

Intelligent Classification Models for Gestational Diabetes: Comparative Study

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To cite this article:

Eboka Andrew Okonji, Okobah Ifeoma Patricia, Oluwatoyin Yerokun Mary. Intelligent Classification Models for Gestational Diabetes: Comparative Study. *Clinical Medicine Research*. Vol. 6, No. 6, 2017, pp. 192-200. doi: 10.11648/j.cmr.20170606.14

Received: April 5, 2017; **Accepted:** October 8, 2017; **Published:** December 7, 2017

Abstract: Diabetes mellitus, a metabolic disease that features high glucose levels in the body with the inability of the body to secrete enough insulin to breakdown glucose, or such a body is resistant to the effects of insulin. Nigeria and other nations of the world have become aware of the inherent threats to life of gestational diabetes in mothers with or without previous cases and its tendencies to metamorphose into Type-II. Our study presents a comparative study of classification models using both the supervised (K-nearest neighborhood and Quadratic Discriminant Analysis) and unsupervised (Profile Hidden Markov Model and Memetic algorithm) methods – which aims at early detection as well as improve early diagnosis via data-mining tools. Adopted dataset is split into: training (in some cases, retraining) and testing to aid model validation. Results show that age, obesity and family ties to the second degree, environmental conditions of inhabitation are critical factors that can increase likelihood. Gestational diabetes in mothers with or without previous cases were confirmed if: (a) history of babies weighing > 4.5kg at birth, (b) insulin resistance with polycystic ovary syndrome, and (c) abnormal tolerance to insulin. Also, PHMM outperforms Memetic algorithm in some cases; while memetic algorithm outperforms PHMM in some cases.

Keywords: Diabetes, Gestational, Fuzzy, Classifiers, Diab Care, Mellitus, Memetic Algorithm

1. Introduction

Diabetes mellitus has now become a general chronic disease that affects about 6% of the global population – so that its avoidance and early detection for effective treatment has become imperative and undoubtedly a critical task for health and economic issue in 21st century (Khashei et al, 2012). Diabetes is a metabolic disease that is characterized by the presence of hyperglycemia or high blood glucose. This result from the body's inability to secrete enough insulin that the body requires for glucose processing as a byproduct of the carbohydrate that we eat, or that the body is resistant to the effects of insulin. Thus, the reason why it is popularly named the *silent killer*. Glucose, as a main source of energy for cells that makes up the muscles and other tissues, is produced from the *food* we eat and in our *liver*. Sugar (or glucose) is absorbed in the bloodstream and enters into a cell by the help of insulin. Liver stores glucose as glycogen so that if glucose becomes low, the liver reconverts the stored glycogen into glucose to normalize the glucose level (Ojugo et al, 2015). Diabetes is a diagnosis from glycemia that is associated with microvascular

disease (Goldenberg and Punthakee, 2013).

Diabetes is associated with range of complications such as risk of blindness, blood pressure, heart and kidney diseases, and nerve damage to mention a few (Temurtas et al, 2009; Ojugo et al, 2016). Its early detection is extremely difficult by experienced physicians, and thus – led to a continued quest for methods to effectively and precisely classify the disease. Khashei et al (2013). Ojugo et al (2015) Various models have been used for its early detection and identification to include: (a) *supervised* classification in which its input variables for the diagnosis are *known*, and (b) *unsupervised* classification in which the variables used for diagnosis and classification are *unknown*. In both instance, a *critical* feat in selecting the appropriate classification model to use is, its accuracy and precision ability in classifying the task at hand.

1.1. Types of Diabetes

Diabetes is generally classified into (Ojugo et al, 2015):

- Type-1 is a chronic condition/state, in which the pancreas secretes little or no insulin, allowing sugar to build up in the bloodstream and cause some real life

threats. Type-1 has no cure as it is insulin-dependent and its causes are *unknown*. Its *symptoms* include: blurred vision, extreme hunger, increased thirst, irritability, incessant urination, fatigue, mood changes, unintended weight loss, vaginal yeast infection (in females), bedwetting etc; Some of its known risk factors include: genetics, family history, age, geography, exposure to bacteria and Epstein-Barr virus in environ, early exposure to cow milk, low vitamin D, early or late introduction to cereal/gluten in baby diet, intake of nitrate-contaminated water, mothers with preeclampsia at pregnancy and babies born with jaundice (American Diabetes Association, 2009; Ojugo *et al* 2016).

