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Genetically Optimized Fuzzy C-Means Data Clustering of IoMT-based Biomarkers for Fast Affective State Recognition in Intelligent Edge Analytics

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Abstract—IoMT sensors such as hearables, moodables, ingestible sensors and trackers have the potential to provide a proactive approach to healthcare. But grouping, traversing and selectively tapping the IoMT data traffic and its immediacy makes data management & decision analysis a pressing issue. Evidently, the selection process for real-world, time-constrained health problems involves looking at multivariate time-series data generated simultaneously from various wearables resulting in data overload and accuracy issues. Computational intelligence of edge analytics can extend predictive capability by quickly turning digital biomarker data into actions for remote monitoring and trigger alarm during emergency incidents without relying on backend servers. But the pervasive generation of data streams from IoMT levies significant issues in data visualization and exploratory data analysis. This paper presents a genetically optimized fuzzy c-means data clustering technique for affective state recognition on the edge. Clustering segregates the biomarker data in chunks and generates a summarized data for each subject which is then genetically optimized to avoid stagnation in local optima. A multi-level convolution neural network is finally used to classify the affective states into the baseline, stress and amusement categories. The model is evaluated on the publicly available WESAD dataset and compares favorably to state-of-the-art with less time complexity. It demonstrates that the use of data clustering technique for numerosity reduction of real-time data stream in intelligent edge analytics which facilitates fast analysis of affective state of the user.

Index Terms—IoMT, Edge Analytics, Data Clustering, Genetic algorithms, Affect

1. Introduction

With the ubiquitous internet connectivity and bandwidth in abundance, IoT (Internet of Things) devices are becoming a part of the mainstream electronics culture. Likewise, the healthcare industry has radically changed as the IoT have recalibrated endless applications within the structure. IoT in healthcare enables interoperability, machine-to-machine communication, information exchange, and data movement that makes healthcare service delivery effective. From the comfort of their homes, patients wear remote medical sensors, referred to as Internet of Medical Things (IoMT) devices & sensors, transmitting their vital signs to health care providers [1]. This data received in near real-time allows doctors and caregivers to monitor an array of vitals, dynamically manage treatment plans, and conduct a consult or intervention over webcam. Further, the data supports predictive analytics, allowing doctors to increase their accuracy of diagnoses by detecting emerging health patterns much faster.

Though the benefits offered are unparalleled and promise useful decision support information, but all this is challenged by a lot of noise created owing to the large volume and variety of information sent at almost light speed. One of the most significant threats that the IoMT poses is of data security & privacy. As these devices capture and transmit data in real-time with no standard data protocols and data ownership regulations, it makes it highly susceptible to hacks and frauds. Moreover, non-uniformity of the connected device's protocols make integration of multiple devices (data aggregation) difficult thereby reducing the scope of scalability of IoT in healthcare. At the same time, data overload and accuracy further create complications. The IoMT devices record a ton of data and utilize it to gain vital insights [2]. However, the amount of data is so tremendous that deriving insights from it is becoming extremely difficult for doctors which, ultimately affects the quality of decision-making. Undeniably, the sheer amount of IoMT data traffic with the rise in connected devices and its immediacy makes data management & decision analysis a pressing issue. That is, despite this proliferation of data, only a small fraction is being used for decision making because the data cannot be stored or transmitted efficiently. As a result, the full value of analyzing the data for timely decision making has not been realized. When healthcare practitioners must make life-or-death decisions, the quality of information at their disposal is critical. Having more specific data — and being able to access it in real time — leads to more informed decisions. IoMT makes this possible through an infrastructure of connected medical devices, software applications, and health systems powered by 5G wireless technology and edge computing, which enables connected devices to process data closer to where it is created. Definitely the new technologies like 5G and edge computing are making healthcare more connected, secure, and efficient [3]. Intelligent edge can be used for intelligently investigating, collecting, storing, monitoring and processing health-related data to provide acceptable, sustainable, and

inexpensive ways of data analytics and decision making in real time with minimum delay, reduced bandwidth consumption and improved response time. It delivers real-time insights via UIs / streaming APIs analyzes, learns & predicts from time-series data, on-the-fly. Edge computing was instituted owing to the phenomenal rise of connected IoT devices with to-fro of information on cloud. At its elementary level, edge analytics is data analytics in real-time which enables computation and data storage at the edge of a network either at or close to a sensor, a network switch or some other connected device. This refutes latency issues associated with real-time data which can affect an application's performance [4]. The typical edge-enabled IoMT-based smart healthcare system consists for four layers, namely the smart user layer, edge computing layer, cloud computing layer and the smart healthcare layer as shown in fig. 1.

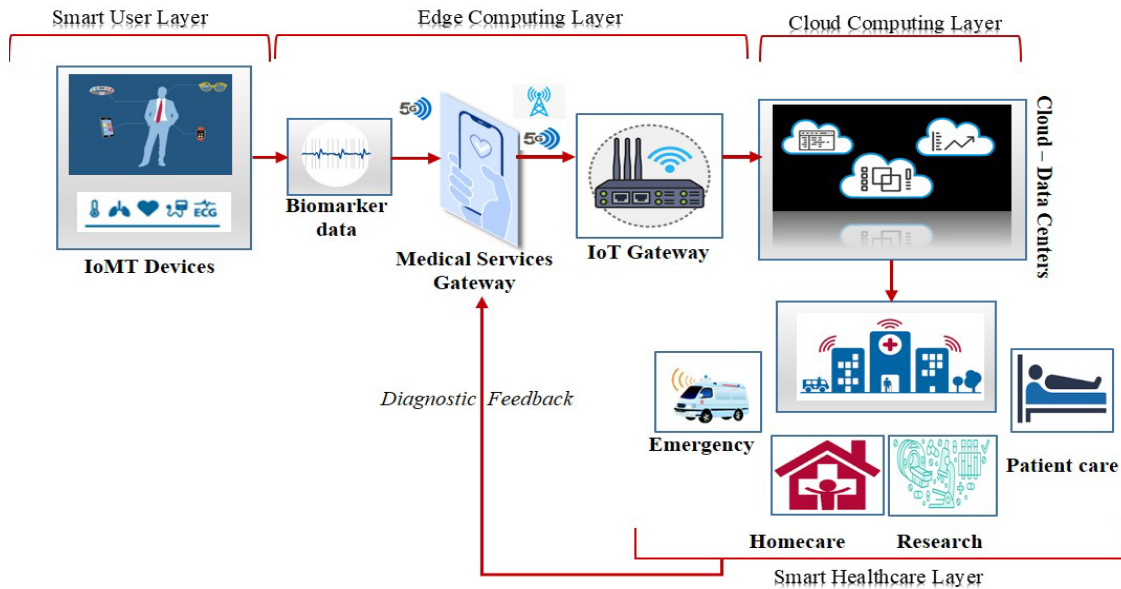


Fig. 1. Edge enabled IoMT-based Smart Healthcare Framework

Both physical and mental health are vital for a stable life with happiness and tranquility. But mental health monitoring is more perplexed and challenging than the physical health monitoring because human psychology varies dynamically, and it is difficult to fetch the patterns of mental behavior [5]. Moreover, as specific events are antecedents of affective reactions and behaviours, it is during the emotion process an individual automatically registers an eliciting stimulus and experiences a feeling state and physiological changes. Biomarkers, which are the measures of observable and quantifiable characteristics of our body, can be used to track the psychological well-being of an individual and monitor mental health. The success of mental health monitoring system depends on this biomarker data acquisition from the patient with mental disorder including historical and hereditary data as well. A typical cloud-based smart mental health monitoring system collects symptomatology through biomarker data and transfers it to the public cloud healthcare service providers to compute the mental state sequence using soft computing techniques. Consequently, the results are provided to the healthcare agent who is responsible for sending the current mental status of the patient to the corresponding hospital or psychologist.

