

An Early Risk Prediction against Covid -19 Based On Adaptive Surf Scale Feature Selection and Sigmoid Recurrent Neural Network for Premature Precaution before Covid Second Wave

Dr. Jagannath Jadhav¹, Dr. Srinivasa Rao Surampudi², Dr. Mukil Alagirisamy³.

Department of electronics and communication engineering
Lincoln University College, Malaysia¹

Department of electronics and communication engineering
Lincoln University College, Malaysia²

Department of electronics and communication engineering
Lincoln University College, Malaysia³

Abstract: The development of new technologies, human nature, and food activities are completely against with nature in recent days. Due to this uncertainty, the new pandemic covid-19 has outbreak globally and spoiled the human life. In this situation, the disease also has improved as a new modified version of influenza like Covid 19 (2.0). So, the Analysis of features becomes mandatory to identify the diseases based on big data analysis. Similarly, most people suffering from diabetes could not have a correct prediction to take proper treatments. Many health care suggestions and treatment handling methods do not predict the right information at the correct time to make a diagnosis. There is no premature process for the treatment based on non-predicted results. Hence, an Adaptive Surf Scale Feature Selection (SSFS) and Sigmoid Recurrent Neural Network Classification (SRNN) is proposed for improving the early risk prediction against the covid. Initially, preprocessing is carried out to verify the records. Then, feature selection is carried out using the surf scale weightage factor, which analyzes the Covid Influence Rate (CIR) and the marginal weight is identified. Each identified weight is ruled into Inter Class Sigmoid Function (ICSF) to activate the iteration recurrent neural network. Finally, the classifier trains the features into a feed-forward layer to produce the classified result. The proposed system produces high performance compared to the previous system as well as recommendations for premature diagnoses.

Keywords: Deep learning, COVID analysis, feature selection neural network, CIR, health care analysis, clustering, prediction.

1. Introduction

Diagnosis becomes important in recent days during Corona research. With similar symptoms to other types of pneumonia, it is an important preventative step. Image screening like C.T. and X-ray is important in that direction of disease prediction. However, using them to boot chest C.T. images and detect COVID 19 is a computationally expensive task. Machine learning technology has the potential to overcome this challenge.

Currently, medical database maintenance is an important issue in the medical field. Care should be taken to provide quality service of patient information covering various disease-related

and diagnostic functions. Medicine Data mining information is so complex that stored data cannot contain missing values and redundant data. Good data production and data reduction are essential before applying a data processing algorithm, affecting mining results. Accurate and consistent noise-free data make diagnostics quick and easy.

The massive amount of data set groups about patient particulars, diagnosis, and prescriptions handled by healthcare industries with more dimensions need deep learning processes. Analyzing the data by processing the image is divided into preprocessing, attribute collection, segmentation, transformation, feature selection, and classification to predict premature treatment data values.

Deep learning algorithms and essence are collections of machine learning positions trying to figure out complex issues by mapping them to different levels. With the development of big data, an important function is to study in-depth academic and optimization outcomes. Attribute-based feature Selection is the bulk capacity analysis of dynamic data in image format for viewing patients screening.

Application of a set of adaptive image processing is well in doing PHR data analysis at multiple levels using different layers of nonlinear information from in-depth training image and database values. Deep learning can extract features based on information obtained through complexity in large data environments, but it is essential to do data mixing before Analysis. The information from PHR is used for information from the screening, and many factors are combined to make decisions, classify and improve.

Feature selection is data that is preprocessed efficiently by data processing technology to minimize data generation. It is very important to identify the most important risk factors associated with the disease in clinical diagnosis. It helps to remove unwanted attributes from continuous, rapid and effective disease data Related feature identifiers.

Classification and prediction whose first application is to train data to create model data processing technology, and as a result, model prediction is used to test the result. Various classification algorithms have been fitted with disease datasets to diagnose chronic diseases, and the results are highly promising. The most important thing is to develop new classification methods that can speed up and simplify diagnosing chronic diseases. Based on the classification results, the best performance needs the concrete methods to improve the performance.

2. Related work

V. Z. Marmarelis (2020) described that the scientific community is accelerating efforts to analyze the dynamics of the COVID-19 epidemic, which is to predict significant epidemiological outcomes, to assist its clinical administration in reasonable planning, and to guide socio-political decision-making in appropriate mitigation measures. According to the established sir system framework, this work includes a population of multiple "vulnerable," "infectious" and "recovery / delete" scores, and should define the dynamic relationship of the first-order differential equation.

