ON THE ANALYSIS OF COVID19 - NOVEL CORONA VIRAL DISEASE PANDEMIC SPREAD DATA USING MACHINE LEARNING TECHNIQUES – RREGRESSION AND SIR MODEL

¹Tahera Begum, ²Dr. Y. Ramadevi, ³A. Sangeetha

¹PG Scholar, M.Tech, Dept of CSE, Chaitanya Bharathi Institute of Technology, Hyderabad, TS.

²Professor and Head, Dept of CSE, Chaitanya Bharathi Institute of Technology, Hyderabad, TS.

³Asst Professor, Dept of CSE, Chaitanya Bharathi Institute of Technology, Hyderabad, TS.

staheraghafoori1997@gmail.com, yramadevi_cse@cbit.ac.in, asangeetha_cse@cbit.ac.in

ABSTRACT- Corona virus are the gathering of viruses that cause different illnesses in birds and vertebrates. In humans, they cause a range of respiratory problems. This undertaking project presents the analysis of the transmission of COVID19 sickness and predicts the scale of the pandemic, the recuperation

rate just as the casualty rate. Here utilized a portion of the notable Machine Learning techniques just as numerical modeling strategies, for example, Rough Set-Support Vector Machine (RS-SVM), Polynomial Regression, Bayesian Ridge Regression and SIR model.

1. INTRODUCTION

Viruses are microscopic organisms that reproduce only within a creature's live cells. Coronaviruses are one of the most well-known viral families that cause a variety of respiratory disorders in living beings.

One of the recent challenges has been determining the extent of Covid's distribution. Anticipating the pandemic with great precision will aid various countries in putting together a plan to combat the spread of infection. For modelling real-world situations, machine learning approaches are commonly used [13],

[14]. Machine learning approaches, in particular, have recently been widely used to predict infections [4],[5],[8].

A portion of the customary methods utilized in guaging of a scourge incorporate time arrangement modeling just as regression modeling. We have picked a portion of the customary just as current machine learning techniques. Support Vector Machine technique has been generally utilized for forecasts while we have contrasted a portion of these customary techniques and a cutting edge technique specifically Recurrent Neural Network (RNN). As there is consistently an incredible level of

vulnerability in the expectation of pandemics we have additionally determined the Mean Square Error (MSE) and Mean Absolute Error (MAE) utilizing the Bayesian ridge technique. The utilization of polynomial regression technique was to track down the best connections between the factors present in the information. We have endeavored to tackle the issue of estimating the pandemic of COVID19 utilizing the machine learning methods expressed previously.

The following is a reminder of the paper's structure. Section II summarises the literature study, section III discusses the machine learning algorithms employed, section IV delves into the results, and section V wraps up the work

2. RELATED WORK

Sujatha and Chatterjee (2020) proposed a model that could be useful in predicting the spread of COVID-2019 by using direct regression, Multilayer insight, and Vector auto regression models on the COVID-19 kaggle data to imagine the epidemiological illustration of the disease and the speed at which COVID-2019 cases spread in India. Yang et al. (2020) proposed a dynamic SEIR model to predict the COVID-19 outbreak apexes and sizes. They employed an AI model that was set up on historical SARS datasets and suggests that the scourges are safe in the future. Machine learning systems developed on stomach Computed Tomography images were used by Barstugan et al. (2020) to introduce the beginning phase region of COVID-19, as designated by the World Health Organization (WHO). Elmousalami and Hassanien (2020) use temporal arrangement models and mathematical specification to connect day level checking models on COVID-19 impacted situations. Rizk-Allah and Hassanien (2020) are familiar with another checking model that looks at and measures the CS of COVID-19 for the next few days based on data reported since January 22,

2020. Rezaee et al. (2020) used a hybrid technique that included the Linguistic FMEA, Fuzzy Inference System, and Fuzzy Data Envelopment Analysis model to come up with a score for covering specific insufficiencies and prioritising HSE risks. Navares et al (2018) presented a response for the issue of expecting each day clinical center affirmations in Madrid in view of circulatory and respiratory cases subject to bio meteorological markers. Cui and Singh (2017) made and applied the MRE speculation for month to month stream forecast with otherworldly force as a random variable. Torky and Hassanien (2020) offered a blockchain-based structure that investigates the possibility of utilising blockchain's shared, timetraveling, and decentralised capacity focal points to create a new system for confirming and recognising dark contaminated COVID-19 sickness cases. GSA-DenseNet121-COVID-19 ward on a hybrid CNN structure is proposed by Ezzat and Ella (2020) using an advancement technique.