Affective state recognition from wearable biosensors can complement context-aware recommendation, mood stabilization, and stress and depression management, especially for mental well-being. Affective states are psychophysiological constructs—meaning, largely, concepts that connect mental and physical processes. Specifically, an affect is a psychological term for an observable expression of emotion [6]. It can be expressed as a tone of voice, a smile, a frown, a laugh, a smirk, a tear, pressed lips, a crinkled forehead, a scrunched nose, furrowed eyebrows, an eye gaze, and changes in heart rate or blood pressure. These modes of expressions or observed manifestations are referred to as biomarkers. An affective biomarker quantifies the affective state of a user using physiological signals, behavioural signals, speech signals, eye gaze and fixation data, and sentiment analysis of social data. These biomarkers can now be measured using sensors in wearable devices like fitness watches, or a chest wearable or with the help of implants such as pacemakers (Fig.2). Real-time data collection using IoMT sensors can lead to terabytes of data in a single day depending upon number of biomarkers being tracked [7].

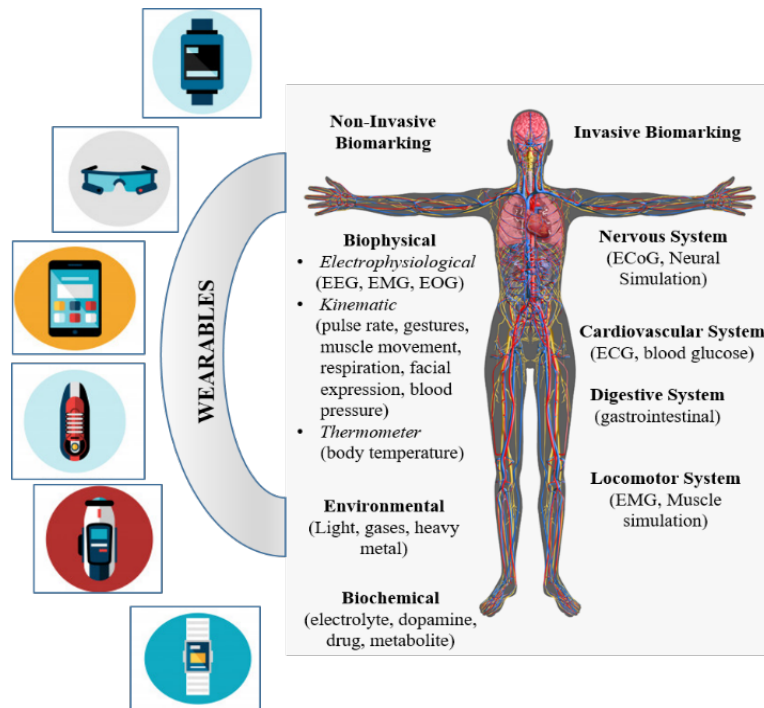


Fig.2. Biomarking using IoMT sensors

Various biomarkers measure different physiological changes in the body, and each indicates some sort of psychological or emotional affect a person is experiencing. That is, to understand the current affective state of a user each biomarker plays an important role. Traditional data management systems handle the storage, retrieval, and update of elementary data items, records and files. Working with IoMT data compels a shorter time span in comparison to the data collected directly from patients. For example, a self-assessment questionnaire data with patient's answers and comments may tend to arrive in a matter of minutes, hours, or days, rather than seconds. Given this, the medical practitioner may have a little more flexibility in deciding which data to select or discard [8,9]. But quite clearly, in the context of IoMT, data management systems must cater to the data streams with phenomenal volume, variety and velocity of data which may need huge storage and make analytical, process and retrieval operations cumbersome and time-consuming. Also, digital biomarkers measuring electrical signals in the body like ECG, EDA, and EMG are analog time-series data which record the physiological state of a body [10,11]. To analyze continuous time-series data it is fragmented into finite intervals. For example, to identify the affective mental state of an individual, the time-series data in the benchmark WESAD (Wearable Stress and Affect Detection) dataset has been broken at interval of 1 second with the sliding window of 0.25 seconds, as effect of a stimuli can occur over a short interval of 2 seconds [12]. The conversion of analog data to discrete values makes a total of 63000000 instances just for a period of 2 hours in this dataset. This huge amount of data is not easy to analyze for any medical practitioner even for few patients on daily basis. Moreover, as physiological changes might occur because of an external stimulus, an individual doesn't encounter changes at every second of the day, which is for the majority of time an individual is in neutral state, leading to wastage of resources to analyze it.

As a result, the medical practitioners are overwhelmed with the unbounded, multidimensional, sporadic, and transient sequence of observations made available along time and might miss on some important information. To resolve this problem, a plausible solution is to have a condensed description of the dataset such that it's still an informative version of the entire dataset [13]. The benefit of using data reduction techniques for intelligent edge analytics is that it facilitates data stream learning to improve risk-based decision making and at the same time can realize federated transfer learning, that is, if the collection device is not capable of training advanced AI models, they may send a summary of their data to a more powerful device (such as a home gateway) which will act as a client in federated learning [14,15]. Motivated by this, this research puts forward a data clustering technique to obtain the data reduction for which the degree of information lost is minimum for intelligent edge analytics. The intent is to consider the biomarkers values which have the potential to minimize variability and maximize benefit [16,17]. To resolve the data overload issue in real-time IoMT data processing, we reduce the size of the data by first performing clustering on

this time-series data and the centroid of the cluster is then used for analysis rather than every instance of the cluster. The proposed model clusters the instances together and then optimize it with the help of genetic optimization to which is then used to generate a summarized data for each patient. Although, fuzzy c-means clustering is easy to implement and has low run time, but its performance is strongly affected by the selection of the initial centroid clusters and as result can be trapped in local optima. Therefore, in order to obtain better clusters, this study combines genetic algorithms and fuzzy c-means clustering. After obtaining clusters, data is summarized by identifying the centroid points of each clusters, having single entity for each cluster generated. Finally, a CNN (convolution neural network) is used that facilitates fast analysis of affective state of the user. The model is evaluated on the WESAD benchmark dataset for wearable stress and affect detection.

The organization of paper is as follows: the next section outlines the related work followed by a brief overview of techniques used in section 3. Section 4 discusses the proposed model and section 5 presents the results and discussion. Conclusion and future work is discussed in the last section.

