

# SOFT COMPUTING TECHNIQUES FOR DENGUE DETECTION: A REVIEW

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**Abstract**—Dengue is a mosquito borne viral disease which occurs frequently affecting in large numbers the people in the tropical and sub-tropical regions. The disease requires medical treatment and may turn out to be fatal if not treated properly or a delay in treatment is reported. Therefore, there is a need for the early detection of the disease so that treatment is being available as and when required. In this review paper, we intend to study and review the various soft computing techniques coupled with bioinformatics for the early detection of Dengue disease. The primary objective of the review paper is to analyze and compare the various soft computing techniques, bio-models used in the existing work, the advantages and the issues associated with them on the Dengue datasets. This paper summarises and compares various techniques used for Dengue Disease detection. The review paper would be helpful in motivating the researchers and in proposing more robust work keeping in mind the issues in the existing work.

**Keywords** — Dengue, Soft Computing, Bioinformatics, Datasets, Detection, Bio-models

## I. INTRODUCTION

Dengue is a major and growing health threat especially in the tropical and sub-tropical regions. Recent facts state that only in India there were 67000 reported cases of Dengue leading to 48 fatalities in 2019. Therefore, the call for its early detection and treatment is vital.

Soft computing is an emergent computer science field which is tolerant to the idea of the partial truth in order to achieve approximate, robust and low-cost solutions to uncertain

Problems. The soft computing techniques are hence forth used in the medical field so as to facilitate medical disease detection and medical diagnosis decision systems.

The work carried out by Choubey et al. [9,10,11,19,28,29] (2016, 2017, 2019, 2020) in the field of bioinformatics and disease detection by using classification served as a major inspiration for us in selecting and working in this field. Bala et al. [26-27] (2017, 2018) have analyzed and compared by using many soft computing, data mining and machine learning methods thunderstorm.

The work carried out by Choubey et al. [19,20,24,25,30] (2014-2017, 2019) gave us a window to explore the various soft computing and machine learning tools used in the classification and detection of diseases and the possibility for those tools to be extrapolated to be used in the detection of Dengue disease. The work carried out could also serve in cases of complications.

Different soft computing techniques have been employed for the detection of Dengue as well. We in this review paper intend to review some of the major work and analyse the advantages and short comings of the work. The study will facilitate in developing a thorough understanding of the work carried out in the field of Dengue disease detection and enabling to possibly device a better solution and method to the Dengue disease detection.

The review article is organized as – the literature Review discussed in and sum up the existing work in a tabular form in Section II and further Discussion and Future Direction has been committed to Section III.

## II. LITERATURE REVIEW

In this section, we review the existing work carried out in the field of Dengue detection using soft computing techniques coupled with bioinformatics by different researchers.

Arifuzzaman et. al [13] (2016) in their paper proposed a system to identify the probability of dengue occurrences based on the neural network and the fuzzy inference algorithm. The paper presents a model which will identify the dengue epidemic based on the time frame of affected people. Fuzzy set was used for flexibility and Adaptive Neuro Fuzzy Inference System to determine infected epidemic rate.

Faisal et. al [1] (2008) in their paper have proposed a novel approach using Self Organizing Maps to establish consequential prognosis factors in Dengue patients. The Self Organizing Maps were used to visualize and decide the critical components that could differentiate amongst the dengue affected patients and the healthy subjects. 35 indicators (17 BIA (Bioimpedance analysis) & 18 symptoms) were investigated with the first SOM based on the BIAs and the second based on the symptoms. u-matrix and the component planes - based hunting the correlation by the Self Organizing Maps was conducted.

Fathima et. al [4] (2011) in their paper have compared the performances of the data mining techniques – (NBC) Naïve Bayes Classifier and (SVM) Support Vector Machines in the prediction of Arboviral disease-Dengue. Random-forest classifier (Gini) was combined with NBC and SVM to evaluate their performances. The operated dataset consisted of 5000 instances with 29 features. The quality was measured on three grounds – Sensitivity, Specificity and Accuracy. SVM (w RF) achieved the best accuracy while NBC (w RF) scored better on sensitivity.

