic liver disease in Sub‑Sahara Africa. Study suggests that large numbers of pregnant women and children were exposed to HBV; And increased efforts should be geared towards preventing new HBV infections are urgently needed in Nigeria.

Keywords: *hepatitis, memetic, simulated annealing, supervised, unsupervised*

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1. Introduction

The (itis) of a liver (hepar), and the burning/swelling of the liver cells is known as hepatitis. There are several sources of hepatitis, comprising of viral infections A, B and C. Others include auto-immune hepatitis, fatty liver hepatitis, spirituous hepatitis and toxin induced hepatitis [1,2,3]. On the worldwide stage, it is predicted that around 250 million people are affected by hepatitis C. Also, it is estimated 400million people are chronic haulers of hepatitis B [4,5].

When a person is infected with hepatitis virus, this virus assaults the liver, causing an instant swelling and redness of the liver [6]. Studies have shown that there is a high probability one may have encountered at least one or more persons with it. Often people with hepatitis virus find it easy to live their lives without letting others know about it – because, hepatitis may be infectious. By doing so, they thwart themselves either from facing the ignorant attitude or sympathy of others. Those living with infectious hepatitis need only take a few precautions to avoid passing the virus around [5,7,8].

The liver is a wedge-shaped organ in upper right side of the body beneath the rib cage. It is considered to be the largest organ and equates to 2-to-3 percent of the overall body's mass. The liver (unlike the heart and stomach) has over 140 functions [4], which includes (not limited to) that it generates the required amount of bile used for digestion, piles up minerals and vitamins, assists in blood clotting (vitamin K), deactivates toxic, regulates energy, sustains hormonal balance, produce amino-acids to build strong muscles and processes sedatives [4]. There is a growing rise in the number of patients fatally attacked by chronic liver diseases – resulting from excess intake of alcohol, inhale of harmful gases, intake of contaminated food and drugs. Thus, liver disease presents numerous concerns in health-care delivery. Chronic liver disease has become a common long-term condition/issue of great concern, to both developed and developing world. There exists many classification heuristics to help in its early identification and diagnosis – as it is vital in and for the survival of the patients [9].

1.1. Symptoms and Diagnosis of HBV

Most infections occur during infancy or childhood, and are rarely diagnosed, since there may be few obvious symptoms. Symptoms of a new infection may not be apparent in children under 5-years of age and adults with a suppressed immune system. Among those aged 5 years and over, between 30-50 percent will show initial symptoms, to include: fever, vomiting, fatigue, nausea, loss of appetite, joint pain, abdominal pain, dark urine, clay-colored stools, jaundice, yellowing of skin and whites of the eyes amongst other symptoms [10]. Acute symptoms appear from 60 to 120 days after exposure to the virus, and they can last from several weeks to 6 months. A person with chronic HBV infection may have ongoing episodes of abdominal pain, persistent fatigue, and aching joints [11,12].

Blood test helps diagnose acute and chronic HBV infection. Screening is available for people with high-risk of exposure or complications from undiagnosed HBV infection. Thus, such screening is recommended for: (a) Infants of mothers with HBV, (b) sex with infected sex partners, (c) unprotected sex with multiple partners, (d) injection drug users, (e) people living with someone who has chronic HBV infection, (f) health-care and public safety workers at risk from occupational exposure from blood-contaminated body fluid, (g) hemodialysis patient, (h) person receiving chemotherapy for cancer, (i) persons from regions with high incidence of HBV, (j) pregnant women. Also, if a woman has HBV during pregnancy, the newborn must be vaccinated and receive hepatitis B immune globulin (HBIG) within 12 to 24 hours after birth [11,13,14].

1.2. HBV Infection in Nigeria

[15] Hepatitis-B is a DNA virus of the family *Hepadnaviridae*, and a causative agent of the hepatitis-B infection. HBV is the most common infectious diseases in the world and a major health problem. [16] WHO estimates a world-population of over 2-billion people with serologic evidence of HBV infection (past and present); And, over 350-million are chronically infected and at risk for HBV-related liver disease. It is over 50-times more infectious than HIV, and 10-times more infectious than Hepatitis-C, as many carriers do not realize they are infected with the virus. It is a common causative of liver diseases, chronic infection and death associated with liver failure, liver cancer and cirrhosis [17,18].

The virus has caused severe endemic in parts of Africa and Asia. The prevalence of HBV varies between 2% in developed countries to about 8% in developing countries, where infection is endemic with sex, age and socio-economic status – all of which unveils as important risk factors for infection [19]. The degree of endemicity often correlates with predominant mode of transmission. The hepatitis disease has enormous impact on health and national economy of many countries, and its severity is highly variable and unpredictable [15,20]. The minimum infectious dose is so low that such practices like sharing of tooth brush or a razor blade can transmit infection [18,21].