2. Literature Review

Mental health is as vital as physical health. Most of the organizations try to arrange motivational sessions or activity sessions to ensure their employees get a ‘mental vacation’ and feel relaxed. This is important as a stressed or depressed person will always find it challenging to focus and so will always take extra time to pursue the same work in comparison to a mentally healthy and relaxed person. As the early stages of mental illness have invisible symptoms, it is not always possible to notice the change until the symptoms are persistent, increase in frequency and severity and interfere with life activities and roles [18]. Thus, early identification and intervention are necessary to recover and reclaim lives. Various artificial intelligence based techniques have been reported to supplement clinical practice in various mental healthcare studies. To analyze the behaviour of a person under stress, researchers have proposed machine learning-based techniques; however, the availability of a WESAD dataset has always been an issue. In 2018, Schmidt [12] created and applied five different machine learning algorithms namely, Random Tree Classifier (RT), Decision Tree (DT), AdaBoost, K Nearest Neighbour (KNN), and Linear Discriminant Analysis (LDA) and given the state of the art results by providing the accuracy of 80%. In 2019, Lin et al. proposed a deep fusion network on the WESAD to optimize the accuracy of the prediction of stress. They used the late fusion method in deep neural networks and divided the model into four sub-networks, one tuned on the chest sensor dataset, and rest three tuned on the wrist sensor dataset, first one on EDA and Temperature, second on BVP and last on ACC. They attained the highest accuracy of 85% and F1 score as 0.86, which was a significant improvement on the result provided by Schmidt et al. [19]. The latest work on stress detection using WESAD is proposed by [20]. They used three classifiers, namely logistic regression, decision tree, and random forest, and rather than evaluating the result into three categories, they added one more output category as meditation. Also, rather than applying each classifier on the complete dataset, they applied it on individual subjects, resulting in an accuracy of 88% to 99% for the individual subject. A deep hierarchal CNN model has been used by Kumar et al on WESAD dataset for affective state recognition [21].

Learning algorithms offer a number of advantages over traditional analytics and clinical decision-making techniques by giving unprecedented insights into diagnostics, care processes, treatment variability, and patient outcomes [22]. Few studies have reported on the edge-IoT based architecture for healthcare analytics [23]. Fadlullah et al. [24] identified that network and computational congestion problems may impact the real-time analytics of the healthcare data and proposed a deep learning based IoT edge analytics approach to support intelligent healthcare for residential users. Chen et al. [25] proffered a cognitive computation based smart healthcare system on the edge to resolve the multimodality, latency and resource issues. In 2020, Alfarraj and Tolba [26] introduced a responsive model for effectively handling IoMT data regardless of the time factor.

3. The Proposed Model

Conventionally, ‘The Things’ include sensors that acquire physical parameter and converts it into a signal suitable for processing (e.g. optical, electrical, mechanical). The acquired data is then transmitted over the network to the cloud for storage & analytics. But for applications that require autonomy (self-driven cars), or that can’t tolerate latency (health care, financial transactions) and applications that require significant bandwidth (smart surveillance system) ingesting data to a distant cloud isn’t a realistic option. As a solution, edge computing enables optimization of cloud by moving the compute close to the source of data, to the *edge*. Executing on device partial computation or on a node closer to the source of data can reduce data that is required to be sent to the cloud and consequently reduce latencies and improve the response time. In edge analytics, data is collected and analyzed directly on the edge and acted upon

in real-time. That is, sensors or devices at the edge collect data and analytics capabilities within the devices enable performing analysis at the edge. If the device needs to take action, it does so by relying on the results of the analysis. Finally, only relevant data is transmitted from the edge to the cloud so businesses can see the big picture by aggregating reduced data (in case of bandwidth constraints) from thousands of devices as shown in fig.3.

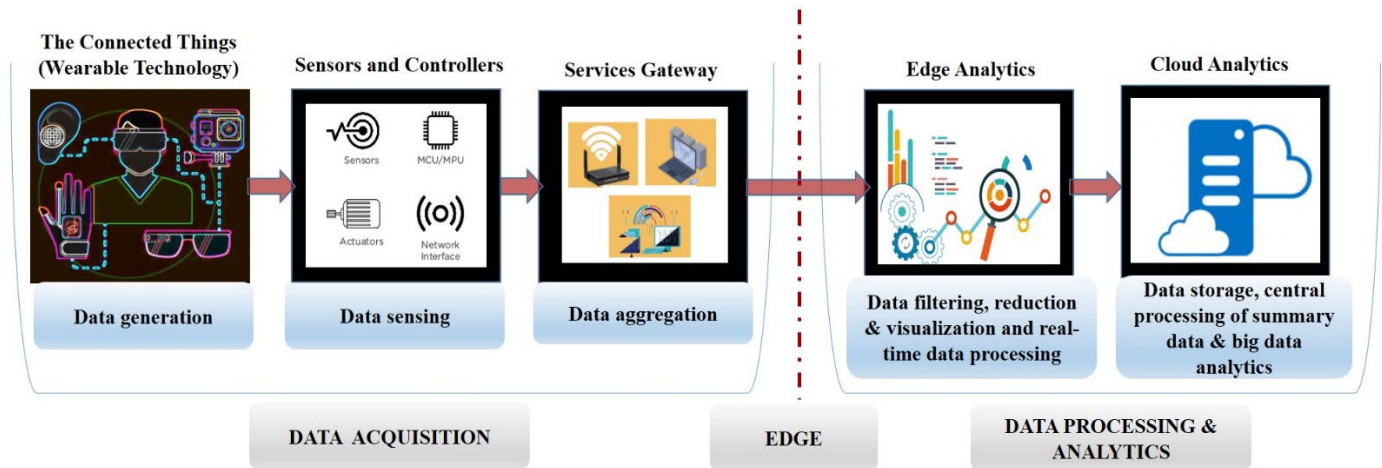


Fig.3. Data Analytics on the Edge

The advantage of edge analytics is two-fold: firstly, to obtain real-time results from IoT devices for visualizations and insights and secondly, to dramatically reduce the amount of data which travels to the cloud. In a life critical domain such as healthcare it is imperative to analyze the data in real-time and operate at the source of data for faster response time. Computational intelligence of edge analytics extends predictive capability by quickly turning digital biomarker data into actions for remote monitoring and trigger alarm during emergency incidents without relying on backend servers. But the pervasive generation of data streams such as the time-series biomarker data from IoMT levies significant issues in data visualization and exploratory data analysis [27].

The data reduction techniques can certainly reduce the size and complexity of real-time data streams by converting it into more coherent and manageable proportions, highlighting the relevant features of the data more clearly and eventually facilitating more accurate and efficient edge analytics. Based on this, the proposed genetically optimized fuzzy c-means data clustering model proffers a fast analytical method for detecting the affective state of the user using data reduction at the edge [28]. The underlying impetus is to create quality clusters with reduced time complexity to get the most significant information. The model has been implemented on the publicly available WESAD dataset, containing data of 15 subjects (patients) measured through IoT-based chest wearable and wrist wearable device for a period of 2 hours with total of 12 biomarkers. These include:

- **Electrocardiogram (ECG):** ECG provides the frequency of cardiac cycles. It is sensed using photo detectors, so is not able to be detected by wrist-wearable devices. (Device: RespiBAN)
- **Electromyogram (EMG):** EMG is used to detect musculoskeletal movements. These signals can detect face and hand gestures. (Device: RespiBAN)
- **Body Temperature (TEMP):** Skin temperature of the subject is measured using a thermistor sensor. Body temperature is negatively correlated with stress. (Device: RespiBAN, Empatica E4)
- **Respiration (RESP):** RESP gives the person inhalation and exhalation rate. The slowed respiration rate shows the level of stress in a user. (Device: RespiBAN)
- **Blood Volume Pressure (BVP):** BVP is the amount of blood in blood tissue during a certain time period. BVP also provides pulse rate and blood flow volume, as it is obtained by photoplethysmography. (Device: RespiBAN, Empatica E4)
- **Electrodermal Activity (EDA):** EDA gives the flow of electricity through the skin. The changes arise in the skin when the brain sends the signal due to different emotion activation. Skin conduction increases when a person is under stress. (Device: RespiBAN, Empatica E4)

- **Three Axis Acceleration (ACC):** ACC gives an indication of different activities like lying, sitting, standing, walking, running and cycling by recording the human movement in all the three dimensions. Fast hand movement over a short time depicts signs of mental stress. (*Device: RespiBAN, Empatica E4*)

Fig.4 depicts the architecture of the proposed model.