- b. Type 2 (adult onset or noninsulin-dependent) diabetes is a chronic condition that affects how the body metabolizes sugar (glucose). It often develops slowly since the body either resists the effects of insulin as produced or does not produce enough insulin to maintain a normal glucose level. Though common in adults, this type is increasingly common now to children with obesity issues. While, there is also no cure for type-2, it can however be managed through proper eating habits, exercising, maintaining a healthy weight and sometimes, diabetes medications or insulin therapy. Its symptoms are increased thirst/hunger, weight loss, frequent urination, fatigue, blurred vision, acanthosis nigricans (areas of darkened skin) amongst others (Peter, 2012; Canadian Diabetes Association, 2014; Ojugo *et al*, 2016). Chinenye and Young (2011) Type-2 diabetes has asymptomatic preclinical phase which is not benign and thus, underscores the need for primary prevention and population screening in order to achieve early diagnosis and treatment. The prevalence of undiagnosed diabetes is been found to range from 4.76% of outpatients attending a family practice clinic, to as high as 18.9% in Nigeria. And such prevalence is higher by 68% in persons of higher socioeconomic status.
- c. Gestational diabetes represents glucose intolerance from onset, and is first recognized during pregnancy. It causes high blood sugar that can affect pregnancy and the baby's health, though the blood sugar usually returns to normalcy soon after delivery. A patient with gestational diabetes is at the risk of type-2 diabetes with each pregnancy and it does not cause any noticeable signs (Canadian Diabetes Association, 2014; Chinenye and Young, 2011).

1.2. Gestational Diabetes Diagnosis: The Nigerian Scenario

Gestational Diabetes Mellitus (GDM) is defined as disorder of glucose tolerance occurring first in pregnancy in mothers – whereas, some experts have viewed and believe GDM to be of same entity with Type-II – wherein the former constitutes the early signs and manifestation of the latter. GDM is endemic around the world and its prevalence differs from one region to another. Its risk factors include: family history of DM in first-degree relatives, child bearing with congenital anomaly, baby weighs more than 4000g or more, dying of unknown

causes at birth, obesity, age greater than 35years amongst other. Various techniques are available to diagnose GDM as to what to test, when to perform such tests and what method is best. Most authors continually favor the early weeks of third trimester (between 26-to28 weeks) of pregnancy as best time to screen for GDM. Its investigations can be divided into *screening* and *definitive* tests (Adebisi *et al*, 2012). The risk factors can be seen in the table 1.

It is a known fact that type-II diabetes has an asymptomatic preclinical phase that is not benign and underscores the need for primary prevention and population screening in order to achieve early diagnosis and treatment. The prevalence of undiagnosed diabetes has been found to range from 4.76% in one study of outpatients attending a family practice clinic to as high as 18.9% in another study. Prevalence of diabetes was found to be higher by as much as 68% in persons of a higher socioeconomic status were earlier studies had reported lower prevalence rates for undiagnosed diabetes in the population – whereas Nyenwe *et al* (2003) reported a 2.8% rate of disease in Port Harcourt and 1.7% in Lagos metropolis in 1988. Arije *et al* (2007) concurred with a satisfactory systolic and diastolic blood pressure control was obtained in only 38.5% and 42.2% of some Nigerian patients attending a tertiary health facility, respectively.