HBV is a blood borne and sexually transmitted pathogen that is spread via contaminated blood or other body fluids (saliva, sweat, semen, vaginal secretion, breast milk, urine and feaces). Transmission can occur when using the same syringe as an infected person, from blood transfusions, body piercing/tattoos, mother-to-child birth, occupational exposure, medical procedures, and sexual intercourse. HBV shares similar transmission routes with HIV, and there are four known transmission modes [4,22] namely: (a) mother-to-child birth (prenatal), (b) contact with infected person, (c) sexual contact, and (d) exposure to blood or other infected fluids. Because HBV can remain stable and infectious on environmental surfaces for at least 7-days, transmission may occur indirectly via contaminated surfaces and other objects like tooth brush, baby bottles, razors, eating utensil, hospitals equipment, contact with mucous membranes, and/or open skin breaks.

HBV disease affects people of all age-groups; But, it has been found from studies to predominantly infect young adults, and acquired sexually or by injecting drug use [12]. Infected persons with HBV are able to clear the virus from their blood stream within 6-months of post infection and develop immunity. Those not cleared after 6-months are certified to have chronic HBV infection. The risk of death from cirrhosis or HBV-related cancer is approximately 25% and this percentage of the entire populace in developing countries have been proven to become chronically infected – as a lot of them, acquired HBV infection from childhood [22]. Nigeria is classified among countries with a highly endemic rate of HBV-infection. And, over 75% of Nigerians are reportedly been exposed to HBV at one time, or another in their lifetime. Though, HBV vaccine are highly effective and successful in preventing the infection as well as other acute or chronic liver disease, HBV infection is still a major problem in Nigeria [20].

2. Materials and Methods

2.1. Data Gathering

Sample data with over 30,000 cases from various hospitals and medical experts across selected hospitals in Nigeria.

Study uses HBV spread as its innovation, to seek convergence time and final number of persons exposed to HBV infection – with these goals: (a) do participants observe the WHO's safe plans, acknowledge HBV's infection high rate of fatality rate with imminent death – if, they do not stay ahead of the endemicity, and (b) the right machinery and measures are needed to steer such new vehicle to help eradicate the HBV propagation in Nigeria as a whole.

2.2. Fact Sheets on HBV in Nigeria

Experiment seeks to explore rate of HBV infection in the Niger Delta Region, and to find the expected number of final adopters (those infected) alongside the graph parameters with the nodes' internal decision rules and position in the graph as they locally interact over time as exposed in the graph-based diffusion model. As such, the study is more interested in the local emergent feats emanating from large-scale effects of such interacting nodes of the entire supply network [21].

3. Experimental Framework: Supervised Versus Unsupervised Models

Various search methods are used to find such tasks solution such as depth search, breadth search, greedy search, iterative deepening, steepest descent, etc. Some search maximizes an objective function, must be feasible (achievable) and optimal (close to best in space). CSTs with dynamic feats make such search tedious and inexplicable to resolve – so that other means are devised to resolve such task. These have yielded in optimization models that search for optimal solution(s), chosen from a set of space that relates data-input with uncontrollable parameters and feats in system, modeled to satisfy all constraints and yield output via a mathematical structure and statistical pattern analysis to yield a new discipline termed Machine learning or soft-computing [23,24].

Machine learning is a branch of artificial intelligence deals with design of models that evolves its behaviour based on empirical (sensors and databases) data, dedicated to resolve tasks via optimization. It exploits numeric data and explores human knowledge via statistical pattern analysis, mathematical models and symbolic reasoning – harnessing captured data features of interest alongside its underlying probabilities to illustrate relations in observed values and learns to recognize complex patterns in dataset to make intelligent decisions [25,26,27].