3. DESIGN AND IMPLEMENTATIONS

We have present the test brings about insight concerning each errand and simultaneously, we have additionally looked at the presentation consequences of our suggested method combines three well-known regression methods: Simple Linear Regression, Polynomial Regression, and Multivariate Regression. The dataset used for the first four errands included the total number of positive cases, recoveries, and deaths from 22/01/2020 (Day 1) to 24/04/2020 (Day 93) in various countries/districts, as well as the name of the country/region and the date. Regardless, region name and absolute positive cases data were used for each of the four assignment dates. Mainland China, the United States, Italy, South

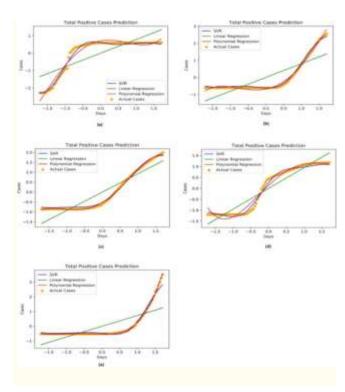
Korea, and India were the primary focus areas for these four projects.

3.1. Predicting the spread of corona virus across regions

The flare-up of Covid-19 is forming into a significant worldwide emergency, and it's beginning to impact significant parts of day by day life. For instance, Bans have been put on area of interest nations, worldwide assembling activities have frequently needed to reduce creation and numerous products exclusively delivered in China have been stopped inside and profoundly influenced out. territories. individuals are beginning to load up on fundamental merchandise. To the point where different regression models were to be used to predict how the virus will spread across various nations and regions in order to predict the total number of positive cases. The fundamental goal of this project was to create and consider regression models that might predict the mobility of all COVID 19 cases from various places, which could aid in the relief of the disease endeavours. The advantage of doing so is that we will have a better idea of the number of cases that will occur, as well as the degree of spread. With this information, the public authority and residents can make legitimate arrangements to deal with the situation by taking measures to limit virus spread through various relief and other basic activities. Anticipating complete number of cases in various areas are show in Fig. 3.

Figure 3 depicts the accuracy of the absolute number of positive cases in Mainland China (a). The expected results for the total number of cases up to day 93 using the Simple Linear Regression approach are 85,492, 73,561 using the Polynomial Regression technique, and 65,795 using the proposed SVR strategy, while the actual number is 68,128. Simple Linear Regression, Polynomial Regression, and SVR

had precision of 62.1 percent, 96.2 percent, and 98.8 percent, respectively.



The total number of positive cases in the United States is shown in Figure 3(b). The expected qualities for the total number of cases up to day 93 using the Simple Linear Regression technique are 1,71,324, 2,95,006 using the Polynomial Regression strategy, and the proposed SVR technique is 2,58,253, though the genuine number was 2,71,590. Simple Linear Regression, Polynomial Regression, and SVR had precision of 65.01 percent, 98.82 percent, and 99.47 percent, respectively. In Figure 3, the total number of expected positive cases in Italy is shown (c). With the Simple Linear Regression method, the expected characteristics for the total number of cases to day 93 are 1,65,154 with the Polynomial Regression technique is 1,85,188 and the proposed SVR technique is 1,83,007, though the real certain cases was 1,92,994. The precision result for Simple Linear Regression, Polynomial