R. F. Sear et al. (2020) described that Dangerous COVID 19 is a huge amount of misconduct on the internet. Use Machine learning to measure the content of COVID 19, health guidance, especially vaccine online antagonist. The development of an anti-VAX community around COVID 19 has received less discussion than the associated vaccine-dependent community. However, it is possible to obtain a broad cross-section of the COVID 19 vaccine in

the anti-VAX community, such as personal surveillance or mandatory fast surveillance for guidance from individuals.

H. Jelodar et al. (2020) described it as the convenient channels for users to discuss health issues and share information based on machine learning prediction. References are carried out from patients' features depending on the classification method.

R. Kavitha et al. (2016) described that cardiovascular classification data are cast-off in the preprocessing phase of the mining procedure of data set from a high-dimensional database. The original database includes data search space and storage space wherein unwanted and irrelevant data are stored. To accomplish organization correctness, the requirement to eliminate needless and immaterial data is essential. The evolutionary discount method is used to wrap high dimensional data with some restrictions to reduce data complexity. The framework itself integrates cardiovascular prognosis for convenience.

U. Haq et al. (2019) described that Using machine learning (ML) models can be very effective in the early stages of diagnosing Heart Disease (H.D.). If diagnosed early, H.D. treatment and recovery can be effective. Assistant Doctors have to be developed through H.D. Identity Machine Learning (ML) technology.

Nair, R et al. (2019) described that extracting microscopic data for disease prognosis is a difficult machine learning task. The higher the percentage and the lower the sample, the higher is the calculation risk. To improve the classification signal-noise ratio, the algorithm can be used to obtain the most appropriate genes' performance. The block-based classification algorithm is then applied to these selected genes' data sets to obtain effective classifiers for future predictions.

Raweh, M et al. (2018) described the development of abnormal DeoxyriboNucleic Acid (DNA) methylation as an important factor in cancer. Understanding its mechanism has become important in the early years for early diagnosis and prognosis. With the advent of high output technologies, many challenges have been overcome to achieve the classification process using DNA methylation data. Higher evolutionary and DNA maturation data can lead to more noise prediction accuracy degradation.

H. Waseem et al. (2019) described that accurate and early predictions of cancer deaths in 2019 are estimated as 9.6 million people approximately. This estimation helps the health care department regulate timely treatment to control the risk of suffering and death. Generally speaking, predictive systems based on Machine Learning (ML) use health data (genetic maps or clinical parameters). Algorithms are there to predict target values for learning cancer. However, forecast accuracy optimization is an important attempt to make accurate decisions.

J. Chiang et al. (2008) described the greening feature selection methods used in the Analysis of gene expression data. It can detect related functions without knowing the number of clusters in advance and determine if the center is approximately correct.

S. Lekha et al. (2018) described that the prognosis for non-invasive diabetes is becoming increasingly important over the past decade. After examining the serum of many people, a

promising alternative to human respiratory blood sugar level and acetone level appear to have shown a good correlation. This interaction establishes acetone as an acceptable parameter for diabetes. The most common data analysis strategy feature is to study biomarkers diagnosed with the respiratory disease using extraction and classification methods. However, applying signals can reduce computational costs and optimal real-time feature selection analysis, such as encountering such problems.

Warda M et al. (2020) described the Rapid growth rate of COVID 19 infection. Due to specific medications, it is possible to control the disease so that early diagnosis patients (COVID 19) cannot be treated. There is an important need to diagnose in the early stages of the disease and immediately isolate the affected person. Many studies are being implemented, but they have not yet introduced satisfactory results. Despite its simplicity, k is very favorable for complex classification problems by classifying adjacent ones. However, it can be easily captured.

S. B. Kotsiantis et al. (2011) described that many candidate features provide the complete characteristics of the classification task that is usually generated by the learning algorithm. However, it is often an inappropriate or excessive learning task for most people, which worsens the performance of the written material with leading accepted algorithm and leads overlap. Learning accuracy and training speed can be significantly impaired by these unwanted features.

Umut Ozkaya et al. (2019) described that Coronavirus (COVID 19) has been declared as infectious disease at the end of the World Health Organization 2019 Global Infectious Disease Recognition. Consent about infections also occurred in the use of Computer Graphics (CD) to provide fast and accurate results in early detection. It is a radioactive pointer showing images of the transformer COVID19 that show different behaviors.

Esteva A et al. (2017) described that early clinical screening and diagnostic skills are followed by dermoscopy biopsy and histological examination. The automatic classification of skin lesions using images is challenging due to the appearance of subtle degeneration of skin lesions. It is possible to make 4, 5 multiple granular material categories and 6, 7,8,9,10,11 integrates of Deep and Convolutional Neural Networks (CNN) to perform general and variable tasks. Demonstrate using a well-trained tip-to-end classification of the presence of a single CNN, direct skin lesion, using only pixels and disease labels input.