Table 1. Dataset Fact-Sheets for Health

Model Feats	Description and Encoded Values
Incubation	Between 3-to-6 months
HBV_PCR	0 for infected and 1 for non-infected patients
Gender	0 for Male Value 1 for Female
Age	In Years
Residence Settlement	0 for Rural, 1 for Semi-Urban and 2 for Urban settlement
Job	Occupational category for Hepatitis 1 for Doctor (Faculty member), 2 for Doctor (Student concession), 3 for Surgeon (Faculty member), 4 for Surgeon (Student concession), 5 for Dentist, 6 for Medical student, 7 for Nursing supervisor, 8 for Nurses, 9 for Nursing student, 10 for Laboratory Technician 11 for Worker, 12 for Paramedic, 13 for Laundry worker, 14 for other medical personnel
Schisto	Schistosomiasis infection is encoded as 0 for NO 1 for YES
Syringe Handling	History of handling syringes on the job 3-to-6-months preceding their enrolment: 0 for Nil, 1 for once in time interval, 2 for dealing twice, 3 for dealing from 3 to 5 times, and 4 for dealing more than 5 times
Needlestick	History of needle injuries in the year prior to enrolment: 0 for Nil, 1 for once, 2 for twice, 3 for 3-to-5 times, and 4 for more than 5 times
ALT	Serum alanine aminotransferase, this enzyme test is measured to see if the liver is damaged or diseased (Normal ranges Female: 32, Male: 42)
AST	An aspartate aminotransferase, this enzyme test is measured to Check for liver damage and Check on the success of treatment for liver disease. (Normal ranges Female: 32, Male: 42)
Hepatitis ELISA	ELISA is a blood test for HCV antibody produced by when it is infected with the hepatitis virus. Value 0 for Negative Value 1 for Positive
HBsAg_ELISA	HBV Surface Antigen, test identifies active infection by the HBV: Value 0: Negative Value 1: Positive

Table 2. Dataset Fact-Sheets for Health

Network Feats	
Population in Niger Delta	Estimated 42million
Country Classification	Lower-middle-income
Gross National Income Per Capita (2016)	$2177.99
Total Health Expenditure of GDP (2017)	3.7%
Per capita Government Health Expense 2017	$3.5
Life expectancy at birth (2017)	52
Human Development Index (2015)	0.527
Median Age In Years (2017)	18
Total Fertility Rate per Woman (2017)	5.5
HBV Detection Period	30 – 180 days
HBV Infection incubation period	4-6months

It aims at a model that when imprecision, partial truth, uncertainty and noise is applied to its input, guarantees high quality output that is void of overfitting. It has led to evolutionary models/algorithms, capable of quantitative data processing to ensure qualitative knowledge. Inspired by behavioral patterns in biological population and evolution laws, it explores 3-dynamic feats: (a) adaptation yield agents void of local minima and high-diverse random factors introduced to slow convergence, balance exploitation versus exploration so that learning feats of change will bias its solution accordingly, (b) robustness estimates the model's effectiveness, and (c) flexible decision with outset uncertainty feats helps to impact a model's future state in forecasts while focusing on its goal and ease of blackbox integration [3,28,29,30].

3.1. Hybrid Gravitation Search Neural Network (GSANN)

GSA is based on Newton's laws of gravity and motion with its main idea, being to consider isolated system of masses, where every mass represents a solution to a certain problem. Law states that particle attracts each other with gravitational force acting between particles are directly proportional to product of their masses and inversely proportional to the distance between them [27,31,32]. Thus, agent's performance depends on its mass as they attract each other via gravitational pull towards those of heavier mass. Agents are randomly initialized with gravitational force defined as [33]:

$$G(t) = \frac{M_i(t) * M_j(t)}{Rij(t) + \varepsilon}\{Xj(t) - Xi(t)\} \tag{1}$$

R_{ij} is Euclidean distance between masses for i and j, G(t) is gravitation force at t with small constant ε – which decreases at t, to control pool and search's accuracy. Total force is:

$$F_i^d = \sum_{j \in kbest, j \neq 1} rand(i) * Fij \tag{2}$$

Acceleration at t, in *d* dimension is directly proportional to force on agent i, and inversely proportional to agent's mass:

$$A_i^d(t) = \frac{F_i^d(t)}{Mij(t)}. \tag{3}$$

Next agent velocity is a function of its current velocity plus current acceleration – to update next position given by X as:

$$V_i^d(t+1) = rand(i) * V_i^d(t) + A_i^d(t) \quad (4)$$

$$X_i^d(t+1) = X_i^d * V_i^d(t+1). \quad (5)$$

Mass is updated as fitness value of agent *i* at time t:

$$Mi(t) = \frac{Fit(i) - worst(t)}{best(t) - worst(t)}. \quad (6)$$

Strongest agents from their fitness route for maximization task is given as:

$$worst(t) = \text{Maximize}_{j \in \{1,2...N\}} Fit(t) \quad (7)$$

$$best(t) = \text{Minimize}_{j \in \{1,2...N\}} Fit(t). \quad (8)$$

At start, agents are located as solution trained in ANN, and passed over to GSA. With each cycle, velocity/position is updated via Eq. 4 and 5; while G/M is found via Eq. 1 and 6. The model stops if an optima is found or stops using its stop criterion (computational expensive). GSA uses exploration ability to navigate and guarantee its choice value for random agents, and exploitation ability to allow agents of heavier masses move slower in order to attract those of lesser mass as well as locate optima, around a good solution in the shortest time possible [27,32,33].

