Machine Intelligent Techniques for COVID-19 Detection: A Critical Review and Analysis

Chekuri Sri Sumanth,
Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation, Vaddeswaram, AP, India,
sumanth.chekuri@gmail.com

Rudra Kalyan Nayak,
Department of Computer Science and Engineering, Koneru Lakshmaiah Education Foundation, Vaddeswaram, AP, India,
rudrakalyannayak@gmail.com

2021 12th International Conference on Computing Communication and Networking Technologies (ICCCNT) | 978-1-7281-8595-8/21/$31.00 ©2021 IEEE | DOI: 10.1109/ICCCNT51525.2021.9579858

***Abstract*—Every human being is discussing a highly addressed topic in the current days which is about the COrona VIrus Disease (COVID) in 2019-2020. The outbreak of corona has affected the human race all over the world, the patient count is increasing day by day, and doctors are in a critically need of computer-aided diagnosis with machine learning (ML) algorithms that will discover and diagnose the coronavirus for a large number of patients. Also, it is more complicated to estimate the discharge time and the criticalness of the patient during treatment. Chest computed tomography (CT) scan was the best tool for the corona diagnosis. Also survival analysis methods in ML outperform better in predicting discharge time. In this, we survey on the COVID 19 diagnosis with a chain of CT scan pictures mined from the COVID-19 data set by using ML algorithms like marine predator, simplified suspected infected recovered (SIR), image acquisition, and some more techniques and also survival analysis techniques of ML. The survey clearly explains the models used up to now which are highly defined for the diagnosis of COVID-19 Virus.**

Keywords—COVID-19 Diagnosis, computer-aided diagnosis, Marine Predator, Simplified SIR model, Suspected Infected Recovered (SIR), Image Acquisition.

I. INTRODUCTION

The pandemic situation of the COVID-19 has become the challenge for every doctor and researcher for exploring new techniques to easily diagnose and detect the coronavirus and due to the less possibility of testing there are so many affected people who are not able to get the tests, and also the test results which are conducted now are viral tests. The tests take more time to result to be gotten. Outbreaks lead to vital situation and may increase with the demand of health center beds and a scarcity of scientific system; medical personnel themselves may also get infected. Also these results are done after patients are critically affected with coronavirus. So, there should be some techniques that would be used to detect the virus in the early stages and the tests should be made very fast. Pertaining to these aspects, some techniques are implemented by some authors and one more task which is mostly important for every COVID-19 affected person or to be affected person is that number of days to be taken for diagnosis of virus and also the criticalness of their disease.

Every person with symptoms of corona who would be in quarantine is provided with a specific weekly common schedule. But there are many patients who took months to be recovered; some are recovered within a week. So, there should be methods to diagnose the corona stage in which the patient is in, and also try to share the info of his recovery period for which he or she should be in quarantine at home or in hospital. For this we need survival analysis methods and also discharge time should be analyzed. Techniques like CT scan image analysis is a very well-known approach for diagnosis of coronavirus, as of earlier research severe acute respiratory syndrome (SARS) and COVID-19 [1] comes under one family whereas SARS was detected by CT images [2] and many other methods likewise COVID-19 can also be detected by CT scan Images. ML methods which are having mostly high value in diagnosing COVID-19 are by image processing methods. Compared with the normal imaging techniques that are used heavily on the human body, ML enables more secure, safe, very efficient, and accurate results. In ML image analysis, image classification, image segmentation, and image acquiring are used as the important features for the image descriptions and are used to classify images by tools like support vector machine (SVM) [3], in these image classification ML techniques placed a high performance. Precise some extra mathematical methods in ML approach are used to predict the recovery time and discharge time, where some data should be analyzed after the coronavirus test results by the CT images [4]. In this survey, we are explaining some of the features related to image processing techniques and we are also explaining the tools used for survival analysis.