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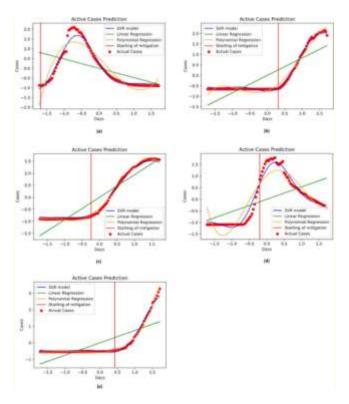
Regression, and SVR were 85.36 %, 99.75 % and 99.41 % separately. The absolute number of positive cases in the South Korean nation is presented Fig 3(d). The expected characteristics for the total number of instances up to day 93 with the Simple Linear Regression technique are 12,733, 10,421 with Polynomial Regression strategy, and 10,266 with the proposed SVR strategy, while the genuine positive cases are 10,718. For Simple Linear Regression Polynomial Regression, and SVR were 90.10 %, 97.28 % and 99.06 % individually The absolute number of positive cases in the Indian nation is plotted in Fig 3(e). Although the real number of positive cases was 24,530, the expected qualities for the absolute number of cases with the Simple Linear Regression strategy is 10,789, with the Polynomial Regression approach is 25,165, and with the proposed SVR strategy is 20,373. Simple Linear Regression, Polynomial Regression, and SVR all had accuracy of 53.04 percent, 99.85 percent, and 98.31 percent, respectively.

3.2. Analysing the growth rates and the types of mitigation across countries

Over the previous few months, various governments have taken various measures to limit the spread of COVID 19. Large gatherings were prohibited, schools were closed, aircraft and other modes of transportation were prohibited, cities were placed under lockdown, and so on. As a result, this work was completed in order to see the consequences of mitigation. The task's major goal was to assess mitigation effectiveness by determining whether there was a link between different methods of mitigation and the rate at which active cases grew. What measures appear to work, which do not, and which are the most successful, for example. Keeping in mind that the rate of growth can be influenced by a variety of country's general (e.g. population density, how much time they had to

prepare for this epidemic before the spread was not much, etc.). Different regression models were used to forecast the number of active cases in a particular location in order to predict how mitigation was affecting the number of active cases across different countries and regions. The purpose of this work is to help us figure out which mitigations are the most effective. The benefit of doing so is that we will have a better idea of how well the mitigations are working, as well as the actions that have been taken thus far, how effective they are, or how many cases have been avoided, and so on. To prepare the dataset for this task, dates were first converted to day numbers, with 22 January 2020 as Day 1 and 24 April 2020 as Day 93. Then, in order of day number, total instances were extracted from each region. The number of current cases was required to calculate growth rates. The total number of deaths and recoveries were subtracted from the total case count day by day to determine the active cases. The day number and active case count were then scaled to provide more precise findings. A linear regression and a polynomial regression model were fitted and shown to the dataset for each impacted country to forecast the number of active cases in that region. The model was fitted with multiple polynomial degrees to see which degree curve suited best in the polynomial regression model. Then, in an urge to seek for better results a proposed SVR model with Radial basis function kernel (RBF) was fitted and visualized to predict the number of active cases in that particular region. The accuracy of each model was then calculated and compared using the Coefficient of Determination to examine how well each model predicted outcomes. Figure 4 depicts the total number of active COVID 19 cases in that region, with the number of active cases on the Y-axis and the number of days on the X-axis. Before using, all of the X-axis and Y-axis values were scaled.

Fig. 4



The increasing rate of the total number of active cases in Mainland China is depicted in Figure 4(a). China has been on complete lockdown since early January, and the total number of active cases in Mainland China is steadily reducing. With the Simple Linear Regression approach, the anticipated values for the total number of instances till day 93 are 1414, while the Polynomial Regression method predicts 6371, with Simple Linear Regression method is 1414, with the Polynomial Regression method is 6371 and the proposed SVR method is 1706, whereas the actual number active cases was 23. The accuracy for Simple Linear Regression, Polynomial Regression, and SVR were 80 %, 85.46 % and 97.01 % respectively. SVR, Polynomial Regression, and Simple Linear Regression all had accuracy of 80%, 85.46 percent, and 97.01 percent, respectively. Figure 4 depicts the rate of increase in the total number of active cases in the United States (b). The United States has chosen a partial lockdown policy rather than a full lockdown, preferring to close