Manivannan et. al [15] (2017) in their paper proposed a method to predict Dengue using K-means Algorithm to predict the number of Dengue affected people under age categories. The model works in four stages – pre-processing the data, feature selection, clustering and prediction of dengue fever. The household Dengue dataset is pre-processed using the R 3.3.2 tool. The missing values in the dataset are filled by the D-win's method. K-means clustering Algorithm proved to be increasing the proficiency of the results and hence was attributed to be the most effective technique to predict Dengue patients with serotypes and when the dataset was fully clustered.

Rao et.al [5] (2012) in their paper proposed a method based on computational intelligence to predict the Dengue diagnosis in real time as well as reducing the number of false positives and false negatives. The method used is based on three broad stages – missing value imputation, a wrapper-based feature selection method with genetic search for extracting a subset of most influential symptoms that can diagnose the Dengue for the feature selection process and an alternating decision tree (ADT) method in ensemble with boosting that generates accurate decision rules. The proposed NM methodology and the modern techniques were compared on the following metrics - specificity (SP), sensitivity (SE), receiver operator characteristics (ROC), and area under ROC (AUC) based on decision parameters of true positives, true negatives, false positives, and false negatives. Also, a stratified k-fold cross validation was employed for evaluating the test error on classification algorithms. The proposed method outperformed modern techniques on all the datasets with the proposed NM method generating 100% accurate decision trees.

Razak et.al [6] (2013) in their paper proposed a model using fuzzy logic system that notifies a patient of suspected Dengue (i.e it is also self-notifiable) and suggest the patient to go consult a doctor or not. The fuzzy logic is the inference engine in the model that is been applied to the rules of knowledge base within the fuzzy. Upon comparison with domain expert i.e the doctor diagnosis the proposed model provided accurate results.

Sasongko et. al [16] (2017) in their paper proposed a method to compare and find the best Backpropagation Algorithm with various optimizations - Multi Layer Perceptron through the various Back-propagation training algorithms – Gradient Descent Algorithm, BFGS Quasi Newton Algorithm, Conjugate Gradient Descent Powel Algorithm, Resilient Backpropagation Algorithm and Levenberg Marquardt Algorithm , for the early detection of Dengue Hemorrhage Fever (DHF). 10 initial symptoms have been used as features for the study. The algorithms were evaluated on the basis of accuracy on the metrics of – Mean Square Error Value, Accuracy Value, Sensitivity Value, and Specificity Value and on training speed on the parameters of - Epoch Value and CPU Time. LM algorithm had the best performance and was found to be robust to outliers in the dataset.

Marimuthu et.al [12] (2015) in their paper proposed a bio-computational model “Sequence Miner” for understanding the relationship between the different dengue viruses. The model also performs classification based on periodic association rules which are derived using the Periodic Association Rule Mining (PARM) and visualizes the results through an interactive tool. The classification is based on the ID3 classifier. The proposed model is found to achieve an accuracy of 96.74%. 10,198 groupings were accurately classified.

Mohsin et.al [8] (2014) in their paper have proposed a Dengue outbreak detection model based on Dendritic Cell Algorithm, which is a Danger Theory algorithm that imitates the human body fighting pathogens. A signal formalization approach based on the cumulative sum (CUSUM) and cumulative mature antigen contact value (cMCAV) is also proposed. The proposed model performs better than the other existing outbreak detection methods and is also found to be robust to inconsistent outbreak signals. Also, the model without a training phase detects detect unfamiliar Dengue outbreak patterns and also differentiates between outbreak and non-outbreak signals with a high detection rate, sensitivity and lower false alarm rate.

Kumar [18] (2018), there are 19 inputs such as headache, temperature, skin rash, muscle pain, body pain, bleeding in gums, fatigue, shivering, nausea and vomiting and based on the symptoms fuzzy rules are made. The risk factor of getting a particular disease gets as output through fuzzy rules. These values are diagnosed afterwards. In the analysing part the fuzzy processing of the system is done. In which the Fuzzification of inputs, then the inference engine processing and then the de-fuzzification is done. The trapezoidal membership functions will be used in fuzzy system. And at last, the output will give the disease and its risk factor.