Lopamudra Dey et al. (2020) described that COVID 19 disease caused by SARS-cov-2 is an epidemic as declared by the World Health Organization on March 11, 2020. In 2020, this covid-19 has caused more than 6 million deaths. Protein-protein interaction (producer price index) plays an important role in the human body's SARS-cov-2 infection process. Recent studies suggest that some human proteins interact with some SARS-cov-2 protein, thereby, many potential interactions are determined.

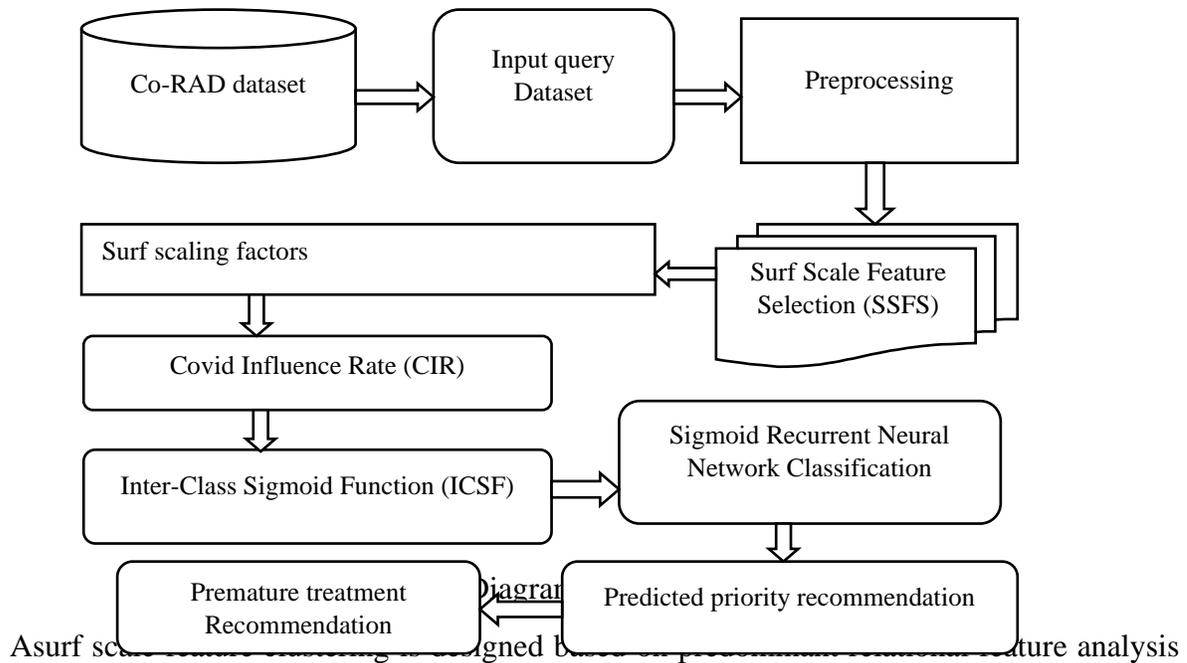
Divya Jain et al. (2018) described that using feature selection and classification technology for diagnosing and prognosis of chronic diseases will be of immense help. A fully functional system that classifies the selection plays an important role in improving accuracy. Evolutionary reduction helps to improve the overall performance of machine learning methods. Disease

Database effect Classification Algorithm Application for diseases, adaptive automated and intelligent diagnostic developing pledge results.

Du, Y et al. (2018) described that Functional imaging data, particularly functional magnetic resonance imaging data, were followed to reflect neural activation function coordination. It is expected to provide potential biomarkers for classifying changes or predicting neural function using the features to classify the data.

3. Adaptive SurfScale Feature Selection and Sigmoid Recurrent Neural Network

This research aims to predict the covid infection for early diagnosis by developing an intelligence system based on a deep learning approach. An adaptive Surf Scale Feature Selection (SSFS) and Sigmoid Recurrent Neural Network Classification (SRNN) are proposed for improving the early risk prediction against the covid. The importance of data selection is based on optimized clustering, feature selection, and classification approaches to reduce data analysis's dimensionality through frequent spectral mapping. This research work intends to minimize the complications of Covid features through the multi-layered approach. An efficient image screening data analysis and physical fitness data analysis model is designed by selecting the frequent relevance of redundant feature arrays.



