

An Intelligent Model Using Relationship in Weather Conditions to Predict Livestock-Fish Farming Yield and Production in Nigeria

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Received September 24, 2019; Revised October 28, 2019; Accepted November 18, 2019

Abstract Soft-computing is an inexact computing art and science that seeks to analyze input so as to yield a predicted, optimal and complete-feasible solution to a complex task for which conventional methods yield a corresponding non-cost effective solution. It achieves tractability, robustness and low-cost to a solution with a tolerance of ambiguity, uncertainty, partial truth, noise, imprecision and approximation as applied to its input. Our study adopts profile hidden markov model to predict fish production yield in Nigeria. In comparison to other models, PHMM misclassification rate of 18.7% and improvement rate of 78.78%; while FGANN (fuzzy genetic algorithm trained neural net) has a misclassification rate of 19.3%, and had improvement rate of 69.30% respectively. Conversely, LDA and K-Nearest neighbourhood had a misclassification error rate of 36.6% and 43.4%; with an improvement rate of 45.83% and 41.79% respectively. We compared the supervised versus unsupervised model and results shows that unsupervised PHMM can more accurately predict future yields in fish production as it forecasts outliers in weather conditions such as rain, sunshine, humidity, and temperature amongst others – as it can greatly improve fish yield in the years ahead.

Keywords: *intelligent models, stochastic, validation, predictions*

Cite This Article: R.E. Yoro, and A.A. Ojugo, “An Intelligent Model Using Relationship in Weather Conditions to Predict Livestock-Fish Farming Yield and Production in Nigeria.” *American Journal of Modeling and Optimization*, vol. 7, no. 2 (2019): 35-41. doi: 10.12691/ajmo-7-2-1.

1. Introduction

Precision Farming (PF) is the art, science and management of a farm, its products and production value chain via principles and technology of process engineering. It seeks to efficiently integrate a management system that attempts to recognize products' needs and its increased yield (typically applied here to fish farm). Precision farming involves processes like animal growth, yield production, disease detection and monitoring, the various dimensions of animal behavior and its physical environ, not limited to thermal micro-environment and emissions of gaseous pollutants [1,2]. Thus, it results in the steady advancement of monitoring and control systems as applied to farming processes that in turn, has led to the development of automatic schemes, machines and models that are now being marketed and understudied [3,4].

The complex and dynamic-chaotic nature of the underlying (man-manufactured and natural) parameters such as early detection for increased yield parameters and postharvest process, which is responsible for

precision farming phenomena has made modeling and its corresponding prediction, a herculean task [5]. Despite advances, parameter selection and accurate model prediction is still a cumbersome task [6,7]. With soft-computing, precision farming is an improvised means that seeks to propagate dataset (consisting of noise, ambiguities and assumptions) as input, which is analyzed to yield a corresponding observed output value. Further tuning will make the model more robust to perform quantitative processing that ensures qualitative knowledge and experience, as its new form of language [8,9]. It achieves this by investigating the underlying probabilities of the data feats of interest; Thus, simulate model's tractability, robustness, low cost-effective solution with tolerance to ambiguity, uncertainties, partial truth, imprecision and noise when applied to its input via machine learning models and heuristics from an evolutionary point. Researchers' quest to enhance stochastic models for better predictions and concise model heuristics will continue as many studies have successfully used them; while aiming at an optimal solution for a task, when given a set of possible solution and search space so that model yields an output guaranteed of high quality, void of ambiguity and perfects its assumptions [10,11].

1.1. Fish Farming and Life History

With a global estimated population of over 12 Billion by 2050, one of the many daunting challenges(s) will be in feeding of such an ever-growing and ever-evolving, multi-faceted society. This is obviously enough to engage the curiosity of researchers and technical experts as well as become a growing concern for leaders of nations the world over [12]. A relatively unappreciated, but promising, fact is that fish has and will always play a major role to placate and proffer a means to satisfying the palates of the world's growing middle income class; And consequently, meet the food security needs of the lower income and poorest groups, in our societies [13,14].