In the study, prediction of the dengue hemorrhagic fever (DHF) in Thailand demonstrated by N. Rachata et. al [22] (2008) automatic prediction system for the DHF was done by utilizing entropy technique and Artificial Neural Network (ANN). Entropy was used by them to extract relevant information so that it can affect the prediction accuracy. The supervised neural network was then applied to predict the future DHF outbreak and the results obtained was Dengue Outbreak Prediction: A Least Squares Support Vector Machines Approach [3] Yuhani Yusof and Zuriani Mustaffa International Journal of Computer Theory and Engineering, Vol. 3, No. 4, August 2011 489 revealed that, by applying the entropy technique, it could yield a better result as the entropy technique produces an accuracy of 85.92% while only 78.16% when the entropy technique is not applied.

The predictive model of the epidemic detection using Multiple Rule Based Classifiers was proposed by Bakar et. al [7] (2011) The classifiers used are Decision Tree (DT), Rough Set Classifier (RSC), Naïve Bayes (NB) and Associative Classifier (AC). Several classifiers are looked over to examine the performance of various rule based classifiers individually and combination of the classifiers. The multiple classifiers can fabricate a significant amount of better accuracy, which is up-to 70% with the rules of a higher quality than using a single classifier.

In the study done by Ibrahim et al. [21] (2005) described that a non-invasive prediction system for predicting the day of effervescence of fever in dengue patients using Artificial Neural Network. They used multilayer feed forward neural networks (MFNN) to develop the system, which is based on the clinical symptoms. The proposed system achieves 90% prediction accuracy.

Martinez et al. [23] (2018) proposed a environment which can contribute to identification of dengue disease using the blood pressure (BP), viral infection (VI), sex (Male or Female) and age factors. It consisted of the Naïve Bayesian classification and WAC-55 for training the model of existing data. Even the patients and the nurses can use this model's method to supply features and get prediction of disease occurrence.

Husin et al. [33] (2018) has presented 4 architectures for prediction of the dengue outbreak consisting of Neural Network and Nonlinear Regression models. This investigation was finished utilizing the dataset of the dengue cases and precipitation level for 5 locales in Selangor. The data were taken from the year of 2004 to 2005. From the undertaken experiment, it was shown that the Neural Network Model yields better result when compared to Non-Linear Regression Model, in all the architectures, and from 4 proposed architectures, the last architecture performs better result.

Davi et al. [32] (2019) proposed a system for serious dengue prognosis using the human genome data and soft computing techniques. In the study, Information obtaining was

performed by Illumina genotyping of all dengue patients and afterward put away into database. The procedure of information pre-preparing was performed to encode and standardize the information into appropriate configuration for the Machine Learning step technique. Highlight determination was performed by them so as to locate the best SNP include set. ANN classifier was prepared to recognize serious dengue anticipation dependent on the highlights recently chose. Their investigation demonstrated that the hereditary setting, characterized by multivariate genomic marks, rather than single individual markers, ought to be the key component of clinical phenotype definition in the hereditarily impacted illnesses. This must be clear outcomes in traditional populace hereditary qualities considers and can clarify the conflicting impacts of the individual hereditary markers that have been seen in the various populaces.

Balasaravanan et al. [31] (2018) performed this study to clear out various disorders that occurred in clinic and it is correlated with respect to the time. Rundown of the dataset is labeled, the component extraction, grouping calculations here are used to investigation the sickness. Highlight vector is created utilizing dataset and order strategy and SMO is utilized to deliver the successful outcome. The model can be utilized to create helps which can anticipate the infection. They have investigated the outcome utilizing Bar diagram and preparing tests which are utilized to test the exactness of their outcome and It is end up being 95% progressively precise. It is wanted to execute the work with nonparametric iterative ascription technique in future. This strategy can be actualized for dataset with discrete characteristics and consistent information.

Najar et al. [17] (2018) showed that Network with bipolar sigmoid initiation work accomplish the best exactness with 55 concealed neurons that is MAE= 0.09417 and MAPE= 3.65969. ELM can be a promising model for chance degree of DHF forecast. In light of our methodology, the best execution is ELM arrange utilizing double actuation work with 50 shrouded neurons where the MAE is 0.08698 and MAPE is 3.00536.

Iftikhar et al. [34] (2019) proposed a model which can predict the risk level or chances of the patient causing dengue fever by using input variables like age, TLC, SGOT, platelets count and blood pressure using fuzzy and soft set theory. They achieved 100% result for the dataset they used. Tarmizi et al. [7] (2013) chose an alternate dengue information property that are utilized for arrangement displaying and the exhibitions are contrasted and the past related work. The exploratory outcomes show that the proposed classifiers improve the exhibition of different techniques. The huge choice of properties in dengue dataset adds to the great outcomes.