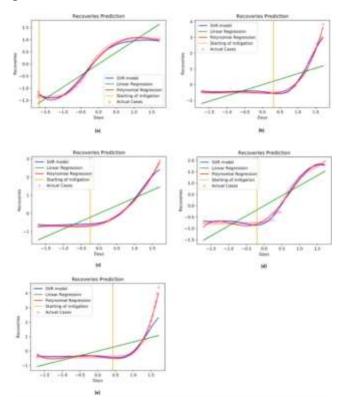
schools and other meeting areas and promote social separation and personal hygiene among individuals (mitigation started around 19th March 2020), and as shown in the figure the total number of active cases of US is not seen to be lowering down. The predicted values for the total number of cases till day 93 with Simple Linear Regression method is 1,22,606, with the Polynomial Regression method is 1,74,969 and the proposed SVR method is 1,56,954, whereas the actual number active cases was 1,51,100. The accuracy for Simple Linear Regression, Polynomial Regression, and SVR were 69.07 %, 97.82 % and 99.46 % respectively. The increasing rate of the total number of active cases in Italy is given in Fig 4(c). Italy went into complete lockdown on March 9, 2020, and the total number of current cases in Italy is not reducing, as shown in this graph. However, the curve has begun to flatten at the top, which is a favourable sign, as the rate of active cases increase has begun to slow. The total number of instances predicted by the Simple Linear Regression technique is 1,08,114, 1,00,262 by the Polynomial Regression method is 1,00,262, and 1,01,910 by the proposed SVR method, however the actual number of active cases is 1,06,527. Simple Linear Regression, Polynomial Regression, and SVR all had accuracy of 87.22%, 99.56%, and 99.51 percent, respectively. Figure 4 depicts the rate of increase in the total number of active cases in South Korea (d). South Korea's lockdown began in early March, and as can be seen in this graph, the total number of active cases in the country is falling at a satisfactory rate The number of active instances on day 93 with the Simple Linear Regression approach is 5270, 2064 with the Polynomial Regression method, and 2200 with the proposed SVR method, however the actual number was accuracy 1843. The of Simple Linear, Polynomial Regression, and SVR was 28.2 percent, 85.3 percent, and 96.76 percent, respectively. From March 24, 2020, India has

been on complete lockdown. Although the total number of active cases in India does not appear to be reducing, despite having such a large population, India's situation is better than that of most other countries. With the Simple Linear Regression approach, the anticipated values for the total number of cases through day 93 are 8733, 19,248 with the Polynomial Regression method, the proposed SVR method is 16,283, whereas the actual number of active cases was 18,252. Simple Linear Regression, Polynomial Regression, and SVR each had accuracy of 55.5 percent, 99.58 percent, and 99.6 percent.

3.3. Predicting how many infected patients will recover

Estimating the number of infected patients who will recover. Because no vaccine for the virus has yet been developed, it's critical to figure out how many patients will recover and when the outbreak will cease. The major goal of this work was to estimate how many people would recover based on previous recovery records. As a result, statistics for the number of recovered patients across different countries were obtained in attempt to forecast how many people will truly recover. The purpose of this work is to assist us figure out how the epidemic will end. In other words, how many patients will be able to recover. The benefit of doing so is that we will be able to estimate the number of people who will recover from the virus using older, wellestablished procedures, as no vaccine or treatment has yet been discovered. We will be able to forecast how long it will take for all of the patients to recover if we can predict how long it will take for the epidemic to stop. To prepare the dataset for this work, the dates were first changed to day numbers, with the 22nd of January 2020 being Day 1 and the 24th of April 2020 being Day 93. Then, in order of day number, the total number of recoveries up to that point were retrieved area by region. The day number and

recovery numbers were then scaled to provide more precise findings. A linear regression and a polynomial regression model were fitted and shown to the dataset for each affected country to predict the number of affected patients who will recover in that region. The model was fitted with multiple polynomial degrees to see which degree curve suited best in the polynomial regression model. Then, in an effort to improve the results. an SVR model with a Radial basis function kernel (RBF) was fitted and visualised to estimate the number of recoveries in that specific location. The accuracy of each model was then calculated and compared using the Coefficient of Determination to examine how well each model predicted outcomes.



4. PROPOSED ALGORITHM

The motivation, as well as a full description of the tasks and proposed approach, are described in this part. COVID 19 is wreaking havoc on individuals, resulting in deaths, misery, and turmoil. Some tasks can be completed in order to examine the impact. These tasks can assist in deciphering and extracting knowledge from COVID 19 data, which can aid a country(region) understanding the virus's spread, facilitating(aware) people, initiating mitigations, determining whether mitigation is having a positive effect, and identifying other factors affecting the virus, among other things. It will assist that country in preparing for what is to come in the near future, thereby saving lives and suffering. The following are the five different activities that were completed in this paper [13]: I) Predicting the corona virus's spread across regions. II) Comparing growth rates and mitigating strategies across countries. III)Predicting the course of the epidemic. IV) Examining the virus's transmission rate. V) Establishing a link between the corona virus and weather conditions. The Support Regression (SVR) model is employed in our proposed work to complete the first four tasks. For the fifth task, Pearson's Correlation [14] is utilised.