Asurf sc... igned b... ure analysis methods to reduce the neural classifier's burden. Figure 1 shows the architecture diagram for the S²FS-SRNNproposed system. The prediction accuracy is improved using multi-factor consideration like scaling features, subset evaluation, object segmentation, and boundary data analysis for redundancy feature evaluation. The optimization of neural classifiers provides the right selection of features inputs for a large dataset and improves the classification accuracy

3.1 Data initialization

Initially, the preprocessing was handled to reduce the features' dimension based on the auction filter which performs the variation in data present in patient records. This verifies the indexing values ordered count and the attributes to the equivalence values, null values, and

empty values. The data preparation checks all features considered as attributes' presence important to getting values cleansing stemmed and filled the nearest values. The preprocessed dataset intakes collection of patient features like temperature, immunity status, cold, cough, ESR, CRP, CT screening, GIS collective data's like social distance through mobile distance observation, etc. The steps given below show that data preparation.

Algorithm

Input: Initialize CO-RAD dataset- Cds

Output: Filter Processed dataset -Fds.

Step 1: Cds= observe collective records labels.

Step 2: compute For. (Cds \rightarrow I at the initialization at J feature)

Step 3: check if empty \rightarrow true

Remove records, check cleansing null attribute, stemming the progress

Step 4: Fds= return rearranged data records

Step 5: end if end for;

Step 6: return as redundant R-Fds

The above algorithm describes the preprocessing stage to reduce the dimension based on an attribute by filtering the values. All the records contain multiple attributes as features referred to the single patient information.

3.2 Surf Scale Feature Selection (SSFS)

The surf scale measures the relational measure, supporting covid direct act under the mean rate of maximum weightage. The feature which improves the c- reactive proteins (CRP) weightage belong states of immunity representation, because the immunity weight is an important feature to be considered.

The surfing factor finds the feature weights to select the scaling values between the class end margins. At each selection, weights are categorized into subgroups based on inner and outer set subgroups. This makes redundant deterministic values to make low dimension data values. In this, redundant feature groups are split into portioned groups, the hypothesis dimensionality space, and, in the subcategory of extracting features, reducing the complexity required to partitioning the data by inner and outer trained set.

Algorithm:

Step 1: Input Phr dataset Co-RAD.

Step 2: Select the label of attributes

Step 3: Check the scaling values of margin weights Mgw

Step 4: Process each data as ForMgw \rightarrow 1=0,1,2,as subdividing attribute partition

Select the relational values of class labels Im \rightarrow {ESR, CRP, IMT}

Compute Low If weight scale Mean rate (Im)

MR \rightarrow inner feature Ot(i*Mgw) = all partitions except i.

Similarly as Where outer set \rightarrow Ot(i), Inner set \rightarrow It(i)

Process up to Ot(i), = the i'th partition as MR

Check initialization For $j = 0, 1, \dots, m$
 Compute social Distance St Measure (Fs) with j components of Fs,
 $I \rightarrow i + Fs$

End loop of (j).

Choose the I.F.s with the s max feature weightage.

Return the Ifs feature

Step 5: Arranged feature as a redundant feature scale and select the scale value.

The selected Ifs feature is redundant which attains the scaling values to find the specific instance of covid influence rate selected based on the Influence rate. The estimation given below shows the deep feature weight age on different factors under the region of covid affection rate, social distance, spreading statistics, PHR immunity margins, economic communication etc.

3.3 Covid Influence Rate (CIR)

The method uses the event similarity based on disease affection rate, social distance, spreading statistics, PHR immunity margins, economic communication, which are measured according to candidate most affected influence calculated by mean rate. Also, the mean rate is referred to as features present in each event class. According to the value of Event Support, a specific event has been selected and produced as a result.

Algorithm

Initialize data source form covid collective source.

For each source s

 For each class l

 For each Decision nodes

 size(N)

 If $Fv(Pl) \in s$ then

$i = 1$

 Count = count +1.

 Compute Feature limits $Fli = \frac{Fv(pi+AmR)}{Fv(marginal\ weight)} \times Fv(NI)$

 Compute spatial data forum Information data rate IrPl.

$IrPl = \frac{Fv(l-1)(Lower\ limit)}{Fv(l-1)(marginal\ weight)} \times Fv(l-1)(NI)$

 Compute Co_Rad -I.R. = $CI / IrPl$

 End

End

ComputeCo_Rad Influence Rate (CIR).

$$ITS = \left(\frac{Fv(Upperlimit)}{Fv(marginal\ weight)} \times Fv(NI) \right) \times Std(IR)$$

If $ITS > Th$, then

$$\text{Add to vulnerable set } VS = \sum(\text{Sources} \in Vs) \cup s$$

End

Stop

The event prediction process is presented above the pseudocode, and the method computes the event support for various event classes. Finally, a single event has been selected as a possible event to produce a result

3.4 Inter Class Sigmoid Function (ICSF)

In this stage, the activation function creates the logical neuron for selecting the features trained into the feed-forward neural network. Each neuron is ruled into logical conditions, making CIR maximum weight intakes by substituting multiple searches and matching class hidden layers. The structural path of layers selects the features according to the Inter Class Sigmoid Function $F(x)$ and inter-class sigmoid values.