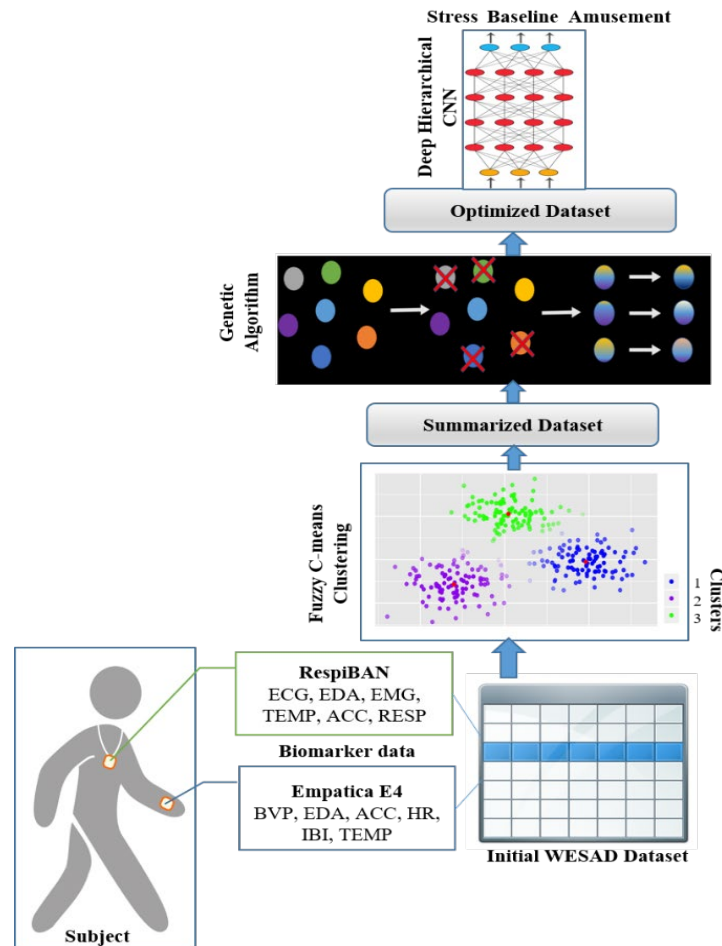


Fig.4. Architecture of proposed model

The model consists of the following four architectural components:

- Fuzzy c-means clustering.
- Genetic algorithm for optimized dataset.
- Data reduction by summarizing the clusters.
- A deep hierarchical model trained using optimized dataset to detect the affective state.

The first component involves defining and initializing clusters for that we used the observation made by Siirtola in 2019 [29], that the affect perceived depends upon the time window taken and the results concluded that affect can be identified with better accuracy with 120 second time window as compared to 15 seconds, 30 seconds, 60 seconds and 90 seconds time window. Analyzing every single second data may not be effective, but at the same time to be quick to detect any physiological change in the body, the data was reduced by margin of 3 seconds. The base hypothesis taken for identifying the best suitable number of clusters for data reduction is chosen similarly by taking different time window and observing the accuracy in each scenario. As WESAD contains the data for a window of 2-hours, i.e., of 7200 seconds, to initialize the clusters, 1440 clusters are used as the model performed optimally with the hypothesis that a physiological change due to any external stimuli will last for at least 5 seconds, as shown in result section. As a person may exist in neutral state before and after an event it is imperative to analyze both these for determining affective state of an individual. Therefore, to distinguish between pre- and post-state of a subject, it is ensured that no two-time varied data belongs to the same cluster with a time criterion added to the initial data table. Time is provided with the numerical value ranging from 1 to 7200, based on the second it belongs to. This extra criterion while clustering ensures

that no pre- and post-data is combined based only on the biomarker measures, as different affective states show different physiological changes in an individual, for some having heartbeat rate 85 could be a warning sign showing a hike, whereas for other it may be average heartbeat rate because of their daily activities. Affect visualization can be done by observing the change in pre- and post-condition, therefore time is an essential feature to understand the affective state.

Fuzzy C-Means performs clustering by iteratively searching for a set of fuzzy clusters and the associated cluster centres that represent the structure of the data as best as possible. Given a number of clusters c , it partitions the data $X = \{x_1, x_2, \dots, x_n\}$ into c fuzzy clusters by minimising the within group sum of squared error objective function. The algorithm stops when either the error is below a certain tolerance value or its improvement over the previous iteration is below a certain threshold. Fuzzy c mean uses fuzzy membership, to cluster the data, it allows an instance to belong to different clusters with different membership value [30]. As the minor change in a single feature may be because of any reason, like pinching by a friend, it last for few seconds, but it may not change the affective state of a user, but certainly brings a physiological change. It is imperative to provide number of clusters for executing the Fuzzy c mean, to identify this optimized number of clusters, we have performed empirical analysis on varying time window hypothesis to identify the most accurate time window clustering by generating clusters based on 3 seconds, 4 seconds, 5 seconds, 6 seconds and 7 seconds. Comparison of different number of clusters has been discussed in the result section. The most accurate results have been shown when the initial clusters were defined using 5 second similarity hypothesis, resulting in 1440 clusters for two hours of period. The 1440 clusters initialized will initially having second tuple of the interval, i.e., first cluster will initially contain 2nd tuple, and 2nd cluster will contain 7th second instance, and so on. Once the number of clusters has been defined, and clusters has been initialized, rest of the tuples are now assigned to each cluster based on the objective function as defined in (1).

$$\sum_{j=1}^k \sum_{x \in C_j} u_{ij}^m (x_i - u_j)^2 \quad (1)$$

$$u_j = \frac{\sum_{x \in C_j} u_{ij}^m x}{\sum_{x \in C_j} u_{ij}^m} \quad (2)$$

where,

u_{ij} is the membership value, i.e. degree to which a particular observation x_i belongs to a cluster c_j .

u_j represents the center of cluster j , which is the mean of all points, weighted by their degree of belongingness to the cluster, as shown in (2).

$(x_i - u_j)$ is the Euclidean distance between i^{th} data and j^{th} cluster's center.

m is the fuzzifier, i.e., it defined the level of cluster fuzziness, it can have any value greater than 1, we have taken $m=2$. The membership value and fuzziness can be computed as shown in (3):

$$u_{ij}^m = \frac{1}{\sum_{i=1}^k \left(\frac{|x_i - u_j|}{|x_i - c_k|} \right)^{\frac{2}{m-1}}} \quad (3)$$

i.e., membership u_{ij} is inversely linked to the distance of an entity from the center of the cluster.