5. METHODOLOGIES

5.1MODULES NAME:

In this section, we go over our model in great detail. We begin by summarising the data set collected from the Johns Hopkins Center for Systems Science and Engineering, as well as the preprocessing strategies investigated. Then, we'll go through the machine learning technique for forecasting pandemic spread.

A. Dataset preparation and data preprocessing

The real-time data from the Johns Hopkins Center for Systems Science and Engineering [12] was used in this project. It is the patients' realtime data. The data includes the areas of the express, the country, the scope, the side effects, the longitude, and the number of instances for each day commencing on January 22, 2020. We considered the venture's updated data set through 07/05/2020. The following methods are used for data pre-handling:

- The data was cleansed, and the faulty attributes were replaced using segment averaging.
- To forecast the spread of the pandemic, the data was altered using Python's Standard Scaler object to achieve a Gaussian dispersion.
- To eliminate outliers, the data were standardised using the logarithmic scale.

B. Mathematical modeling using SIR Model

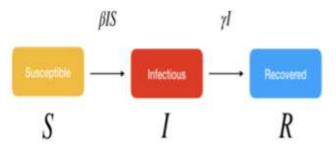


Fig. 1 Block diagram representation of the SIR Model

The SIR Model [3] is a fictitious numerical model designed to predict irreversible illnesses. It is determined using differential condition modelling. The model is depicted diagrammatically in Fig.1 and is described as follows:

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Goal: The model aims to find the relation between the dependent and the independent variable.

Time 't' is regarded as the independent variable. One group considers individuals, whereas the other considers a subset of the population.

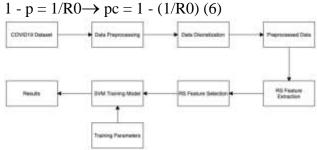
For more precision, we considered a group made up of a subset of the population.

The following is the model's definition: a) Susceptible (S): The person has not received the disease, but she may become infected as a result of transmission from sick people. b) Infected (I): The person has been infected with the disease. b) Recovered/Deceased (R): The disease can result in one of two outcomes: the person either survives and develops immunity to the disease, or the person dies.

- βis a measure that indicates the rate of disease transmission from one individual to another. It is determined by the likelihood of contact and the likelihood of disease transmission.
- \triangleright γ is a metric that describes the pace of recovery over a given time period.
- ➤ People gain immunity when they have been healed. People who die naturally are not taken into account.
- > The number D is considered to indicate the number of days required to recover from the infection. It comes from the word.γ.

R0 is the basic reproduction number of the disease. It gives the average number of people affected by another person. It is used to estimate the Herd Immune Threshold (HID). $ds/dt = -\beta IS$ (1) $di/dt = \beta IS - \gamma I$ (2) $dr/dt = \gamma I$ (3) $D = 1/\gamma$ (4) Balanced state of the disease is obtained by multiplication of the basic reproduction number by the percentage of nonimmune people and is equal to 1. $R0 = \beta/\gamma$ (5) Let the number of immune people be p. Then the stable state of the

pandemic can be represented as: $R0(1 - p) = 1 \rightarrow 1 - p = 1/R0 \rightarrow pc = 1 - (1/R0) (6)$