Exponential representation of Inter Class Sigmoid Function is logistic functions, which are represented as.

$$\text{The function } f(x) = \begin{cases} y = 1 & \text{if } \sum_{i=1}^n w_i x_i \geq b \\ y = 0 & \text{otherwise} \end{cases} \dots(1)$$

where $f(x)$ in equation (1) remains the logistic activation of neuron trained with Inter Class Sigmoid Function.

$$y = \frac{1}{1 + e^{-(w^T x + b)}} \dots(2)$$

The Inter Class Sigmoid Function $e^{-(w^T x + b)}$ exponential point represents the sigmoid function. The neurons weight W iterates the input function to the Inter Class Sigmoid Function neuron. The weightage are activated at each neuron ℓ at the weight at feed into b hidden layer to Compute \hat{y} as Compute $\ell(w, b)$, the iteration be tuned and w and b with trained neurons and feed layer.

$$w_{(t+1)} = w_t - \mathbb{N} \Delta w_t \text{ at weightage level } b_{(t+1)} = b_t - \mathbb{N} \Delta b_t \dots(3)$$

Iterate till the end the neuron gets the closer mean value get trained by neurons. The calculation of the terminal output produce the derivative weights in Inter Class Sigmoid Function

This Inter Class Sigmoid Function finalizes the neuron iteration based on $F(x)$ logical conditions that make the neural layer tuning function. Each iteration is tuned according to the Maximum weight observed from the trained class beyond the disease influence rate limit. If any distinction of neurons is selected as per weightage of class labels, the adjusted with support features called relational features.

3.5 Sigmoid Recurrent Neural Network Classification

This classifier initiates the selective features at spectral points into internal layer whose calculation collective weightage neurons are correspondingly forming optimized hidden neurons trained with activation function. Hidden neurons can intercede between the outside information and network yield with correlation features with logical representation. Intermittent numerals haveformed more than one recurrent to form feed forward layer. It might comprise a separate layer of neurons with every neuron serving its yield motion back to the various neurons' contributions based on the decision carried. This reduces the search reputation on the classifier to the closest weightage.

Algorithm:

Step 1: Construct anInter Class Sigmoid Function with neural network

Step 2: Initialize scaling vectors as features input

Step 3: fix the sigmoid rule Max set Limits of feature index Fsi to each neurons

Step 4: Compute the search feature closer Neurons

$$Fsi(Fst \rightarrow w.xi+b) \geq y - \epsilon i, \epsilon y \geq 0, 1 \leq y \leq n$$

Step 5: for executing fsi as Max feature Mx

Step 6: compute all scaling features according to their fitness best-case measure

All input data samples $x = x_i w_{ij}$ *definesthesequences*

$$Z_{ij} = x_i w_{ij}; Z_j = \sum_i Z_{ij} + X_j = g(Z_j)$$

Sort all the features to index F as cluster Fci

$$f(xfci) = \sum_i ir_i$$

Step 7: The remaining features at Max point Ci as for

Step 8: Computing forward layerCi as for all scaling j

Step 9: Compute xci,j Indexed weight modification

Produce optimal class \rightarrow new, ci,j

Indexing class \rightarrow $X_{new, ci, j} = X_{ci, j} + \alpha * (X_{best, ci} - X_{ci, j}) * r^2$

Step 10: Compute the scaling marginal if xci,j= x is the best, ci class then

Fix margin winner class $X_{new, ci} = \beta * Center_{ci}$

Step 11: Add class Maxi,j and update xnew,ci,j

$$Center_{ci, d} = \frac{1}{nci} \sum_{l=1}^{nci} x_{ci, l, d}$$

Step 12: end if

Step 13: Scaling end cluster

Step 14: Max Point end

Step 15: for all class c_i in the features, do

Step 16: attain to modify the new scaling features weight in class c_i by

$$Class\ st = \frac{1}{2n} \sum_{i=1}^n (\hat{x}_i - x_i)^2 + \beta \sum_{j=1}^m KL(p|\hat{p}_j) + \frac{\lambda}{2} \sum_{i=1}^n \sum_{j=1}^m \theta_{ij}^2$$

Step 17: end for

18: Calculate scaling weight closer by the newly created class

$$P(F_{max \rightarrow c}) = X_{\omega \in A} p(\omega) \text{ where } p(\omega) \geq 0$$

Step 19: create priority, Max, ascending index until $t < \text{MaxGen}$

$X_{\omega \in A} p(\omega) = 1$ in highly recommendation set of $X = \{x_1, x_2, \dots\}$

Step 20: Recommend the weighted Max class.