The output derived from the first component is a summarized data table, reducing the size by a large margin. For each subject, data can be represented as 1440*17. Initially an individual subject has total of 4498417 instances, a raw discrete decision matrix of subject have 17 attributes, one for time, 8 for wrist-based sensor (5 for BVP, EDA, HR, IBI, TEMP and 3 for ACC, as ACC records the movement of the individual in all 3 directions.) collected through Empatica E4, and 8 from a chest based sensor (5 for ECG, EDA, EMG, TEMP, RESP and 3 for ACC) collected by RespiBAN, where biomarker values of Empatica E4 is variation from a predefined base value, RespiBAN.

The second component of the proposed model optimizes the clusters, by generating the optimal mapped data to the clusters by minimizing the objective function. As the main issue with a partition clustering fuzzy C-means is that it requires Apriori specification of the number of clusters and moreover, this clustering is done on the basis of homogenous data points whereas as discussed with the real-time IoMT time series data analysis, considering the pre- and post-data temporal correlations is important, that is, as the physiological change can be observed for more than 5 seconds, the number of clusters can be defined by dividing the time frame accordingly. Therefore, optimizing the clusters are important. A genetic model typically has an initial random population of individuals or solutions, which in this case is provided by the solutions generated by fuzzy c mean, followed by the fitness evaluation of these individuals,

using a fitness function. Once, the fitness function value has been generated for each individual the following procedure is repeated until one of the terminating conditions has been met. First, select the best individual, based on fitness value. Then, generate new population, by using crossover and mutation. Thirdly, evaluate the fitness of new population. And at last, replace the poor performer with new best performers.

This process is repeated until either the number of iterations set has been completed or no new solution can be generated, or the fitness of new population comes to be lower than already existing individuals. The steps involved in the second phase are:

- *Initialization:* Generally, the initial population is generated randomly, allowing the entire range of possible solutions (the search space). But for our normalized dataset, we start by initializing all the initial clusters formed by Fuzzy C-Means as the initial population generation.
- *Selection:* In our problem the Fitness function calculates the position of centroids obtained through fuzzy c-means. This is done repeatedly till the centroids keep moving. This produces an optimised separation of alternatives into clusters. Once better individuals are determined, they replace the worst individuals in the group and the process is repeated. The breeding of the new generation is done through two Genetic operators: crossover or mutation.
- *Crossover:* Crossover is a genetic operator used to change or "evolve" an individual from one generation to the next. It is analogous to reproduction and biological crossover, upon which genetic algorithms are based. For our dataset, any 2 individuals are chosen for a single-point crossover to produce new children.
- *Mutation:* Mutation alters one or more gene values in a chromosome from its initial state. For our normalized dataset, a Uniform mutation is applied which adds a unit uniform random value to the user defined upper and lower bounds for that gene. The resultant mutants are then operated on by the fitness function.
- *Termination:* Termination can be done on the basis of the following conditions:
 - An optimised solution is obtained.
 - The highest ranking solution's fitness is about to or has plateaued such that successive iterations no longer produce better results.

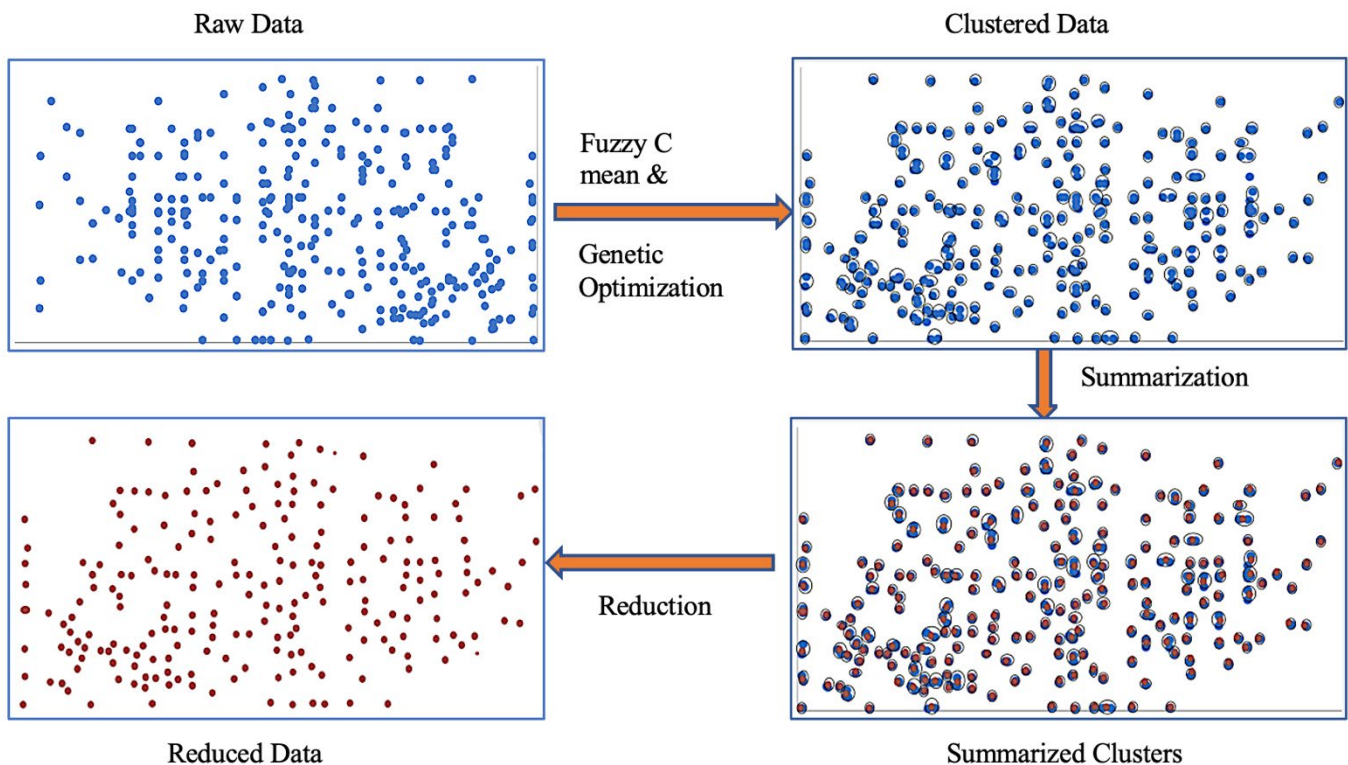


Fig.5. Data Reduction Procedure

Thus, the first and second component together generates a clustered data that further helps to reduce the size drastically, to speed up the further analysis [31]. Various techniques such as dimensionality reduction, numerosity reduction, and aggregation can be used to reducing the high-dimensional dataset into a smaller, meaningful and interpretable dataset while retaining the important characteristics of the original data. The data reduction techniques can be applied to obtain a reduced representation of the data set that is much smaller in volume, yet closely maintains the integrity of the original data. That is, mining on the reduced data set should be more efficient yet produce the same analytical results. We have used Numerosity reduction technique, which reduce the data volume by choosing alternative, smaller forms of data representation by using parametric or non-parametric methods. The parametric methods assume the data fits some model, estimate model parameters, store only the parameters, and discard the data (except possible outliers), for example, log-linear or regression whereas the non-parametric methods do not assume models. In the proposed work, we have used Fuzzy C mean and genetic algorithm to identify the optimized clusters. Where Fuzzy C mean combines the overlapped dataset and allows each instance to belong to more than one cluster. And then Genetic algorithm optimizes the clusters by identifying the most relevant instances together. Once the clusters have been identified, each cluster is represented by just one instance having median value of each attribute. This reduces the size of data directly to the total number of instances chosen at the initial level. Although the size has been reduced drastically, but accuracy of the model depends highly on the number of clusters. As the main issue with a partition clustering fuzzy C-means is that it requires Apriori specification of the number of clusters [32], the proposed work does have a high bias, but it has been reduced by validating the model with different experimental setups, each having different number of clusters. Figure 5 highlights the first three components of the work illustrating the procedure of data reduction.