ANN first yields candidates of low fitness in training, and if better solutions are not found, best individuals are chosen after a number of runs, until optima is found. ANN uses its exploratory search of multiple individuals; while GSA uses it flexibility in finding a better optimal point, even when a local maximas are present. Factors to be defined: (1) ANN: number of runs, dataset for calibration, pool representation of dataset, size and cross validation function; and (2) with GSA: parameters G, M and positions – updates to choose fittest candidates and recomputed to track individuals of value 0.8. Though, ANN finds individuals of low fitness with G, M and position of agents (rules) updated to enter GSA early enough till state of energy 0 is reached – implying a solution is found [26,27,32,33].

3.2. Genetic Algorithm Trained Neural Network (GANN)

GA as inspired by Darwinian evolution consists of a dataset chosen for natural selection with potential solutions. Individuals with genes close to its optimal solution, is fit as determined by fitness function. Based on laws of selection, GA generates better rules via 4-operators [34,35]: initialization, selection, crossover and mutation. Cultural GA is one of the many variants of GA with 4-beliefs thus: (a) Normative – specific range of values to which an individual is bound, (b) Domain has information about task, (c) Temporal has information about the search space available, and (d) spatial has topographical data about the task with time as a specific feat. In addition, CGA has an influence function that ensures that individuals (altered or not) conforms to a pool that does not violate its belief space and reduces number of possible individuals generated till an optimum is found. GA's strength is in parallel traversing with solutions from randomly generated initial pool continuously evaluated via its fitness function [26,27,31,32,36].

For GANN, ANN initializes model via its fitness function to select new pool for crossover/mutation as [26,27,31,32]:

a. Crossover – We adopt tournament selection (to help maintain diversity) in the random selection of chromosomes so that as new offspring are generated with every iteration, a lesser number is chosen and continues till one is chosen as parents. The goal is not to create a best rule (global optimum), but set of rules good enough to detect intrusion (many local maxima). Model chooses two-random cross-over points in chromosome between the parents, to yield two new children.
b. Mutation: Each gene chromosome may (or not) change depending on probability of mutation rate. Mutation improves population diversity needed.

The generated rules are used to evaluate the remaining dataset, and the aim of testing is to gather information of how well the rules created, can detect attacks. Two methods are used for testing namely: (a) use existing rules in a rule-based HBV detection decision support system, and (b) build tailored rule for HBV detection. The proposed design requires tailored rules created from traffic and fed back for detection.

3.3. Simulated Annealing Trained Neural Network (SANN)

Inspired by annealing, the model seeks to strengthen glass and crystals – so that it is heated until it liquefies. Then slowly cool so that as molecules settles into low energy states, it tracks and alters an individual's state, constantly evaluating its energy via its energy function. Its optimal point is found via a series of Markov chain under different thermodynamic state [26,27,31,32]. Its neighbouring state is found by randomly changing an individual's current state via a neighbourhood function. If state of lower energy is found, individuals move to it. If neighbourhood has higher energy, individuals move to that state only if an acceptance probability condition is met. If not met, individual remains at current state. Acceptance probability is difference in energies between current and neighbouring states. Temperature is initialized as high, so that individuals incline towards higher energy state – allowing individuals to explore a greater portion of space, preventing its being trapped in local optimum. As the model progresses – its temperature reduces with cooling and individuals converge towards lowest energy states till an optimum point. ANN first yields candidates of low fitness in training, and if better solutions are not found, best individuals are chosen after a number of runs, until optima is found. ANN uses its exploratory search of multiple individuals; while SA uses it flexibility in finding a global optima [32].

Factors to be defined: (1) ANN: number of runs, dataset for calibration, population representation of dataset, size and cross validation function; And (2) SA (with ANN complete), what neighborhood size and energy function is employed to choose fit candidates till solution is found. Temperature schedule is applied that randomly re-initialize network for series of Markov chain. Neighbourhood function is applied to randomly change individual energies. The fitness function is recomputed to track individuals of low energy state but with threshold value of 0.8 to enter

SA early enough to apply temperature schedule needed. Thus, a moderated Markov chain is used that accepts the states with energies of lower or equal to current state's energy. It runs till state of energy 0 is reached (solution is found). SA and ANN, shares the same fitness function [31,32].