Fish represents 16-percent of all animal-protein as consumed globally. This proportion will increase as consumers with rising incomes seek higher-value seafood, and as aquaculture yearns to meet the increasing demands. Aquaculture continues to grow at an impressive rate world over, as it has helped to produce more fish-food as well as kept the overall price of fish down, and made fish and seafood more accessible to consumers [2,15,35]. Adequate funds will help the industry create an emergence of new cum safer technologies, their adaptation to local conditions, and their adoption in appropriate settings [16]. To supply fish with sustainable production without depleting productive natural resources and without damaging the aquatic environment is a huge challenge as fish continue to experience excessive and irresponsible harvesting; while *natural* (environmental, diseases etc) and *man-made* (pollution) conditions continue also to adversely affects production and account for early mortality syndrome in aquaculture [4,14,17].

The feeding pressure for aquaculture has steadily increased from 1930s to the middle 1960s, has also remained high till this day, and will increase over the next few years. Fishing history is observed fishing mortality to have increased between 1932 to 2005; And, assumed a constant 68-percent average yearly that has remained constant (though, has been deemed higher than what is considered precautionary for the NorthEast Arctic cod) at a record average of 40-percent yearly [4,15].

1.2. Evolutionary Model and Precision Farming

Evolutionary models lends itself to resolve complex task by exploiting observed data whose underlying probability feats are found as it explores knowledge and symbolic reasoning expressed as mathematical model to yield a heuristic method tolerant to noise, uncertainty and ambiguities. It exhibits the feats of (a) robustness, (b) flexibility, and (c) continuous adaptation in model designed cum simulated, in its bid to resolves a constraint satisfaction tasks, and mimics agents in search of optimal solution (food and survival) in a domain space. Mostly inspired by behavioral pattern and natural laws of biological evolution [2,18,19].

Evolutionary predictive models are based on simulations are developed to explore environmental constraints that select observed spatial and temporal spawning patterns and life-histories of the species [20]. [14] inquired into fish livestock production for evolutionary-based

reproductive model strategy in adult fish and its usage as a passive transport for early life stages. The study was poised to harness the evolutionary success of spawning, as quantified when patterns at population level emerge after many generations from constraints at the individual level via selective process. As a result, several self-sustaining populations are identified considering different sets of selective constraints. Spawning patterns were aimed at better match of the observed mean spawning pattern with two selective environmental constraints associated using: (a) the threshold temperature of 14°C, which the development of early life stages is ensured, and (b) avoidance of offshore currents that constitute a loss of spawning products. Their results indicated that simulated recruitment patterns are more realistic when considering the constraint of reaching the nursery area. The study did help to identify, temporally and spatially, environmental factors important for fish recruitment, spawning and production, and hierarchical establishment of these factors.

1.3. Problem Statement

Fish production systems aim to satisfy the needs, if they fit into resource base or environ, and if they are socially/economically viable. Macro-level factors may also have significant influence with environmental implications, both on/off farm, for development of sustainable systems. The current state of fish systems reflects their evolution in response to changing circumstances.

The need arose from these:

- Existing studies in improving fish yield are tied to a single recognizable feat, and as thus – also proffer dedicated model. Our study model aims to create a profile for weather conditions that improves fish yield.
- Most evolutionary stochastic models use hill climbing method, whose solutions are trapped at local minima because their speed shrinks as the model(s) approaches its optima.
- Resolving conflict in its structured learning and statistical dependencies imposed by data feats and by the heuristics adapted, is often tedious.

1.4. Rational of the Study

The rationale for this study is to interpret African experience via analysis of their evolution, current status and to consider its relevance for fish yield and planning with specific attention to Nigeria.

2. Material and Methods

Table 1 displays weather condition series that seems fairly stationary with strong seasonal components and the presence of outliers. Our immediate concern is to choose appropriate variables that can exert significant influence on rainfall so as to consequently increase fish yield. We select these parameters as inputs by inspecting the correlation values of rainfall with each of the other variables. Additionally, we use the historical data as below for the study.

Table 1. Weather Parameter for Asaba (2000-2014)

Year	Mean Rainfall (mm)	Mean Temp °C	Average Fish Yield in kg
2000	2000	34	47
2001	1652	41	45
2002	1902	50	62
2003	1672	35	43
2004	989	33	41
2005	1902	37	42
2006	2108	41	65
2007	2711	45	52
2008	1502	39	49
2009	981	23	37
2010	1972	39	59
2011	1678	32	47
2012	2032	45	45
2013	1901	33	37
2014	1420	39	42

3. Proposed Model

3.1. Markov Chains

A Markov chain describes a series of state with its associated probabilities to transit between states, if the transition probabilities depend only on current state (not on previous states). The Markov chain has no memory for a first order; while, n th order Markov chain depends both on current and its $n-1$ previous states. We represent in our example of simple DNA sequence using a Markov chain process as: P_{AT} is probability of the transition from state A to T; while P_{TA} is probability of the transition from state T to A, and so on respectively given that in the DNA chemical code, A = Adenosine, C = Cytosine, G = Guanine, and T = Thymine [21,22,23].