This forms subset correlation data points on hidden layers for a considerable number of layers comparable with original weightage to categorize the class. All the layers are nonlinear. Activation function figures out the internal result of the input vector and the heaviness of that unit constructs worldwide approximations to I/O mapping. Only the synaptic weights must be scholarly found to classify the result to produce high performance.

4. Results and Discussion:

The proposed adaptive Surf Scale Feature Selection (SSFS) and Sigmoid Recurrent Neural Network Classification (SRNN) for improving the early risk prediction against the covid using python framework and its performance in restricting the pandemic are measured. The performance of the method has been validated under various parameters. The method has been validated for its performance using different data sets with dissimilar methods CNN (Convolution Neural Network) based Covid Infection Transmission Analysis (CNN-CITA) with monitoring rate called screening National Care (NC). The results obtained have been presented in this section.

Table 1: Details of a Data set

Parameters	Value
Tool Used	Python framework
Data set	GIS, Covid Data set
Number of regions	35
Number of Users	1 million
TimeLine	3 months

The data set is used to evaluate the proposed algorithm's performance, as presented in Table 1. According to the details in Table 1, the method's performance has been measured and presented in this section.

Table 2: Performance on Infection Transmission Analysis

Performance on Infection Transmission Analysis			
Methods	3 Lakhs users	5 Lakhs Users	1 Million Users
Infection Disease System	72	76	79
Hygienic Measures	76	79	83
Screen NC	79	84	86
CNNCITA	86	91	97
S ² FS-SRNN	89	92	98

The performance of infection transmission analysis produced by different methods has been measured and presented in Table 2. The results indicate that the proposed S²FS-SRNN approach has produced higher performance in infection transmission analysis.

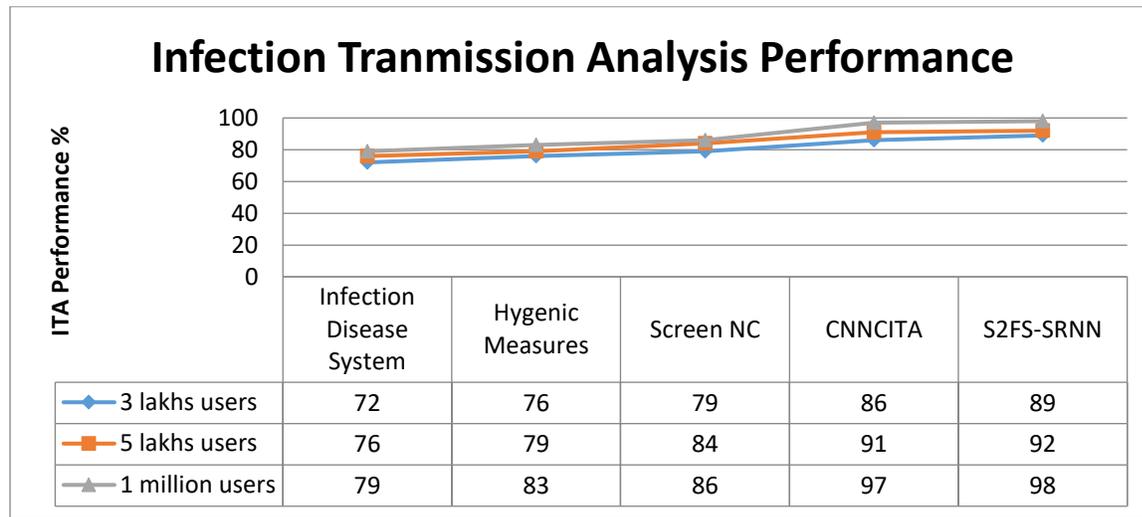


Figure 2: Analysis of Infection Transmission Analysis

The performance in analyzing and identifying the infection transmission produced by the different methods is measured and presented in Figure 2. The proposed S²FS-SRNN approach has produced higher performance than other methods.