The Table I contain the summary of the existing work carried in the field of Dengue disease detection year wise.

Table I – Summary of the existing works for the Dengue Disease Detection

Authors and Ref. No.	Techniques Used	Purpose	Dataset Used	Advantages	Issues	Accuracy
Faisal et al. [1] (2008)	- SOM (Self Organizing Map) - BIA (Bioimpedance Analysis) - u-Matrix	Using SOM to establish consequential prognosis factors in Dengue patients	Dataset taken from University Kebangsaan Malaysia Hospital	The determination of the significant prognosis factors enables early and robust determination of the disease	The dataset should contain sufficient in order to give rise to meaning clusters	SOM Quantization Error (QE) = 2.03 Topographic Error (TE) = 0.012 BIA: QE = 1.13 TE = 0.033
Bakar et al. [2] (2011)	Decision Tree (DT), Rough Set Classifier (RSC) and Naïve Bayes (NB)	To understand single classifier can be less effective	Dataset from National University of Malaysia Medical Center.	Proposed method was considered to be more effective than single classifier	Less Complicated Method can be achieved	Variable for different models
Yusof et al. [3] (2011)	Least Squares Support Vector Machines (LS-SVM) Radial Basis Function (RBF) neural network predictor Back Propagation (BP) neural network predictor	To show that the LS-SVM prediction model outperformed the Neural Network model in terms of prediction accuracy and computational time.	Dataset on dengue cases and precipitation level gathered from five regions in Selangor.	Least-squares support-vector machines able to get great speculation capacity contrasted with NNM, in this manner improving the forecast precision and MSE.	Future research is required to consider other attributes such as humidity, temperature etc.	85.92%
Fathima et al. [4] (2011)	- SVM (Support Vector Machines) - Naïve Bayes Classifier - Random-Forest Classifier (Gini) - R	Compare the performances of data mining techniques – Naïve Bayes Classifier and Support Vector Machines in the prediction of Arboviral disease-Dengue	Clinical Dataset: About 5000 instances with 29 parameters from Chennai and Tirunelveli hospitals and diagnostic labs	The findings can be extended to other classification tasks in bioinformatics	.....	90.7 %
Rao et al. [5] (2012)	- ADT (Alternating Decision Trees) - Wrapper based features subset selection algorithm - k-fold cross validation - ROC (Receiver operator	A method based on computational intelligence to predict the Dengue diagnosis in real time as well as reducing the number of false positives and false negatives	Probable cases from labs of ELISA.  Machine Learning data repositories of Keel and University of California	Imputation of MV's in proposed algorithm on Machine Learning data repositories of Keel and University of California better than other existing imputation algorithms. Time complexity of the proposed	The findings may not be geographically independent	99%

	characteristics)					
Bin Razak et al. [6] (2013)	<ul style="list-style-type: none"> <li>- Fuzzy Logic</li> <li>- UiTM</li> <li>- Centre of Area (COA),</li> <li>- Centre of Sums (COS)</li> <li>- Mean of Maxima (MOM)</li> </ul>	A model using fuzzy logic system that notifies a patient of suspected Dengue and suggest the patient to go consult a doctor or not	Knowledge Base: Doctor will be interviewed	System can be employed at UiTM medical unit	System Limitations	.....
Tarmizi et al. [7] (2013)	<ul style="list-style-type: none"> <li>Decision Tree (DT)</li> <li>Artificial Neural Network (ANN)</li> <li>Rough Set Theory (RS)</li> </ul>	Choice of various dengue information characteristics are utilized for arrangement displaying and the exhibitions are contrasted and the past related work	Dengue dataset collected from Public Health Department, Selangor State	Decision Tree and Neural network are commonly used but rough set theory provides a better knowledge	Further analysis required	.....
Mohsin et al. [8] (2014)	<ul style="list-style-type: none"> <li>- Danger Theory</li> <li>- Dendritic Cell Algorithm</li> <li>- Cumulative Sum (CUSUM)</li> <li>- Cumulative Mature Antigen Value (cMAV)</li> </ul>	A Dengue outbreak detection model based on Dendritic Cell Algorithm	SARS Dengue Outbreak Dataset	Even without any training phase the Dendritic Cell Algorithm based outbreak detection model is able to detect unfamiliar Dengue outbreak patterns	The model is still not an real time agent based model	94%
Marimuthu et al. [12] (2015)	<ul style="list-style-type: none"> <li>- Periodic Association Rule Mining (PARM)</li> <li>- RECFIN Algorithm</li> <li>- Amino Acid Component based Classification (AAAC)</li> <li>- ID3 Classifier</li> <li>- Point Accepted Mutation (PAM)</li> <li>- BLOCK SUBSTITUTION MATRIX (BLOSUM)</li> </ul>	Build a bio-computational model “Sequence Miner” for understanding the relations between the different dengue viruses	Dataset: National Center for Biotechnology Information (NCBI)	The relationship between dengue serotypes predicted can be helpful in developing an effective vaccine for the dengue disease.	4-serotype model is under development	96.74%