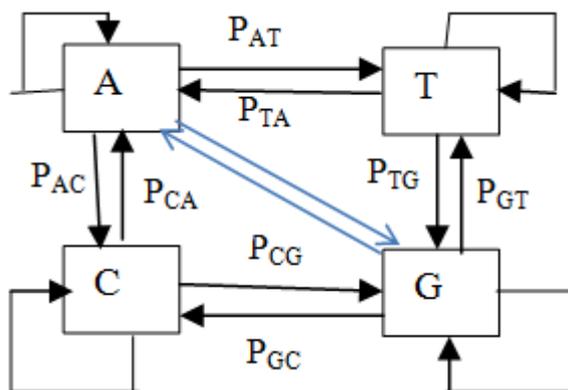


Figure 1. State Transition / Automata Diagram

Each arrow represents transition probability of a specific base followed by another base. Transition probabilities are calculated after observing several DNA sequence and corresponding transition probability matrix yields a compact representation of the transition probabilities – noting that a Markov chain leads to a corresponding Markov model; And, that each event depends only on the previous event. Transition probability

from state of observed symbol s to another state t is given by Eq. 1 [22,24]:

$$a_{st} = P(x_i = t | x_{i-1} = s) \text{ for } 1 \leq s, t \leq N \quad (1)$$

where N is the number of states and x_i is the state at step i . The sum of transition probabilities from each state equals 1 since these transitions represent a probability distribution as the probability associated with each step of/in the model.

With Bayes Theorem, the probability of sequence relative to the given model is computed below noting that $P(x_i)$ is the probability of starting at the first state x_i , and “begin”/“end” state helps accommodate the first and last symbols of its output sequence.

$$\begin{aligned}
 P(x) &= P(x_L, x_{L-1}, x_{L-2}, \dots, x_1) \\
 &= P(x_L | x_{L-1}, x_{L-2}, \dots, x_1) P(x_{L-1} | x_{L-2}, \dots, x_1) \\
 &= P(x_L | x_{L-1}) P(x_{L-1} | x_{L-2}) \dots P(x_2 | x_1) P(x_1) \quad (2) \\
 &= P(x_i) \prod_{i=2}^L a_{x_{i-1}x_i}.
 \end{aligned}$$

3.2. Higher Order Markov Chain / Model

Here, current event depends on more than one previous event. An n th order Markov process over m symbols is represented as a first order Markov chain with mn symbols. Thus, given a series of observations (i.e. output sequence) from a Markov process, we wish to determine which state generated each observation. Consider N buckets with a given distribution of coloured balls in each. Note that we are well aware of the distribution of the balls in each bucket as well as the rule for determining which of the bucket to select from. Being a Markov process, this rule for choosing the bucket from which we can select from depends on the previous selection [24].

Suppose, we are given a sequence of colours corresponding to the balls that were selected, but we do not know which buckets they were selected from. That is, the Markov process itself is hidden – we would like to gain information about this hidden process through the observations – that is, the colour of the balls selected. So far, we only outlined the basic structure of a hidden Markov model, the problem can be solved using the hidden Markov model approach using this simple example where:

- ✓ O : the observation sequence
- ✓ T : is the length of the observation sequence
- ✓ N : number of states in the HMM process
- ✓ α – is the alphabet for the model
- ✓ M : number of symbols in the alphabet
- ✓ A : the state transition probability matrix
- ✓ a_{ij} probability of the state transition from i to j
- ✓ $b_i(k)$: probability of observing k in the state i
- ✓ B : probability distribution of the observations (one distribution for each Markov process)
- ✓ $\lambda = (A, B, \pi)$ and it represents the HMM

HMM is given by $\lambda = (A, B, \pi)$ where the matrices of A, B and π may or may not be known, depending on the task we are trying to resolve. Thus, the model can be suited for any of the following tasks [23]:

- a. **Problem 1:** Compute probability model yields an observation sequence if given $\lambda = (A, B, \pi)$ and observation sequence O , compute $P(O/\lambda)$.
- b. **Problem 2:** Uncover the HMM $\lambda = (A, B, \pi)$ and an observation sequence O to determine most likely sequence of states $X = (x_1, x_2, \dots, x_T)$ that could have produced the sequence.
- c. **Problem 3:** Given observations and parameters N and M , determine $\lambda = (A, B, \pi)$ that best fits observed sequence O . Train model to fit data. Remarkably, HMM training requires no *a priori* assumptions about the model other than we outlining parameters N and M , which specifies the size of the model.