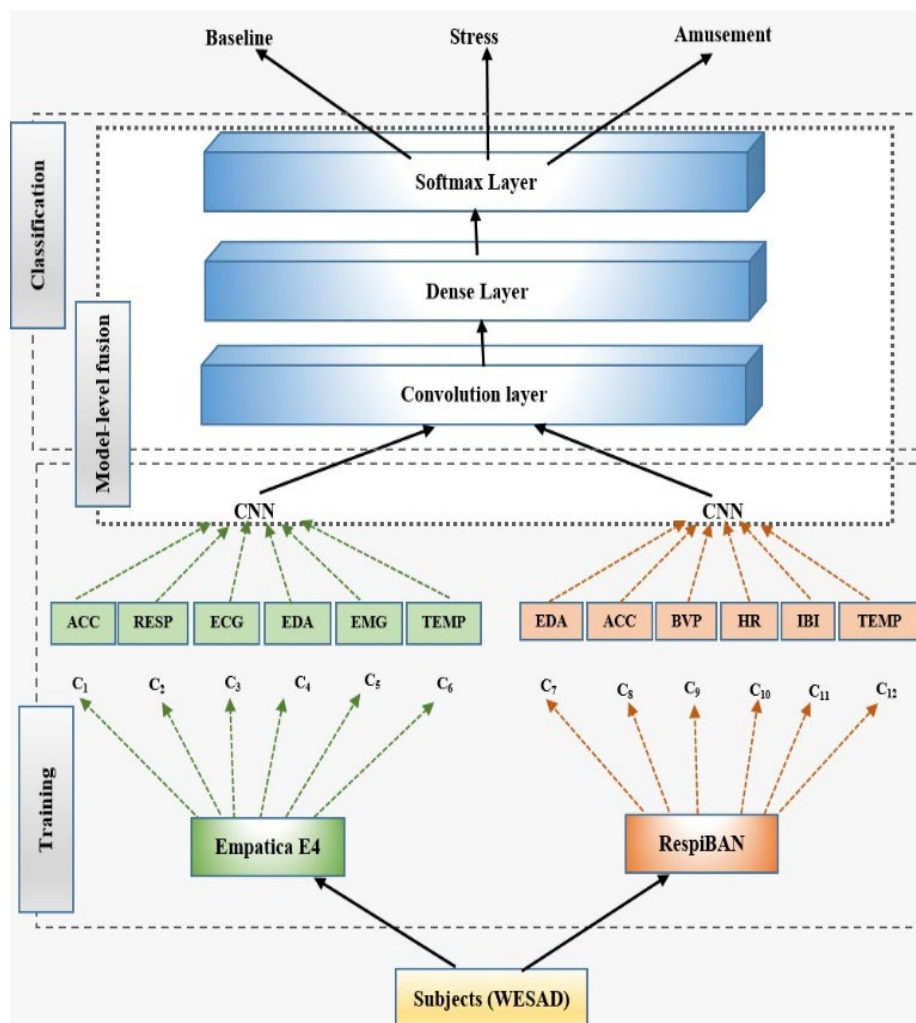


Fig. 6. Architecture of Deep Hierarchical Model

After generating the optimized summarized data or information table, it is given as an input to the fourth final component, i.e., deep hierarchal model to train and detect the affective state of an individual [21]. CNN is a sequence of convolutional layers, interspersed with activation functions. It is a deep neural architecture which has the power of self-tuning & learning skills by generalizing from the training data, it enhances feature extraction. The proposed Deep Hierarchal CNN model comprises of three levels, at first level ten 1-dimensional CNN (1D-CNN) layers were used to train the model on individual biomarkers, the output of first level was transformed to second level having two 1D-CNN, one each for generating an output for each wearable device (RespiBAN, & Empatica E4) and finally using model-level fusion the results of two 1D-CNN were combined to classify the affective state of an individual. After the data has been fetched in the scalable format, data is still astronomical and exists as individual units, so we apply the 1D-CNN over each feature signal by constructing a separate CNN (C_n). Once all the C_n s gets trained, the input is passed in as subject manner, i.e., all the features of a subject at one sliding window or at a particular time is passed through the second level 1D-CNN, and the output of the two CNN layers is then passed into the primary model that classifies the subject at a particular instance into one of the three classes defined during the training phase using SoftMax layer. As each subject produces different bio-signals while being in stress, amusement or baseline, the convolution network while predicting can map a single instance into different classes having different probabilities, therefore application of logistic regression is very important to determine the final output class of the subject at a given instance. Due to 3 classes, SoftMax function is applied on top layer to map the output with highest probability class. The proposed hierarchical network is shown in figure 6.

Each subject's data contains signals from two different sensor devices, RespiBAN recorded with 700Hz signal, the C_n s created for each of these feature is 1-D CNN with input layer 700×1 except for ACC which is provided with input layer of 700×3 , as the ACC signals contain 3 dimension data. The C_n s for features recorded with Empatica E4, have different sized input layers, for ACC 32×3 , BVP has 64×2 , TEMP and EDA have input size of 4×1 input layer. 65% of data is used to train the model, i.e., ten subjects are used to train the model, and rest 35% i.e. 5 Subjects data is used to test the data, and 20% of the data (2 subjects) is used to validate the model. 53% of the total instances belong to the baseline class, 30% belongs to stress class, and 17% belong to the amusement class. Algorithm 1 depicts the step-by-step sequence of the proposed model:

Algorithm 1: Proposed Model

Input: WESAD data, k =number of clusters,
Output: Ac – Accuracy obtained
1: **Begin:** Choose the initial Cluster centroid
2: **Initialize:** Fuzzy Membership Matrix, $U = [u_{ij}]$
3: **Repeat while** ($U^{(k+1)} - U^{(K)} < \text{threshold}$)
4: Calculate new Euclidean distance
5: Calculate new Cluster Centroid
6: Update the Fuzzy Membership Matrix
7: **End-while**
8: **Initialize:** Fitness Population = U
9: **Define** Tournament for fit individuals
10: **Repeat While** (New Child \notin Population)
11: **Select** Fit individual \leftarrow Random from Fitness Population
12: **Select** Child1 & Child 2 \leftarrow Random from Fitness Population less chromosome
13: $\text{Fit1} \leftarrow \text{Fitness}(\text{Child1})$
14: $\text{Fit2} \leftarrow \text{Fitness}(\text{Child2})$
15: $\text{Optimal Child} \leftarrow (\text{Fit1} > \text{Fit2}) ? \text{Child1} : \text{Child2}$
16: **Select Parent** \leftarrow Tournament (Fitness Population)
17: **Define** Crossover
18: **Define** Mutation
19: **End-while**
20: Calculate new Cluster Centroid
21: **Define** new Information Matrix
22: Update Information Matrix with only cluster centroids
23: **Train** \leftarrow Information Matrix
24: **Return** (Ac)