Diabcare Nigeria in 2008 took a sample study conducted across 7-tertiary health centers in Nigeria with the objective of assessing clinical and laboratory profile, evaluating the quality of care of Nigerian diabetics with a view to planning improved diabetes care. Clinical parameters studied include: diabetes types, anthropometry, blood pressure, chronic complications of diabetes and treatment types. Laboratory data assessed include: fasting plasma glucose (FPG), 2 Hour post-prandial (2-HrPP), glycated haemoglobin (HbA1c), urinalysis, serum lipids, electrolytes, urea and creatinine. A total of 531 patients, 209(39.4%) males and 322(60.6%) females enrolled. Results indicate the mean age of the patients was 57.1±12.3years with mean duration of diabetes of 8.8±6.6years. A majority (95.4%) had Type-II 2 diabetes compared to Type-I (4.6%) using a $p < 0.001$ significance. Mean FPG, 2-HrPP glucose and HbA1c were noted at 8.1±3.9mmol/L, 10.6±4.6mmol/L and 8.3±2.2% respectively. Only 170 (i.e. 32.4%) male and 100 (i.e. 20.4%) female patients achieved the ADA and IDF glycaemic targets respectively. About 72.8% patients did not practice self-monitoring of blood glucose and hypertension is found in 322 (i.e. 60.9%) patients, with a mean systolic BP of 142.0±23.7mmHg and mean diastolic BP of 80.7±12.7mmHg (Chinenye and Young, 2011).

Its complications include: peripheral neuropathy 59.2%, cataracts 25.2%, cerebrovascular disease 4.7%, retinopathy 35.5%, nephropathy 3.2% and diabetic foot ulcer 16.0%. It is obvious that the status of Diabetes Care in terms of glycaemic control, control of cardiovascular risk factors, management practices and presence of late complications of diabetes were below the optimum expected; And most screening conducted in pursuance of early detection that are based on risk factors have been found to be insensitive as well as resulted in an increased false positives rates of methods adopted for these

test as a little above 40% of these cases are missed. Also, no screening method is consistently reliable. Thus, the rationale for this study to early detect GDM in mother as maternal mortality has been seen to be on increase (Ojugo et al, 2015).

The *idea* is to advance for early diagnosis and detection of GDM and Type-II in mothers (with or without previous cases) using intelligent classification (supervised and unsupervised) model. This task seeks to allow model to propagate observed data as input – as the model seeks to uncover the underlying probability of data feats of interest, even with the data fed in as input consisting of ambiguities, noise and impartial truth. The model will seek to yield an output that is guaranteed of high quality and void of ambiguities. These models, further tuned can become robust and perform quantitative processing to ensure qualitative knowledge and experience, as its new language (Ojugo et al, 2013, Heppner and Grenander, 1990).

2. Materials

2.1. Dataset Used

Table 1. Risk factor for GDM and Clinical Parameters for Encoding Dataset Schema Used.

Attribute Name	Clinical Associates
Family Relatives	Type-2 DM in 1st-Degree Relatives
Number of Pregnancy	1 or more
Plasma Glucose Tolerance	History of abnormal glucose tolerance
Diastolic Blood Pressure	
Triceps skin fold thickness	Body Mass Index > 30kg
Diabetes Pedigree Function	Type-2 or GDM in previous pregnancy
Age	35years and above
Obesity	BMI > 30.0kg/m ²
Ethnicity	African-American, Hispanic, Asian-American, Pacific Islander etc
Insulin Resistance	Polycystic ovary syndrome
Large Babies	History of babies >4.5kg at birth
Malformation	Birth of a malformed child
Perinatal Events	Unexplained perinatal loss
Maternal Birth/Large Babies	< 2.5kg or >4.5kg

Some statistical information of attributes is given in Table 1.

The data set consists of 768 samples, about two third of which have negative diabetes diagnosis and one third with a positive diagnosis. The data set is randomly split into equal size of training and test sets of 384 samples each.

2.2. Statement of Problem

The problem statements are as follows:

1. Being a silent killer makes its early detection, critical and imperative – as an unchecked scenario leads to increased maternal mortality. The use of supervised diagnosis is becoming redundant as it sometimes yields inconclusive results due to *unknown* inputs. Studies show conditions not even related to diabetes (but with symptoms similar or mimics type of diabetes class). Such classification results in increased rate of false-positives (*unclassified* symptom) and true-negatives (to classify symptom as diabetes when it is not). Proposed model seek to

effectively group data into definitive classes of diabetes (GDM) via evolutionary *unsupervised* models that employs predictive data-mining rules and reinforcement learning (Section III).