3.3. Experimental Framework

[20,21,22] describes Hidden Markov model as adapted in diabetes classification problem, for which we have the probability from one transition state to another as in Figure 1. Adapting such, the Hidden Markov Model is a double embedded chain that models complex stochastic processes. Markov process is a chain of states with probabilities associated to each transition between states. In an n -order Markov, its transition probabilities depend on *current* and $n-1$ *previous* states as seen in Figure 1. A Hidden Markov model process determines state generated for each state observation in a series (solution space). In fisheries production, a rule not accepted by the trained HMM, yields high misclassification of either a false-positive or true-negative result. The traditional HMM scores data via clustering based on profile values or score criterion. The probabilities of initial set of rules are sampled – then grouped into production yield such as **High**, **Moderate**, **Low** and No-yield class types. Model maintains a log in memory to help reduce unclassified rules (and errors of true-negatives and false positives in production).

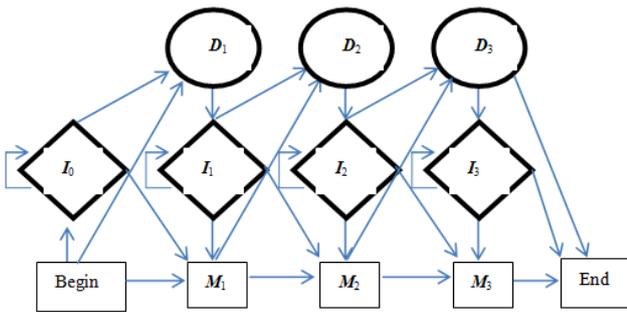


Figure 2. PHMM with 3-Match States

As adapted to fisheries production and spawning, O is each rules contained therein to define various parameters of the various class types, T is time taken by each rule to classify data, N is the number of unclassified rules that results in false-alarm rates, M is the number of rules that are 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; the general idea is still intact [20,21,22,23] as seen in Figure 2.

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 class type (or those not) contained in the Bayesian net. We then use the profile HMM to score codes and make decision. The circles are **delete** state that detects rules as classified into the various fish yield classes, rectangle are the **insert** states that allows us to **accurately** classify rules that have been previously unclassified into a class type and it then updates knowledgebase for classified false-positives and true-negative; while diamonds are **matched** states that accurately classifies rules of parameters into variants of similar symptom or still unclassified rules, as in the standard HMM [20,21,22].

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 model; But, are positional-dependent (in contrast to standard model). Also, the emission probabilities are derived from the Bayesian net, which represents our training phase. Finally, **match** states allow the model to pass through gaps, existing in the Bayesian network to reach other emission states. These gaps prevent model from over-fitting and overtraining as seen in Figure 2 [20,21,22,23]. We then adopt a forward algorithm to compute probabilities for each possible case recursively by reusing scores calculated for partial sequences using Eq. 3 to Eq. 5 respectively as thus:

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

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

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

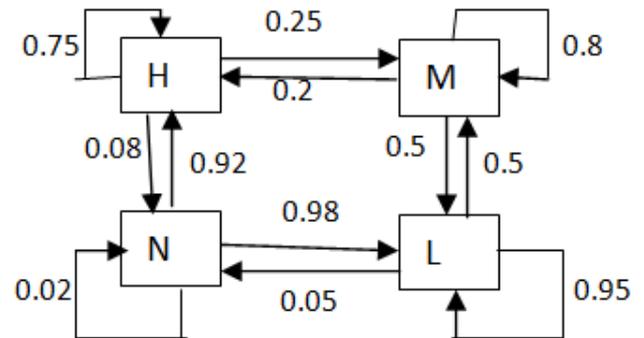


Figure 3. Actual State Transition with yield $P(x)$

Thus, from Table 2, our range of yearly fish yield is:

- a. High Yield if the amount of fish size, produced ranged between 55kg and above
- b. Moderate Yield if the amount of fish size, produced ranged between 40kg-to-54kg.
- c. Low Yield if the amount of fish size, produced ranged between < 40kg.
- d. No Yield if all the fish died.