C. Prediction using RS-SVM

SVM is a traditional machine learning technique that is used for forecasting. The Rough Set (RS) Attribute Reduction SVM was used. To reduce the complexity of SVM, the RS is used as a front preprocessor. This strategy improves forecast precision. The fundamental idea behind the RSbased SVM algorithm is to reduce extra and irrelevant input. The design of the RS-based SVM system used in the experiment is depicted in Fig.2. It uses a heuristic technique and is greedy algorithm. categorised as experiment, Algorithm 1 [3] was utilised. The First Algorithm Reducing Greedy Attributes Algorithm A decision-making mechanism is used as input. R = C E, V, f > DS = U, R = C E, V, f >Output: A DS reduct, marked as Redu 1. P = POSc(E) 2. Put C into array c, put Φ into array Redu 3. K = 0 4. while pos <> k do 5. j = 1 6. for $i \leftarrow 1$ to |c| do 7. ifPOSRedu \cup C[i] [E] 8. K = $POSRedu \cup C[i]$ [E] 9. J = i 10. $Redu = Redu \cup$ c[j] 11. Delete the element c[j] from array c 12. for $i \leftarrow 1$ to |Redu| do 13. if POSRedu - Redu[i](E) = P then 14. Delete the element Redu[i] from array Redu This algorithm works as follows:

- The reduction set is assumed to be vacant.
- Criteria of grouping are set according to the test.
- ➤ The characteristic having the best order capacity is picked.

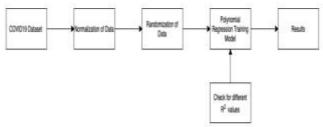
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The test is repeated iteratively until a specified reduction set of qualities is obtained.

D. Prediction based on Polynomial Regression is a type of regression analysis. Polynomial regression is a form of quadratic direct regression [2]. The benefit of using polynomial regression is that it overcomes the dependency between elements that may not be direct [17]. The engineering of the polynomial regression-based system employed in this test is depicted in Fig.3. We employed polynomial regression of the fifth degree. The decision was made to use fifth degree polynomial regression since the bent had the option of appropriately fitting the data. In the fifth - degree polynomial regression prediction, the trade-off between predisposition and change was the smallest. The design of the polynomial regression-based system employed in the investigation is depicted in Fig.3.

E. Prediction utilizing RNN Recurrent Neural Networks (RNN) structure a class of neural network algorithms having an inner memory in each hidden layer[16]. It saves data that has recently been calculated. RNNs are recurrent because they use the same parameters for each cluster of contributions to each hidden layer. The loads and inclinations for each concealed layer are used to process the information sources. When the yield is generated, it is duplicated and resent into the recurrent network. Short-Term Memory Capacity (LSTM)



networks utilize an enhanced version of recurrent neural networks, which makes it simpler to recall past data in memory [15]. We used the LSTM approach to forecast the rate of pandemic casualties. The important advantage of using LSTM is that it is a viable technique for organising, measuring, and forecasting temporal arrangement models with varying slack lengths. The model is trained with help of a back engendering system

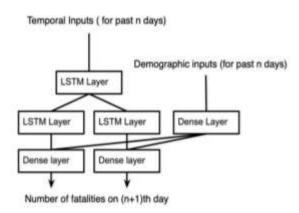


Fig.4 The design of the RNN model utilised in the trial is described in detail. The analysis took into account 5 layers of temporary contributions, as well as 5 layers of demographic data sources. A total of 250 ages were considered in order to improve the prediction's accuracy. The dataset was divided into two parts: a preparation set and a testing set.

F. Computation of MSE and MAE

In our test, calculating Mean Square Error and Mean Absolute Error was critical. The Bayesian estimators were used to forecast the spread of the epidemic. The Bayesian method contains the assumption of earlier dispersion, which aids in minimising the lack of back predicted worth. An assessor is seen as a ludicrous appropriation, and thus serves as the danger work. If there is a decrease in Bayesian danger among all of the estimators in the expectation, the assessor is known as the Bayes assessor. The misfortune work is regarded to be a genuine-valued ability L(, a). 'a' refers to the gauge, whereas " refers to the true worth of the boundary. The most significant advantage of

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ISSN (Print): 2204-0595

ISSN (Online): 2203-1731

using a Bayesian assessor-based technique was that it could be improved as more up-to-date data became available in the database.

5. CONCLUSION

The study in this paper was based on the data set provided by the Johns Hopkins Corona Virus Resource Center. We had communicated one of the most well-known machine learning formulas and were able to achieve extremely good results. Among the machine learning models submitted for the testing, the proposed SIR model was the most effective. The results are useful in anticipating and limiting the spread of any scourges or pandemics for any country or the entire planet. The test in the examination of this data set is that it is always growing and the number of cases is rapidly increasing. A few future works will combine the organisation of traditional machine neural networks with learning approaches.

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