4. Result Findings and Discussion

4.1. Model Result Findings and Validation

Figure 1 – Figure 6 describes the accuracy with which each hybrid model classifies the HBV as well as its corresponding errors of ***false***-positive (error rates in classifying rules that exhibits HBV symptoms as emergent – when in truth they are not really HBV) and ***true***-negatives (error rates in not accurately classifying a rules as HBV signature emergent).

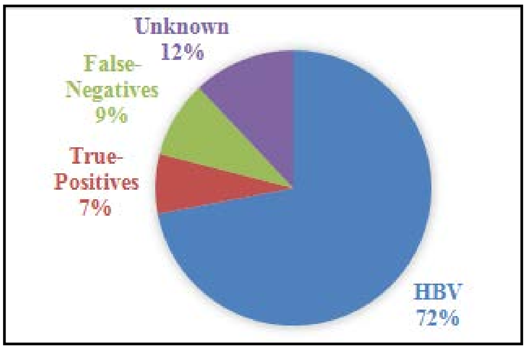

Figure 1. HBV Detection Using GSANN

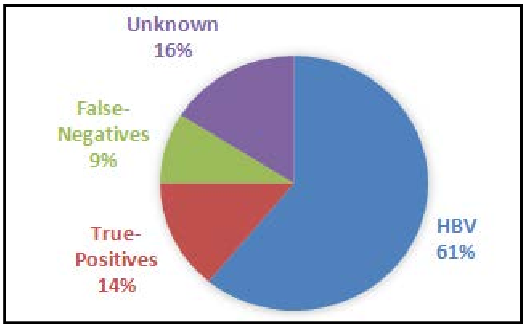

Figure 2. HBV Detection Using SANN

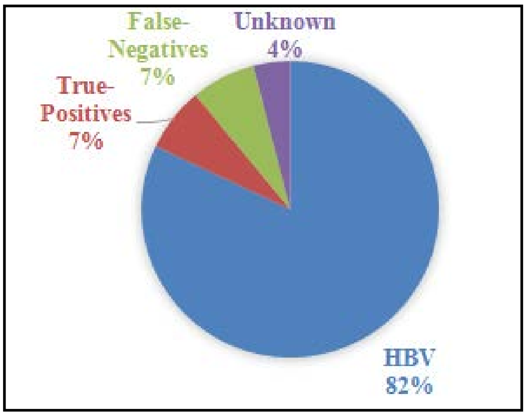

Figure 3. HBV Detection Using GANN

4.2. Classification Accuracy

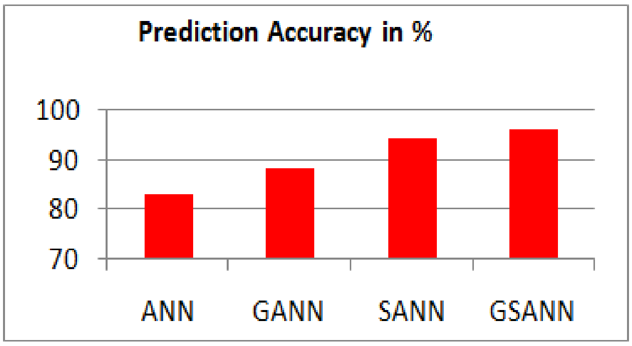

Figure 4. Prediction Accuracy of Algorithms in percentage

4.3. Processing Speed

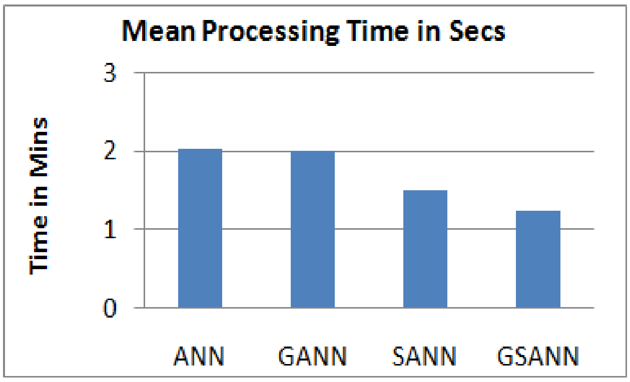

Figure 5. Processing time in Seconds

4.4. Convergence Time

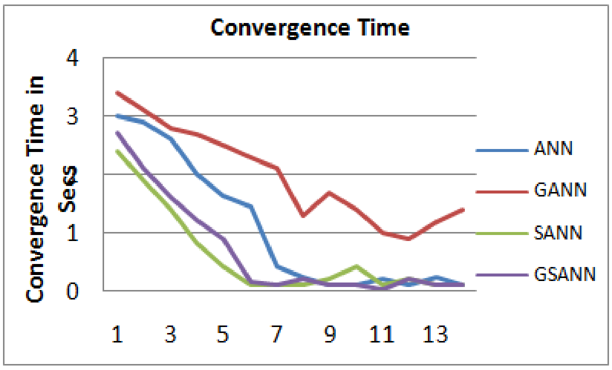

Figure 6. Convergence time of matches

Using a Python implementation of various matching algorithms, we compared algorithms based these feats as seen in Figure 4, Figure 5 and Figure 6 respectively.