Table 3: Analysis of false ratio

False Ratio on Infection Transmission Analysis			
Methods	3 Lakhs users	5 Lakhs Users	1 Million Users
Infection Disease System	28	24	21
Hygienic Measures	24	21	17
Screen NC	21	16	14
CNN-CITA	14	9	3
S ² FS-SRNN	11	7	2

The false ratio produced by different infection transmission analysis approaches has been measured and presented in Table 3. The proposed S²FS-SRNN approach has produced less false ratio compared to other techniques.

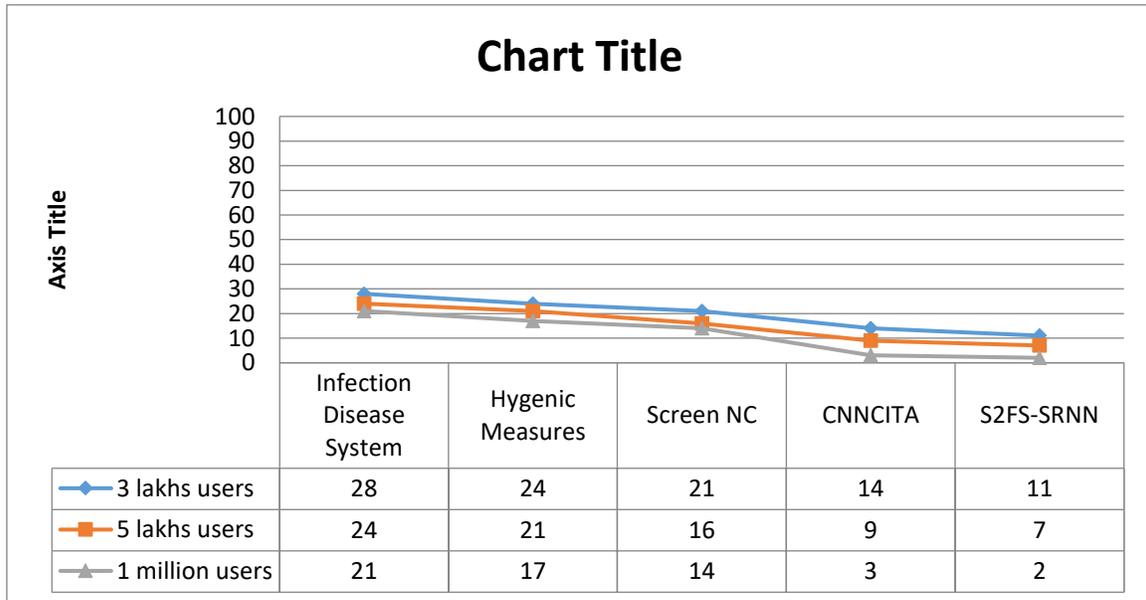


Figure 3: Analysis of false classification ratio

The performance in falsely classifying the infection transmission is measured, and the false ratio is computed for different conditions according to the number of persons in each region. According to that, the proposed S²FS-SRNN approach has produced less false ratio than other methods.

Table 4: Analysis of time complexity

Time Complexity in Millie Seconds			
Methods	3 Lakhs users	5 Lakhs Users	1 Million Users
Infection Disease System	73	79	89
Hygienic Measures	69	74	83
Screen NC	56	69	78
CNNCITA	14	21	29
S ² FS-SRNN	10	15	18

The time complexity introduced by different methods is measured and presented in Table 4, which shows that the proposed S²FS-SRNN approach has produced less time complexity than other techniques.