2. Hybrid models have been employed in many studies on diabetes. However, there are tradeoffs to be made as well as conflicts that needs to be resolved such as the conflict imposed on the model by the various underlying statistical dependencies that exist between the various heuristic method being adopted by the hybrid as well as the conflict imposed on the hybrid model by the dataset used. The proposed model resolves this (Section III) via the creation of profiles that assigns scores to rules that effectively classifies data into various types or classes of diabetes.
3. Many datasets often consist of ambiguities, imprecision, noise and impartial truth that must be resolved via robust search. Also, speed constraint that often gets such solution trapped at local minima (resolved in Section III).
4. Parameter(s) selection can be quite a daunting task when searching a solution space for a complete and optimized solution that will aid effective and efficient classification in a certain domain. Careful selection is required so that the system does not result in model over-fitting of data as well as overtraining cum over-parameterization (resolved in Section III) as the model seeks to discover underlying probability of the data feat(s) of interest.

3. Intelligent Proposed Model

We seek to compare various supervised model (LDA and Support Vector Machine) against the unsupervised models (Hidden Markov Model and Fuzzy Genetic Algorithm Trained Neural Net Model) to measure their comparative performance.

3.1. Linear Discriminant Analysis (LDA)

LDA is a very simple and effective supervised classification method with wide range of applications. Its basic theory is to classify compounds (rules) dividing n-dimensional descriptor space into two regions separated by a hyper-plane that is defined by linear discriminant function. Discriminant analysis generally transforms classification tasks into functions that partitions data into classes; Thus, reducing the problem to an identification of a function. The focus of discriminant analysis is to determine this *functional* form (assumed to be linear) and estimate its coefficients. LDA was first introduced in 1936 by Ronald Aylmer Fisher and his LDA function works by finding the mean of a set of attributes for each class, and using the mean of these means as boundary. The function achieves this by projecting attribute points onto the vector that maximally separates their class means and minimizes their within-class variance as expressed in Eq. 1 as follows:

$$X'S^{-1}(X_2 - X_1) - \frac{1}{2}(X_2 + X_1)'S^{-1}(X_2 - X_1) > c \quad (1)$$

where X is vector of the observed values, X_i ($i = 1, 2, \dots$) is the mean of values for each group, S is sample covariance matrix of all variables, and c is cost function. If the misclassification cost of each group is considered equal, then $c = 0$. A member is classified into one group if the result of the equation is greater than c (or $= 0$), and into the other if it less than c (or $= 0$). A result that equals c (set to 0) indicates such a sample cannot be classified into *either* class, based on the features used by the analysis. LDA function distinguishes between two classes – if a data set has more than two classes, the process must be broken down into multiple two-class problems. The LDA function is found for each class versus all samples that were not of that class (one-versus-all). Final class membership for each sample is determined by LDA function that produced the highest value and is optimal when variables are normally distributed with equal covariance matrices. In this case, the LDA function is in same direction as Bayes optimal classifier (Billings and Lee, 2002), and it performs well on moderate sample sizes in comparison to more complex method (Ghiassi and Burnley, 2010). Its mathematical function is simple and requires nothing more complicated than matrix arithmetic. The assumption of linearity in the class boundary, however, limits the scope of application for linear discriminant analysis. Real-world data frequently cannot be separated by linear boundary. When boundaries are nonlinear, the performance of the linear discriminant may be inferior to other classification methods. Thus, to curb this – we adopt a decimal encoding of the data to give us a semblance of linear, continuous boundaries.

3.2. *K*-Nearest Neighbourhood (KNN)

The *K*-nearest neighbour (KNN) model is a well-known supervised learning algorithm for pattern recognition that first introduced by Fix and Hodges in 1951, and is still one of the most popular nonparametric models for classification problems (Fix and Hodges 1951; 1952). *K*-nearest neighbour assumes that observations, which are close together, are likely to have the same classification. The probability that a point x belongs to a class can be estimated by the proportion of training points in a specified neighbourhood of x that belong to that class. The point may either be classified by majority vote or by a similarity degree sum of the specified number (k) of nearest points. In majority voting, the number of points in the neighbourhood belonging to each class is counted, and the class to which the highest proportion of points belongs is the most likely classification of x . The similarity degree sum calculates a similarity score for each class based on the *K*-nearest points and classifies x into the class with the highest similarity score. Its lower sensitivity to outliers allow majority voting to be commonly used other than the similarity degree sum (Chaovalitwongse, 2007). We use majority voting for the data sets to determine which points belongs to neighbourhood so that distances from x to all points in the training set must be calculated. Any distance function that specifies which of two points is closer to the sample point could be employed (Fix and Hodges, 1951). The most