4.5. Discussion of Findings

Top rules have same fitness range [0.8, 0.8065] and are estimated 80% good to be used in detection – to imply the achievement of generating a bunch of good rules, rather than a single optimum rule – is better in intrusion detection. 10-out-of-22 rules have destination port as -1, so that the rules looks out for connections from any destination port. This increases the chances of detecting intrusion, improves the generality of rules, and provides for new attack types and its corresponding rules to be added to knowledgebase. The rule generator used a population of 400, w1 = 0.2, w2 = 0.8, 5000 epoch-evolutions and 0.05 probability of a gene to be mutated respectively.

After training and testing models, the results are thus

a. GSANN was run 15 times (to eradicate biasness) and took 102econds to find optima after 322 iterations (at best). It was able to generate each time, multiple local maxima (good rules) and its time varied between 89 seconds and 54minutes. Convergence time depends on fitness function of weights with G, M and position updates of rules and individuals in the pool.
b. SANN was run 15 times, took 62seconds to reach optima after 380 iterations. It generated at intermittently multiple local maxima (good rules) and its time varied between 62 seconds and 40minutes. Convergence time depends on initial population, the temperature schedule applied and series of random walks applied to pool. It is to be noted that SA is most useful in the generation of best rule (and not set of better rules, goal of this study).
c. GANN was run 15 times (to eradicate biasness) and took 89seconds to find optima after 280 iterations (at best). It was able to generate each time, multiple local maxima (good rules) and its time varied between 102seconds and 70minutes. Convergence time depends on how close initial population is to solution and on mutation applied to individuals in the pool.

4.6. Rationale for Choice of Algorithms

Most mathematical, machine learning models are inspired by evolution, biological and behavioral population. They search a space via hill-climbing method which is flexible, easily adapts to changing states and suited for real-time app to guarantee high global convergence in multimodal task. Initialized with random pool, it allocates increasing trials to regions of high fitness to find optima. Once a peak is found, model restarts with another randomly chosen, starting point. Its simplicity, well suited for dynamic feats/phenomena of many local maxima – makes them appropriate. Each random trial is done in isolation and as search progresses, it allocates its trials evenly over space and still evaluates as many points in regions found to be of low fitness as in regions found to be of high fitness. Its demerit is its inadequacy for linear model with small regions surrounded by low fitness – making such functions/models, difficult to optimize.

4.7. Implementation Tradeoffs

Result trade-offs includes [26,27,31,32]:

a. Result Presentation: Researchers often display flawed and unfounded results, to validate new/modified model rather than re-test limitations, insufficiency, biasness and inabilities of existing ones. This is because negative results are less valuable and most of such models aim to curb the non-linearity and dynamism in the phenomena they are predicting alongside discovering feats and underlying properties of the historic datasets used, to train, cross validate and test such models.
b. Efficiency **–** modeler sand researchers can often use figure to show how well their prediction is quite in agreement with observed values (even with their limited dataset used for training the model that is often times squeezed). Some plot for observed and predicted values are often not easily distinguishable – as such modelers do not even provide numerical data to support their claim for their system (though their model is in good agreement with observed values). Some measure of goodness does not provide the relevant data.
c. Insufficient Testing: Validation compares observed on predicted values. Many studies suffer from inadequate dataset. If model aims to predict dynamic state, such ability should not be demonstrated with misleading results of limited dataset; and inconclusive and unclear contributions. Model must be adequately tested with methods laid bare so that process can be repeated to validate the usefulness and authenticity of such models.
d. Model validation is not an undertaking to be carried out by a researcher or research group; but rather, a scientific dialogue. Improper model applications and ambiguous results often impede such dialogue. This study aims to greatly minimize confusion in study of model as well as their corresponding implementation in IDS.