Arifuzzam et al. [13] (2016)	<ul style="list-style-type: none"> <li>- Fuzzy Logic</li> <li>- ANFIS (adaptive Neuro Fuzzy Inference System)</li> <li>- PPI (Percentage of people infected)</li> </ul>	A system to identify the probability of dengue occurrences based on neural network and fuzzy inference algorithm	Institute of Epidemiology, Disease Control and Research and Centre of Disease Control annual report Bangladesh	Use of fuzzy set Use of time frame of infected people to model the system Pin point epidemic rate	The findings are geographically independent No biological factors considered	-
Naiyar et al. [14] (2017)	Machine Learning Classifiers	Used all the machine learning techniques to detect dengue and the technique with best accuracy was considered	Dengue Dataset of different regions and counties such as Brazil, Malaysia, Singapore on the basis of patient attributes	All the techniques were compared and Microarray suite software gave the best results	Different datasets used for the comparisons with different attributes	.....
Manivanna et al. [15] (2017)	<ul style="list-style-type: none"> <li>- Dengue serotypes DENV1 to DENV4</li> <li>- R 3.3.2 Tool</li> <li>- K-means algorithm</li> <li>- D win's Method</li> </ul>	Use K-means Algorithm to predict the number of Dengue affected people under age categories	Dataset: Dengue clustering data collected from Ho Chin Mi, Vietnam	Proper handling of missing values using D wins method	4-serotype model is under development	.....
Sasongko et al. [16] (2017)	<ul style="list-style-type: none"> <li>Backpropagation Algorithm</li> <li>Multi Layer Perceptron (MLP)</li> <li>Gradient Descent (GD)</li> <li>BFGS Quasi-Newton (BQN)</li> <li>Conjugate Gradient Descent - Powell (CGD)</li> <li>Resilient Backpropagation (RB)</li> <li>Levenberg Marquardt (LM)</li> </ul>	To compare and find the best Backpropagation Algorithm with various optimizations for the early detection of Dengue Haemorrhage Fever (DHF)	Dataset: The data was collected from the following dates - March'16 to April'16 by Dr. Karyadi Semarang	Can effectively handle outliers on the dataset	Dataset is minimal	99.28%
Najar et al. [17] (2018)	Extreme Machine Learning	Model of Extreme learning machine is a lot less difficult and more viable than the regular feed forward neural system	Central Bureau of Statistics Jakarta, Jakarta Health Agency, Indonesia.	Better than Neural Networks, Support vector machines and back propagation	Limited dataset Geographic limitations	MAE is 0.08698 and MAPE is 3.00536