common distance metric used in *K*-nearest neighbour is the Euclidean distance (Viaene, 2002). The Euclidean distance between each test point f_i and training set point f_s , each with n attributes, is calculated via Eq. 2:

$$d = [(f_{t1} - f_{s1})^2 + (f_{t2} - f_{s2})^2 \dots + (f_{tn} - f_{sn})^2]^{\frac{1}{2}} \quad (2)$$

In general the following steps are performed for the *K*-nearest neighbour model (Yildiz *et al.*, 2008): (a) chosen of k value, (b) distance calculation, (c) distance sort in ascending order, (d) finding k class values, (e) finding dominant class.

A challenge in *K*-nearest neighbour is to determine optimal size of k that acts as a smoothing parameter. A small k is not sufficient to accurately estimate population proportions around test point. A larger k will result in less variance in probability estimates (but for risk of introducing more bias). K should be large enough to minimize probability of a non-Bayes decision, and small enough that all the points included, gives an accurate estimate of the true class. Enas and Choi (1986) found optimal value k depends on sample size and covariance structures in each population and on the proportions for each population in the total sample. For cases where the differences both in covariance matrices and between sample proportions are both small or both large, it is found that optimal k is $N^{3/8}$ (N is number of samples in the training set). If and when there is a large difference between covariance matrices, and a small difference between sample proportions (or vice-versa), the optimal value k is determined by $N^{2/8}$ (Enas and Choi, 1986).

This model presents several merits (Berrueta *et al.*, 2007) in that: (a) its mathematical simplicity does not prevent it from achieving classification results as good as (or even better than) other more complex pattern recognition techniques, (b) it is free from statistical assumptions, (c) its effectiveness does not depend on the space distribution of the classes, and (d) when the boundaries between classes are not hyper-linear or hyper-conic, *K*-nearest neighbour performs better than LDA.

However, Enas and Choi (1986) found that LDA performs slightly better than *K*-nearest neighbour when the population covariance matrices are equal, a condition that suggests linear boundary. As the differences in covariance matrices increases, *K*-nearest neighbour performs increasingly better than the linear discriminant function. However, despite these merits of the model, the demerits of the *K*-nearest neighbour models includes that model does not work well if large differences are present in samples in each class. *K*-nearest neighbour provides poor information about the structure of the classes and of the relative importance of each variable in the classification. Laos, it does not allow a graphical representation of the results, and in the case of large number of samples, computation become excessively slow. In addition, *K*-nearest model requires more memory and processing requirements than other methods. All prototypes in the training set must be stored in memory and used to calculate Euclidean distance from every test sample. The computational complexity grows exponentially as number of prototypes increases (Muezzinoglu and Zurada, 2006).

3.3. Bayesian Profile Hidden Markov Model (PHMM)

Ojugo et al (2016) describes the Hidden Markov model as used in examination scheduling. Adapted to GDM diabetes classification problem, probability from one transition state to another is as in figure 1. The PHMM is a double embedded chain that models complex stochastic processes (Bhusai and Patil, 2011; Masoumeh, Seeja, and Afshar, 2012). Markov process is a chain of state probabilities associated to each transition between states. In n -order Markov, its transition probabilities depend on *current* and $n-1$ *previous* states. A HMM process determines the state generated for each state observation in a series (output sequence). For GDM diabetes analysis, a rule not accepted by the trained HMM, yields high probability of either a false-positive or true-negative result (Ojugo et al, 2016). Traditional HMM scores data via clustering based on profile values. Probabilities of initial set of rules are sampled – then classified into GDM or non-GDM class. HMM maintains a log in memory to help reduce high true-negatives (rules of symptoms with semblance of diabetic feats) and high-false positives (unclassified rules for diabetes). Thus, our HMM is initially trained to assimilate normal behaviour of the various types or diabetes class/types. It then creates a profile of the rules, classifying them into type-1, type-2, gestational and other profile ranges were possible (Tripathi and Pavaskar, 2012; Ojugo et al, 2016).