4. Results & Discussion

The proposed model was initially applied on the original WESAD dataset with 12 bio-signals. WESAD contains a time series data, but to process it, analog signals were converted to digital values at the interval of 1 second, but since the variation can be observed at each second, a sliding window of 0.25 seconds was chosen to monitor the changes affective psychological state of an individual. To evaluate the model, WESAD was pre-processed by applying min-max normalization for standardization so each subject have test results in the same range. To train the deep hierarchal model, the output class was converted into numerical values, by assigning 1 for baseline affective state, 2 for stress, and 3 for amusement, whereas for undefined cases were considered as baseline. The model was evaluated using 5-cross validation, each having 65% of data for training i.e. 10 subjects were used for training and 5 subjects were used for testing the model. At last the model was validated using 20% of data (3 subjects). Deep hierarchical model was executed on a 2.7 GHz INTEL core i5 with 16GB RAM system and was evaluated in terms of accuracy, F1-Score and execution time. The average accuracy attained by each subject during validation in each cross-fold has been shown in table 3, along with the F-1 score and the execution time in seconds to evaluate each subject. The average model accuracy of 87.7% is achieved with the best subject-level accuracy of 96.98% achieved for Subject 2. The accuracy curve of the model is shown in fig. 9. It is observed that the accuracy of the model varies from 72% to 96%, whereas the F-1 score ranges from 0.612 to 0.998. The average accuracy achieved by the proposed model is better than the state-of-the-art results.

As the impact of each stimuli on a subject can be observed for few seconds, the data reduction is done by clustering the data which belongs to a certain time window and subsequently optimizing the clusters. To find the best time window, in which the affective state can be detected accurately while having fast execution time, the proposed architecture was evaluated 5 times, first on clusters having summarized bio-signals of 3 seconds, i.e. with 2400 clusters, second time model was implemented on 1800 optimized clusters, with initially each cluster having data of 4 seconds. Similarly the model was tested on 1440 clusters (5 second window frame), 1200 clusters (6 sec window frame) and lastly on 1030 clusters having 7 second window frame. Each time after defining the number of clusters on the basis of time frame, the data was initially sorted into each cluster using fuzzy-c mean clustering using Euclidean distance, and then to find the optimized clusters, genetic algorithm was applied. Once we obtained the optimized information matrix, it was pre-processed to scale the data, and then provided as an input to train the deep hierarchal model using 5-cross validation, each with 65% data for training, 35% for testing and 20% for validation.

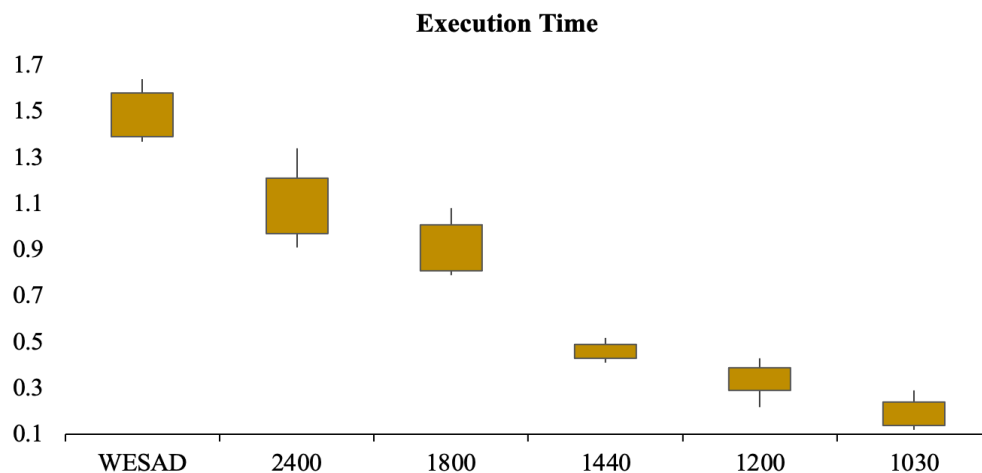


Fig.7. Execution time of different clusters

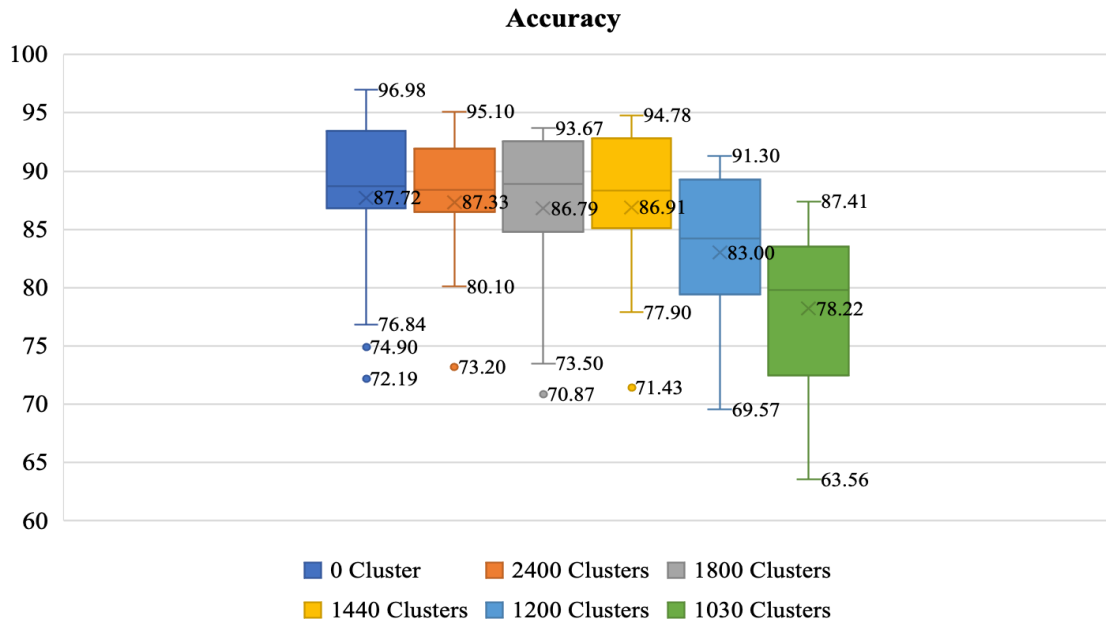


Fig.8. Accuracy of different clusters

The execution time taken for each subject ranges from 1.37 seconds to 1.64 seconds, with an average execution time of 1.51 seconds. The variation in execution time and accuracy in each case can be visualized in figure 7 and 8 respectively. It was observed that the average model accuracy slightly reduced with increase in reduction ratio of the data, but the execution time was reduced considerably with the summarized data. The optimal trade-off between accuracy and execution time was observed with 1440 clusters, having time frame window of 5 seconds. As we increase the time frame window to reduce the number of clusters, the execution becomes fast, but the accuracy declines as well. Therefore, we propose clustering the data at an interval of 5 seconds which can reduce the latency time and can provide an accurate detection of the affective psychological state of an individual.