Sandeep Kumar [18] (2018)	Fuzzy Rules Inference Engine Artificial Neural Network	System will diagnose the 5 diseases Malaria, Dengue, Tuberculosis (TB), Chikungunya, Elephantiasis based on fuzzy rules and ANN	19 Factors Dataset headache, temperature, skin rash, muscle pain, body pain, bleeding in gums, fatigue, shivering, nausea and vomiting	Output disease and risk factor can be achieved	Not accurate for very common diseases and hence more research to be done	-
Balasaravan et al. [31] (2018)	Artificial neural Network (ANN) Classifiers Vector Error Correction Model (VECM)	Develop an architecture using ANN to detect dengue	Dengue Dataset from medical agency having 10 attributes	ROC of Naive Bayes = 0.874 Accuracy of ANN = 92% Accuracy of CART = 88%	Further Research can improve the accuracy rates	95%
Davi et al. [32] (2019)	Single Nucleotide Polymorphisms (SNPs) Support Vector Machine (SVM) Artificial Neural Network (ANN)	To construct a soft computing approach which can predict dengue fever severity based on the human genome data	Human-Genome-Data	Proposed method can be applied to many diseases at any stage, even before infection has started, and can utilize the broad choice of human sample tissue.	Further research needed	.....
Iftikhar et al. [34] (2019)	Fuzzification fuzzy sets soft sets Reduction of soft sets Gaining soft rules Analysis of soft rules	To demonstrate the exact percentage of the risk level of dengue fever automatic circumventing for possible imprecisions	Data of 30 dengue patients was collected who were treated at Holy Family Hospital Islamabad	More precise and useful as compared to traditional methods and they achieved 100% results	Further research required as its data set is only limited to the patients of one hospital	.....

### III. DISCUSSION AND FUTURE DIRECTION

In this section, the authors have emphasis on the future direction over the existing work, as to what the existing work can be extended too.

Dengue is a viral mosquito borne disease. The magnitude of illness caused by the disease varies from sub-clinical disease i.e no signs or symptoms to severe dengue which is marked by severe complications like severe bleeding, drastic fall in platelet count, organ impairment and or plasma leakage. The incidences of Dengue have increased vastly recently and much more than the reported cases due to rise in asymptomatic cases. According to reports from the WHO, the total number of cases of Dengue reported to WHO have increased 15 folds in the last two decades with reported deaths also increasing 4.5 times. And at major risks are people in sub-tropical and tropical countries which often are characterized by breeding grounds for contagious diseases and poor healthcare facilities. Therefore, looking at the gravity of situation it is extremely important that early detection of the Dengue is made possible given the amount of people at risk. The official figures at risk according to

WHO are 390 million people worldwide with about 70% of them in Asia.

Therefore, a need for a robust, efficient and accurate detection technique is imminent. In this direction the authors have discussed various techniques used for Dengue Disease detection in the existing works. The techniques are then analyzed and compared on the basis of their advantages, issues and detection accuracy with an aim that the study would yield a robust, accurate and efficient detection technique. The authors have also discussed future works over existing works of some exciting papers in this section. After reviewing the papers thoroughly, the authors found some limitations in these existing works. One of the major limitations was the global usability of results due to the use of localized datasets in the studies. For eg., There is no guarantee that the result obtained in [15] would hold robust for detection in India. Also, other limitations included the use of 4-serotype model, which is still under research, some models relying heavily on systems and some yielding unsatisfactory accuracies.

The future work over some of the existing works is discussed in Table II.

For future work, the authors would suggest a more globalized approach and preparing and testing models under different datasets. The authors would also suggest tweaking

the mathematical parameters like the ROC, accuracy, efficiency, MAPE, MAE, topological error etc. towards betterment. The approach should be such that it provides early, robust, efficient and accurate, detection and assist in decreasing healthcare costs.

TABLE II – FUTURE WORK

Authors and Ref. No.	Existing Work	Future Work
Rao et. al [10] (2012)	Predicts the Dengue diagnosis in real time as well as reducing the number of false positives and false negatives	Intensive studies based on the findings will lead to better clinical management and virological monitoring of Dengue disease
Mohsin et. al [5] (2014)	Dengue outbreak detection model based on Dendritic Cell Algorithm	Will be extended to a real time agent- based model
Arifuzzaman et. al. [6] (2016)	System identifies the probability of dengue occurrences based on neural network and fuzzy inference algorithm	Narrow the field of data to sub-districts to have a clearer insight of the epidemic situation and also consider different biological factors to improve the accuracy of the model
Balasarayanan et. al. [19] (2018)	Architectural model using ANN to detect dengue	Data tuning methods can be added to make the data more precise.
Sandeep Kumar [20] (2018)	System that diagnoses 5 diseases Malaria, Dengue, Tuberculosis (TB), Chikungunya, Elephantiasis based on fuzzy rules and ANN considering several attributes.	Fuzzy rules and ANN are more resource demanding so alternative methods should be found out to improve the performance in normal systems.

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