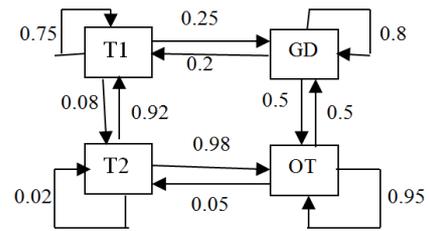


Figure 1. Actual State Transition with $P(x)$

The Profile HMM as a variant of HMM, proffers solution to the fundamental problems of the HMM by: (a) makes explicit use of positional (alignment) data contained in observations or sequences, and (b) allows null transitions, where necessary so that the model can match sequences that includes insertion and deletions (Ojugo et al, 2014). Used in GDM early detection, O is each rules contained therein to define the various symptoms of GDM diabetes type, T is time it takes each rule to classify data input, N is number of unclassified rules and those with symptom semblance that results in false-alarm rates, M is the number of rules accurately classified, π is the initial state or starting rule, A is state transition probability matrix, a_{ij} is the probability of a transition from a state i to another state j , B contains the N probability distributions for the codes in the knowledgebase from where profiles have been created (one rule for each state of the process); while HMM $\lambda = (A, B, \pi)$. Though, parameters for HMM details are incomplete as above; But, the general idea is still intact (Ojugo et al, 2016).

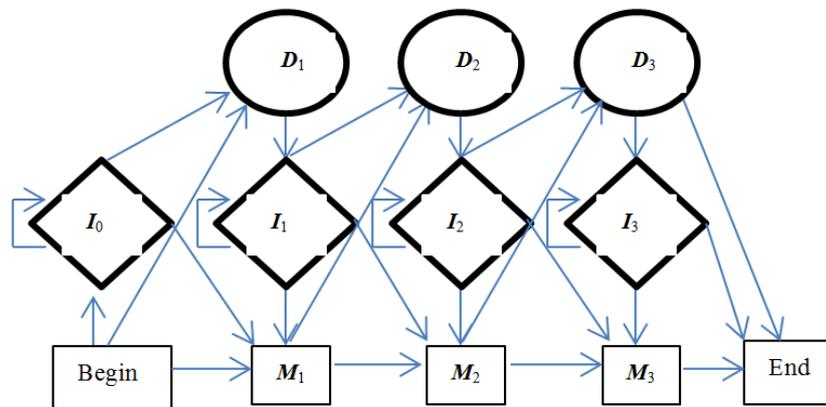


Figure 2. PHMM with 3-Match States.

We can also align multiple codes (data) rules as sequence with significant relations. Its output sequence determines if an unknown code is related to sequence belonging to either of the diabetes (type class) or its variant (or those not) contained in the Bayesian net. We then use the profile HMM to score codes and make decision. Circles are *delete* state that detects rules as classified into GDM-diabetes types, rectangle are *insert* states that allows us to *accurately* classify rules of symptoms that have been previously unclassified inputs into a class type and consequently, update knowledgebase of the classified false-positives and true-negatives; diamonds are *matched* states that accurately classifies rules of symptoms into variants of similar symptom or unclassified rules, as in standard HMM (Ojugo et al, 2014; 2016). Delete and insert are emission states

in which an observation is made as PHMM passes through all the states. Emission probabilities, corresponding to B in standard HMM model is computed based on frequency of symbols that can be emitted at a particular state in the model; But, are positional-dependent (in contrast to standard model). Also, the emission probabilities are derived from Bayesian net, which represents our training phase. Finally, *match* states allow the model to pass through gaps, existing in the Bayesian net to reach other emission states. These gaps prevent model from over-fitting and overtraining as in figure 2 (Ojugo et al, 2016). Our forward algorithm computes (recursively) probabilities of all possible case by reusing scores calculated for partial sequences using Eq. 3 to Eq. 5 respectively as thus:

$$F_j^M = \text{Log} \frac{e^{M_j(x_i)}}{qx_i} + \log(aM_{j-1}M_j \exp(F_{j-1}^M(i-1))) + aI_{j-1}M_j \exp(F_{j-1}^I(i-1)) + aD_{j-1}M_j \exp(F_{j-1}^D(i-1)) \quad (3)$$