Table 1. Performance of Proposed Model

| Subjects | WESAD | | | Summarized WESAD | | |
|----------------|--------------|--------------|----------------|------------------|--------------|----------------|
| | Accuracy | F-1 Score | Execution Time | Accuracy | F-1 Score | Execution Time |
| S1 | 93.39 | 0.946 | 1.64 | 92.81 | 0.925 | 0.52 |
| S2 | 96.98 | 0.983 | 1.53 | 94.03 | 0.974 | 0.49 |
| S3 | 88.70 | 0.612 | 1.61 | 87.95 | 0.721 | 0.48 |
| S4 | 95.07 | 0.929 | 1.47 | 92.81 | 0.934 | 0.46 |
| S5 | 74.9 | 0.968 | 1.58 | 71.43 | 0.815 | 0.42 |
| S6 | 87.92 | 0.855 | 1.39 | 88.56 | 0.837 | 0.51 |
| S7 | 86.79 | 0.860 | 1.56 | 84.2 | 0.892 | 0.47 |
| S8 | 72.19 | 0.684 | 1.37 | 71.5 | 0.656 | 0.43 |
| S9 | 87.24 | 0.798 | 1.44 | 88.3 | 0.813 | 0.41 |
| S10 | 92.73 | 0.935 | 1.52 | 91.8 | 0.908 | 0.46 |
| S11 | 93.46 | 0.834 | 1.48 | 94.78 | 0.851 | 0.51 |
| S12 | 87.24 | 0.858 | 1.39 | 86.78 | 0.893 | 0.48 |
| S13 | 88.72 | 0.931 | 1.62 | 87.34 | 0.899 | 0.44 |
| S14 | 76.84 | 0.649 | 1.59 | 77.9 | 0.715 | 0.49 |
| S15 | 93.56 | 0.917 | 1.42 | 92.5 | 0.878 | 0.43 |
| Average | 87.7 | 0.852 | 1.51 | 86.8 | 0.848 | 0.46 |

ACCURACY

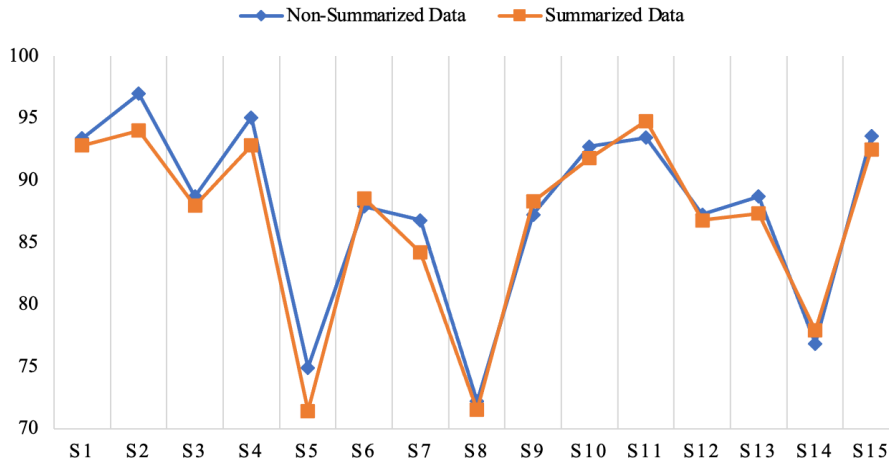


Fig. 9. Accuracy of Summarized vs. Non-Summarized Data

The accuracy and execution time comparison of both the original WESAD and the summarized WESAD is shown in table 1 and in figs. 8 and 9. The table shows the performance of the proposed model in terms of average accuracy, F1-score, and execution time of each subject after 5-cross validation for original WESAD dataset, and the summarized WESAD with 1440 clusters with time frame window of 5 seconds for clustering. In case of summarized data, best accuracy of 94.78% was achieved for Subject 11, with an average accuracy of 86.8%. And the execution time taken for each summarized subject data ranges from 0.41 seconds to 0.52 seconds, with an average execution time of 0.46 second. It is observed that the accuracy of the model varies from 71.4% to 94.78%, whereas in case of non-summarized the accuracy varied from 72% to 96% as shown in figure 9. Figure 10 highlights the time variation the model has shown while execution for summarized vs. non-summarized data.

EXECUTION TIME

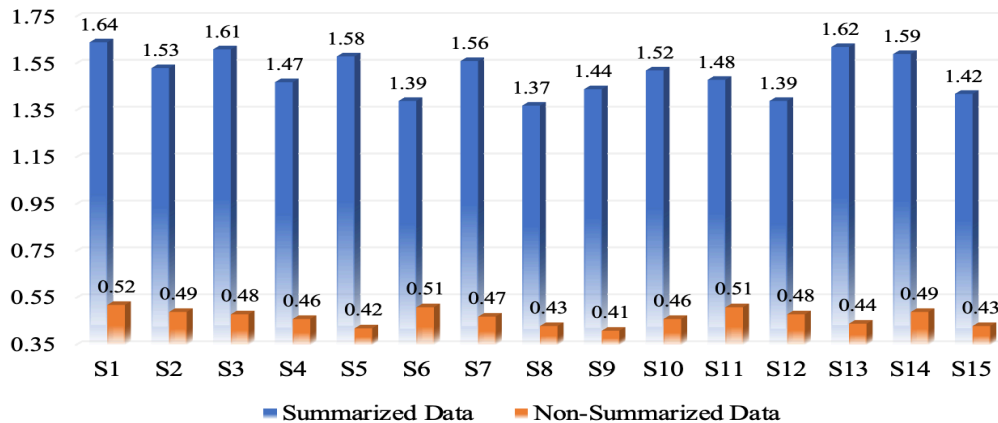


Fig. 10. Execution Time of Summarized vs Non-Summarized Data

Quite clearly, the decline in accuracy over the summarized data is insignificant as the average model accuracy reduces by 1% as compared to a significant reduction of 27.7% in the execution time. The reduction in accuracy could have been due to reduction in the size of training data. It is plausible to train the model on complete data and then evaluating it on reduced data for better accuracy. Also, as validated from the results obtained, the accuracy of the model depends upon the subject's data, as different individuals have different level of stress under same scenario and the expression of stress is also different for each individual. To understand the affective state of a person it is required to have the health profile of the subjects like medical history, traumas faced along with continuous monitoring using IoMT-based wearable devices. The proposed model currently only takes the subject's bio-signals of 2 hours under controlled lab environment, but this trained model can work as a base model for real-time analysis over the intelligent edge with continuous modifying weights for each individual at the cloud server.

5. Conclusion

Affective state recognition from wearable biosensors on the basis of varying available criteria represents a complex decision problem. The real-time data which is continuously collected from the wearable devices is massive, less structured and heterogeneous. Moreover, identifying the affective psychological state of an individual in a real-time environment needs fast execution time and high accuracy. With the availability of IoMT-based trackers various bio-signals can be measured but to have fast estimation of affective state bringing the computing power to the edge of the network helps address the challenge of data build-up, mostly in closed IoT systems. The ultimate goal is to minimize cost and latency, while controlling network bandwidth and the major benefit intelligent edge analytics brings is the reduction of data required to be transmitted and stored in the cloud. We proposed an optimized Fuzzy C-means data clustering technique that generates a summarized data for each subject in WESAD. A CNN model with hierarchical capabilities is then used to train and detect the affective state of an individual. The results show a significant reduction of 27.7% in the execution time with an insignificant decline in average model accuracy by 1%. Undeniably, the intelligent edge analytics can fast track the affective state analysis of an individual, sending emergency signals at the time of higher stress or anxiety attack to the medical professional for the required help.

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