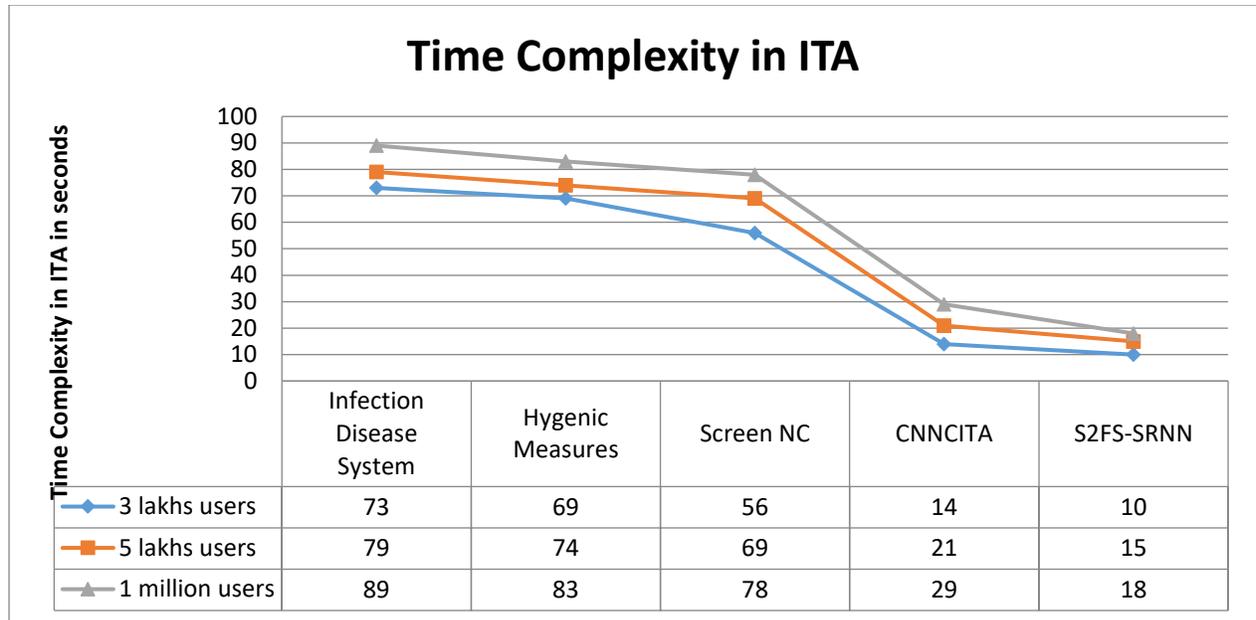


Figure 4: Analysis of Time Complexity

The time complexity incurred by different methods in analyzing the infection transmission is measured and presented in Figure 4. The proposed S²FS-SRNN approach has produced less time complexity in ITA than other methods.

5. Conclusion

This paper concludes that the new intent, an adaptive Surf Scale Feature Selection (SSFS) and Sigmoid Recurrent Neural Network Classification (SRNN) for improving the early risk prediction against the covid, has performed the early prediction of COVID – 19 for premature treatment. This method has produced an efficient relational feature analysis for identifying the most rate of disease influence rate. The features are in redundant form to make the importance of real entities belonging to the virus parameters. This relational data help identify important feature dependencies to make delight weightage using prediction rate. The identified features are trained into the feed-forward neural network. The neural network gets a deep activation function to classify the result. This proposed system has produced 98% best performance than the previous methods and recommendation for precautions against covid spreading.

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About the Authors:



Dr. Jagannath Jadhav received his Bachelor degree in Electronics and Communication Engineering, in 2012 and Master of Engineering degree in Communication Systems in 2015 and Ph.D in Engineering in 2020. He is a Renowned Researcher and Global Scientist having 3 Patents published in Indian patent journal and expert reviewer in many journals. He is an Academician, Researcher, Author, Writer, Inventor and Innovator, Scientist (Consultant and Orator). He is pursuing his **Post doctoral fellowship** from **Lincoln University College**, Bharu, Kelantan, **Malaysia** working on **Infection rate of Pandemic disease like covid19**. He was awarded with the **certificate of excellence** in reviewing in recognition of an outstanding contribution to the quality of the International Journal of Environment and Climate Change. He has been awarded with the **BEST RESEARCHER AWARD** on September 5, 2020 on Teacher day by the **GLOBAL EDUCATIONAL AWARD 2020** and has Strong synthesizing, writing, and information technology skills: wrote scientific articles in international peer-reviewed journals, as well as the highly technical replies to the questions raised by the reviewers.



Dr. S.Srinivasa Rao, received the B.Tech degree from Madras Institute of Technology, Anna University, and the M.Tech and Ph.D from JNTU Hyderabad, Telangana, India. Presently working as Professor and Head of the Department at Malla Reddy College of Engineering and Technology, Secunderabad. He has 24 years of experience in the field of teaching. He is a member of professional bodies like IEEE, ISTE and IETE.



Mukil Alagirisamy received her Bachelor degree in Electronics and Communication Engineering, in 2005 and Master of Engineering degree in Communication Systems in 2007 and Ph.D in Engineering in 2012. She completed her PDF in 2015. She started her career as a lecturer at Hindustan Engineering College, India. She was working as an Assistant Professor at B.S. Abdur Rahman University, India. Later she joined as a Lecturer at Stamford College, Malaysia. Currently, she is working as an Associate Professor and Coordinator for Master of Science in Electrical, Electronics and Telecommunication Engineering programs at Lincoln University College, Malaysia. She has 12 years of experience in teaching subjects like Data Communication, Analog and Digital Communications, Digital Signal Processing and Satellite Communications. Her research interests are in Sink mobility patterns, Clustering, Modulation, Data Aggregation and Compressive Sensing Techniques for Wireless Sensor Networks.