5. Conclusion

Hybrids are quite difficult to implement as modelers seeks to resolve the structural differences and corresponding data must be appropriately encoded so that model can exploit numeric data and efficiently explore the domain space to yield an optimal solution. Modelers must adopt an effective parameter selection and adjustment of weights/biases so as to avoid *overfitting, over-training* and *over-parameterization* of the model. Encoded through the model's structured learning, this will help address issues of statistical dependencies between the various heuristics used, highlight implications of such a multi-agent populated model as well as resolve conflicts in data feats of interest. Thus, as agents create/enforce their own behavioural rules on the dataset, hybridization should be able to curb this (as CGA does for this model in its belief space and operators as applied) to display the underlying probabilities of interest. Models serve as educational tools to compile knowledge about a task, as new language to convey ideas as experts gain better insight to investigate input parameter(s) crucial to a task, and its sensitivity analysis helps to reflect on theories of system functioning. Simple model may not yield enough data; while complex model may not be fully understood. Detailed model helps us develop reasonably applicable models even when not operationally applicable in larger scale. Its implementation should seek its feedback as more critical rather than seeking an accurate agreement with historic data. Since, a balance in the model's complexity will help its being understood and its manageability, so that the model can be fully explored as seen in [26,37].

References

[1] Hodgson S., Harrison R.F., Cross S.S., (2006). An automated pattern recognition system for the quantification of inflammatory cells in hepatitis-C-infected liver biopsies, Image and Vision Computing, 24: pp1025-1038.

[2] Moriishi K., Atsuura, Y.M., (2003). Mechanisms of hepatitis C virus infection, Antivir. Chem. Chemother 14: pp. 285-297.

[3] Ojugo, A.A., Otakore, O.D., (2018b). Improving early detection of gestational diabetes via intelligent classification models: a case of the Niger Delta region of Nigeria, SciEP Journal of Computer Science & Application, 6(2): pp 82-90.

[4] WHO, Hepatitis C global prevalence, Weekly Epidemiological Record (World Health Organization), 74, 1999, pp. 421-428.

[5] Wilkins, T., Zimmerman, D and Schade, R.R., (2010). Hepatitis B: diagnosis and treatment, American Family Physician, 81(8), pp 965-972.

[6] Ojugo, A.A., Yoro, R.E., (2018). An intelligent lightweight market basket associative rule mining for smartphones cloud-based app, Adv. in Multidisciplinary and Scientific Research, 4(3): pp79-90.

[7] Fattovich G., Schalm S.W., (2000). Hepatitis C and cirrhosis, in Hepatitis C, T.J. Liang, J.H. Hoofnagle, San Diego, Academic Press, pp. 241–264 eds, 2000.

[8] Lawrence S.P., (2000). Advances in the treatment of hepatitis C, Advanced in International Medicine. 45: pp .65–105.

[9] Esrra, M.H., Mai., S.M., (2014). A study of support vector machine algorithm for liver disease diagnosis, American J. Intelligent Systems, 4(1): pp9-15.

[10] Ursem, R., Krink, T., Jensen, M., Michalewicz, Z., (2002). Analysis and modeling of controls in dynamic systems. IEEE Transaction on Memetic Systems and Evolutionary Computing, 6(4), pp.378-389.

[11] Ojugo, A.A., Eboka, A.O., (2018). Modeling computational solution of market basket associative rule mining approaches using deep neural network, SciEP Digital Technologies, 3(1): 1-8.

[12] Ojugo, A.A., Okobah, I.P., (2018). Prevalence rate of the hepatitis B virus infection in Niger Delta Region of Nigeria: a graph-based diffusion heuristic model, Int. Journal of Computer Application, 179(39): pp27-33.

[13] Ojugo, A.A., Eboka, A.O., Yoro, R.E., Yerokun, M.O., Efozia, F.N., (2015). Hybrid model for early diabetes diagnosis, Mathematics and Computers in Science and Industry, 50: 176-182, ISBN: 978-1-61804-327-6, ISSN: 2227-4588.

[14] Ojugo, A.A., Eboka, A.O., (2018). Comparative evaluation for performance adaptive model for spam phishing detection, SciEP Digital Technologies, 3(1): pp9-15.

[15] Aminu, M., Okachi, E.E., Abubakar, S.M., Yahaya, A., (2013). Prevalence of hepatitis B virus surface antigen among healthy asymptomatic students in a Nigerian University. Ann Afr. Med., 12:55-60.

[16] Emechebe, G.O, Emodi, I.J., Ikefuna, A.N., Ilechukwu, G.C, Igwe, W.C., Ejiofor, O.S., et al. (2009). Hepatitis B virus infection in Nigeria – A review. Niger. Med. Journal, 50:18-22.