$$F_j^I = \text{Log} \frac{e^{I_j(x_i)}}{qx_i} + \log(aM_jI_j \exp(F_j^M(i-1))) + aI_jI_j \exp(F_j^I(i-1)) + aD_jI_j \exp(F_j^D(i-1)) \quad (4)$$

$$F_j^D = \log(aM_{j-1}D_j \exp(F_{j-1}^M(i))) + aI_{j-1}D_j \exp(F_{j-1}^I(i)) + aD_{j-1}D_j \exp(F_{j-1}^D(i)) \quad (5)$$

3.4. Fuzzy Genetic Algorithm Trained Neural Network Model

The GANN is initialized with if-then rules. Individual fitness is computed as 30-individual are selected via the *tournament* method to determines new pool and individuals for mating. Crossover and mutation is applied to help *net* learn dynamic and non-linear feats in the dataset and feats of interest using a multi-point crossover. As new parents contribute to yield new individuals whose genetic makeup is combination of both parents, mutation is reapplied and are allocated new random values that still conforms to belief space. Number of mutation applied depends on how far CGA is progressed on the network (how fit is the fittest individual in the pool), which equals fitness of the fittest individual divided by 2. New individuals replace old with low fitness so as to create a new pool. Process continues until individual with a fitness value of 0 is found –

indicating solution is reached (Ojugo *et al.*, 2013).

Initialization/selection via ANN ensures that first 3-beliefs are met; mutation ensures fourth belief is met. Its influence function influences how many mutations take place, and the knowledge of solution (how close its solution is) has direct impact on how algorithm is processed. Algorithm stops when best individual has fitness of 0 (Dawson and Wilby 2001). Model stops if stop criterion is met. GANN utilizes number of epochs to determine stop criterion.

4. Result Findings and Discussion

4.1. Model Performance

Ojugo *et al.* (2013) Performance is evaluated via computed values: mean square error, mean absolute error, mean relative error and coefficient efficiency as thus:

Table 2. Model Convergence Performance Evaluation.

Model	MSE	MRE	MAE	COE	Class. Accuracy %
LDA	0.87	0.79	0.75	0.581	42
K-nearest	0.67	0.55	0.56	0.481	51
PHMM	0.46	0.31	0.23	0.853	90
FGANN	0.46	0.37	0.46	0.818	86

Table 3. Clinical Parameters and Association.

No	Attribute Name	μ	σ
1	Number of Pregnancy	3.8	3.4
2	Plasma Glucose (2 Hours)	121	32
3	Diastolic Blood Pressure	69.1	19.4
4	Triceps skin fold thickness	20.5	16.0
5	Two Hour Serum Insulin	79.8	115.2
6	Body Mass Index	32.0	7.9
7	Diabetes Pedigree Function	0.5	0.3
8	Age	33.2	11.8

4.2. Result Findings and Discussion

To measure their effectiveness and classification accuracy, we adopt the misclassification rate of each model as well as its corresponding improvement percentages of the proposed model in comparison with those of other classification models for the diabetes data in both training and test data sets as summarized in Table 2 and Table 3, respectively. The equations for the misclassification rate and its improvement percentage of the unsupervised (B) model against those of the supervised (A) model, is respectively calculated as follows:

$$\text{Misclassification Rate (MR)} = \frac{\text{No.of Incorrect Diagnosis}}{\text{No.of Sample set}} \quad (6)$$

$$\text{Improvement Percentage} = \frac{\text{MR(A)} - \text{MR(B)}}{\text{MR(A)}} \times 100 \quad (7)$$

Table 4. Misclassification Rate of Each model.

Model	Classification Errors	
	Training Data	Testing Data
LDA	36.6%	34.9%
K-Nearest Neighbourhood	43.4%	39.7%
PHMM	18.7%	15.8%
FGANN	19.3%	18.3%

Table 5. Improvement Percentage.