From transition diagram of Figure 1, we compute the probabilities of each state of fish yield to give the Figure 3.

4. Discussion of Findings

4.1. Model Performance

[9,25,26,27,28] Performance is evaluated via computed values as thus:

Table 2. Model Convergence Performance Evaluation

Model	MSE	MRE	MAE	COE	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

4.2. Result Findings and Discussion

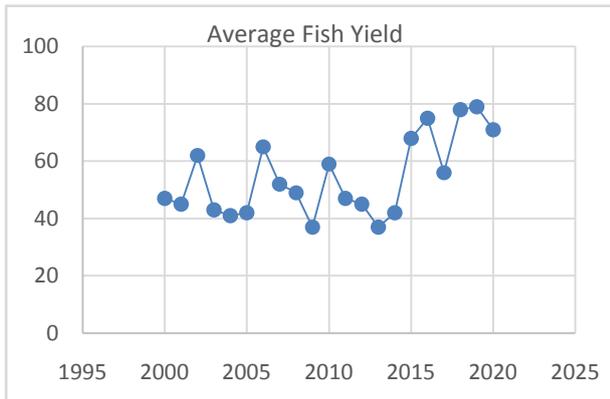


Figure 4. Shows Average Fish Yield

Result shows significant increase in fish production yield in the years ahead. This can be attributed to proper management of the natural habitats as well as favored weather conditions such as rain, sunshine, humidity and temperature.

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 3 and Table 4, 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 [8,29,30]:

$$\begin{aligned} & \text{Misclassification Rate}(MR) \\ &= \frac{\text{No. of Incorrect Diagnosis}}{\text{No. of Sample set}} \end{aligned} \tag{6}$$

This is used to compute the rate at which the model is able to predict the future yield of fish

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

This is used to compute the rate at which the model is able to improve after resulting in *false*-positive (indicate that the yield will increase when it actually decreases and vice versa) and *true*-negatives (when there are tendencies to result in increased fish production, but the parameters selected and the forecast was proved as wrong) result [31].

Table 3. Misclassification Rate In Comparison to Other Supervised/Unsupervised models

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

Table 4. Improvement Percentage In Comparison to Other Supervised/Unsupervised models

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

When compared to other models, results from Table 3 & 4 indicates that the *unsupervised* model especially the PHMM has lowest error on test portion of the data set in comparison to supervised models used. PHMM had misclassification rate of 18.7%, while FGANN (fuzzy-set genetic algorithm trained neural net) has a misclassification rate of 19.3%, and had 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 was 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 [12,32,33,34].

4.3. Result Tradeoffs

[9,20,21,22,25-28] notes that various trade-offs in prediction result can often fall under these categories:

- a. **Result Presentation** – researchers often display flawed results, modify/build new models rather than re-test limitations, biasness and inabilities of existing ones – since negative results are less valuable. Data driven model aim to curb non-linearity and dynamism in historic datasets, used to train/test it, unlike knowledge models.
- b. **Efficiency** – modelers use figure to show how well their simulations is in agreement with observations (even with their limited data that is squeezed) with lines for observed and simulated runoff that are not

easily distinguishable. Some do not provide numerical data; but their model is in 'good agreement' with observations. Some measure of goodness does not provide the relevant information.

- c. **Insufficient Testing** – Validation is a comparison of computed versus observed values, and many studies suffer from inadequate data. If a model aims to simulate more than runoff, such ability is demonstrated in unfounded results with limited data and misleading results and conclusions.
- 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. The aim of this thesis to a greatly minimize confusion in hydrology models as well as proffer data driven models that will aid in simulation of RR.

5. Conclusion/Recommendations

Models are useful fictions and/or representation of reality as their primary value is their use as an intellectual tool, to help us better understand and reflect reality. Thus, they support experts in making estimates about the future. Very simple models do not provide enough new data, whereas very complex models are not understandable. A model's application as an intellectual tool requires less accurate numerical agreement between simulations and observations, but rather re

Thus, these recommendations are made:

1. Parameters are a major source of uncertainty. Model should have input ranges as computed via Monte-Carlo Integral methods.
2. Multi-criteria training with adequate datasets can help to reduce parameter uncertainty.
3. Prediction is of limited practical use, without clear data about reliability and accuracy.

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