[17] Edo, A.E., Edo, G.O., Ohehen, O.A., Ekhator, N.P., Ordiah, W.C., (2015). Age and diagnosis of type-2 diabetes in Benin City Nigeria, African J. Diabetes Medicine, 23(1), pp18-19.

[18] Musa, B.M., Bussell, S., Borodo, M.M., Samaila, A.A., Femi, O.L., (2015). Prevalence of hepatitis B virus infection in Nigeria, 2000-2013: a systematic review and meta-analysis, Nigeria J. Clinical Practice. 18: pp183.

[19] Dongdem, J.T., Kampo, S., Soyiri, I.N., Asebga, P.N., Ziem, J.B., Sagoe, K.. (2012). Prevalence of hepatitis B virus infection among blood donors at the Tamale Teaching Hospital, Ghana. BMC Res Notes, 5: pp115.

[20] Ado, A, Alhassan, S., Chonoko, U.G., Samaila, A.U., (2010). Sero-prevalence of hepatitis B surface antigen (HBsag) among blood donors attending Ahmadu Bello university teaching hospital (ABUTH), Zaria, Nigeria. Bajopas, 3: 20−2.

[21] World Health Organization (2013). Hepatitis B and C, Immunization, Vaccines and Biologicals. [online]: http://www.who.int/immunization/topics/hepatitis/en/.

[22] WHO, Hepatitis C (Fact Sheet No. 164), World Health Organization, Geneva, 2000.

[23] Barakat, N.H., Bradley, A.P., Barakat, M.N.H., (2010). Intelligible support vector machines for diagnosis of diabetes mellitus, IEEE Transactions on Information Technology in Biomedicine, 14(4), pp 1114-1120.

[24] Khashei, M., Eftekhari, S., Parvizian, J., (2012). Diagnosing diabetes type-II using a soft intelligent binary classifier model, Review of Bioinformatics and Biometrics, 1(1), pp 9-23.

[25] Guo, W.W and Xue, H., (2011) An incorporative statistic and neural approach for crop yield modelling and forecasting, Neural Computing and Applications, 21(1), pp109-117.

[26] Ojugo, A., Eboka, A., Okonta, E., Yoro, R.E., Aghware, F., (2012). GA rule-based intrusion detection system, J. of Computing and Information Systems, 3(8), pp 1182-1194.

[27] Ojugo, A.A., Yoro, R.E., (2013a). Computational intelligence in stochastic solution for Toroidal Queen, Progress in Intelligence Computing and Applications, 2(1), pp 46-56.

[28] Chinenye, S and Young, E., (2011). State of diabetes care in Nigeria: a review, The Nigerian Health Journal, 11(4), pp101-106.

[29] Coello, C., Pulido, G and Lechuga, M., (2004). Handling multiple objectives with particle swarm optimization, In Proc. of Evol. Computing, 8: 256-263.

[30] Ojugo, A.A., Otakore, O.D., (2018a). Seeking intelligent convergence for asymptotic stability feats of Prey Predator retarded equation using supervised model, Computing, Information Systems, Development Informatics & Allied Research Journal, 9(2): pp93-102.

[31] Ojugo, A.A., Emudianughe, J., Yoro, R.E., Okonta, E.O., Eboka, A., (2013b). Hybrid neural network gravitational search algorithm for rainfall runoff modeling, Progress in Intelligence Computing and Application, 2(1), pp 22.

[32] Ojugo, A.A., R. Abere., A.O. Eboka., M.O. Yerokun., R.E. Yoro., C.C. Onochie., D. Oyemade., (2013c). Hybrid neural network model for rainfall runoffs: comparative study, Advancement in Sci. Engr. Res., 1(2): 47-55.

[33] Ojugo, A.A., (2012). Artificial neural net gravitational search algorithm for rainfall runoff modeling in hydrology, unpublished PhD Thesis, CS Department: Ebonyi State University Abakiliki, Nigeria.

[34] Ojugo, A.A., Ben-Iwhiwhu, E., Kekeje, D.O., Yerokun, M.O., Iyawa, I.J.B., (2014). Malware propagation on time varying network, Int. J. Modern Edu. Comp. Sci., 8, pp25-33.

[35] Reynolds, R., (1994). Introduction to cultural algorithms, Transaction on Evolutionary Programming (IEEE), pp.131-139.

[36] Perez, M., Marwala, T., (2011). Stochastic optimization approaches for solving Sudoku, IEEE Transaction on Evol. Comp., pp.256-279.

[37] Heppner, H and Grenander, U., (1990). Stochastic non-linear model for coordinated bird flocks, In Krasner, S (Ed.), The ubiquity of chaos (pp.233-238). Washington: AAAS.