Model	Improvement %	
	Training Data	Testing Data
LDA	45.83%	41.16%
K-Nearest Neighbourhood	41.79%	43.09%
PHMM	78.78%	76.33%
FGANN	69.30%	69.91%

Tables 4 and 5 shows *unsupervised* model has lowest error on test portion of the data set in comparison to supervised models used. PHMM/FGANN had misclassification rate of 18.7% and 19.3% respectively – with an improvement rate of 78.78% and 69.30% respectively. Conversely, the supervised models in LDA and K-Nearest neighbourhood had a misclassification error rate of 36.6% and 43.4% respectively; while showing an improvement rate of 45.83% and 41.79% respectively. Also, it is observed that though the *K* - nearest neighbour scores were quite sensitive to relative magnitude of

different attributes, all attributes are scaled by their z - scores before using K - nearest neighbour model in tandem with Antal et al (2003).

4.3. Related Study

Barakat et al (2010) adopts SVM by using an additional intelligent module to transform black-box SVM model to an intelligent SVM's diagnostic model with adaptive results that provides a potential model for diabetes prediction. Its logical rule set generated had prediction accuracy of 94%, sensitivity of 93%, and specificity of 94%. Extracted rules are medically sound and agree with outcome of relevant medical studies.

Khasei et al (2012) adopted a feed-forward multi-perceptron network in their study. Such networks must be expanded and extended to represent complex dynamic patterns and/or cases such as this, since it treats all data as new – so that previous data signals do not help to identify data feats of interest, even if such observed datasets exhibits temporal dependence. Consequently, this has practical implementation difficulty as large nets are not easily implemented. However, *Jordan* net overcomes such difficulty via use of its internal feedbacks that also makes it appropriately suitable for such dynamic, non-linear and complex tasks as its output unit is fed-back as input into its hidden unit with a time delay, so that its outputs at time $t-1$, is also input at time t . Also, Ojugo et al (2015).

The *rationale* for the choice of techniques adopted is to compare between: (a) supervised versus unsupervised model, (b) seek a measure to lay claims to superiority of a class of models (supervised/unsupervised) over the other for the task at hand, (c) compare clustering (profile) versus hill-climbing heuristic, and (d) measure the convergence behavior and other statistic between PHMM and FGANN. On this latter, it was observed that PHMM converged after 253-iterations; while FGANN converged after 213-iterations. And though, FGANN is significantly better and outperforms PHMM in some tasks; while PHMM have been found to outperform FGANN in classification accuracy.

We *note*, model's speed is traded-off for greater accuracy of classification, more number of rule set generated to update the knowledge database for optimality and greater functionality.

5. Conclusion and Recommendations

As for GDM, its risk factors are many and must be assessed regularly in all pregnant women. Placental mass and hormonal changes during pregnancy may contribute to the pathogenesis of GDM. Insidious onset of most cases of GDM necessitates a diligent search and screening, and while, we advise that RBG, FBG, and OGTT to be used in GDM diagnosis (as agreed by Opta and Nzeribe, 2013). A significant number of cases of GDM in pregnancy require insulin for treatment. There is now increasing evidence, that sulphonylureas and metformin are safe in pregnancy. The management and follow-up of GDM is for life.

Furthermore, our study employed *supervised* (K -nearest neighbourhood/LDA) and *unsupervised* (PHMM/FGANN as

benchmark for classification of GDM) models – and consists of 5-phases: (a) train models with available data, (b) determine minimal fuzziness via the obtained weights and same criterion, (c) delete outliers in data, (d) compute membership probability of output, and (e) assign output to appropriate class by largest probability. Four known intelligent classification models: LDA, K - nearest neighbour, PHMM and FGANN are used to show their classification efficiency for early prognosis of GDM. The hybrid unsupervised models outperforms, and is better than K -nearest and LDA (alongside other traditional classification models).

The unsupervised models do not assume the shape of the partition, unlike the linear and quadratic discriminant analysis. In contrast to K - nearest neighbour model, the proposed model does not require storage of training data. Once the model has been trained, it performs much faster than K - nearest neighbour does, because it does not need to iterate via individual training samples. Proposed model does not require experimentation and final selection of kernel function and a penalty parameter as is required by the support vector machines. Our proposed model solely relies on a training process in order to identify the final classifier model. Finally, the unsupervised models does not need large amount of data in order to yield accurate results.

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