II. LITERATURE SURVEY

A. Marine Predators Algorithm, Ranking Based Diversity Reduction Strategy [5]

Marine Algorithms were proposed to mimic ideal methods of marine predators in discovering their prey. They utilize the low methodology for the time being while there is low utilization of prey and use the Brownian method for bountiful prey [6]. In the making of chest CT images of 21 corona patients in china [7], researchers is covered that CT clean examination included pneumonic parenchymal ground glass method and also consolidated respiratory reports, once in while with an familiar morphology as well as a fringe lung application. Along these lines, they built up a

calculation that could remove the littler comparative areas that can show diseases with the COVID-19 infection. Numerous division techniques are evolved like area-based division [8], edge-based recognition [9], choice based grouping [10], and edge-based division [11]. The threshold-based segmentation technique is better [12-14] thus; the creators utilized as the primary algorithm. In this work multilevel, optimal thresholds are utilized to develop a well-known multi-level technique, the main one is Kapur's entropy [15], where it decides optimal threshold esteems depend on the entropy in the divide areas. In this, standard marine predators algorithm (MPA), very improved MPA are developed to defeat the multi-threshold picture division issues.

B. Ranking Based Diversity Reduction Technique (RDR) [5]

The authors suggest an algorithm to figure out the successive number of emphasis in which every molecule couldn't recognize a superior arrangement. When distinguishing the unique terrible particles those neglect to locate a superior arrangement inside a back to back number of iterations [16]. The ranking based diversity reduction technique (RDR) makes these atoms to be refreshed with the best arrangement found so far to decrease the good ways from the prime result [17]. In near future, this algorithm can be used in shading picture division methods and also in diverse clinical methods.

C. Simplified Suspected Infected Recovered (SIR) Model [18]

Mathematical approaches have expanded more thought and care in the investigation of illness transmission and also in the medical field [19-20]. One of the mathematical methods is the SIR model [21]. This SIR model was first implemented to examine the plague 100 years back [22]. Colossal development is practiced in the dynamical plague model since the mid-twentieth century [23]. In current decade, some reasonable factors influence pandemic transmission and those are associated with the incomparable SIR model, for instance, this model considers the agonizing stage [24], susceptible exposed infectious recovered susceptible (SEIRS) model follow the general population and age of the diseased [25]. SIR model includes birth and infection days [26]. Highly powerful models will be expected for the unequivocal plague. Consider this example; dynamic models were developed for the control of spreading Human Immunodeficiency Virus (HIV), SARS, and the Middle East Respiratory Syndrome (MERS). In this model SIR and ML methods are pooled with the dynamical prototype and made a deal with the plague gauge [27-29]. For the improvement of SIR model, it needs to choose a couple of key boundaries for instance: the population rate and the departure rate precisely or quantifiably [30]. Nevertheless, the SIR models consider more factors that are needed to be described for more data with additional limits. Of course, in the improved model, some efforts are made. As an example, outstanding key conditions were used as a two-compartment model i.e. susceptible infectious (SI) model that can be moreover called a stochastic technique that is used for SARS detection [31,32]. The authors attempted to introduce a model to predict the pandemic of the 2019-nov depending on the streamlined SIR. The epidemiological info was dissected initially to acquire a sensible assessment of key boundaries whereas disease rate. Contamination and the evacuation rate are zeroing, a few more tests are needed to be done to mimic the spreading of corona under various degrees by hostile to pestilence measuring and clinical consideration.

D. Structured Latent Multi-View Representation Learning [33]

By a computer related clinical assurance, a couple of methodologies subsequently learn request from the models that are reliant of features removed with a pro before [34]. Regardless, some of them are the only mater to a single kind of features beside these lines can't be researched well on the basic information of various types of features. Fortunately, multi-level depiction learning offers gadgets to handle different kinds of heterogeneous features [35]. Existing multi-level depiction learning methods can't give guarantee to the information satisfying and promising the unique structure. This will make them overfit the planning data to hurt the testing stage presentation. Considering this assessment, authors proposed a different framework for rectifying these problems to withstand the standard point to perceive the corona from community acquired pneumonia (CAP). These various sorts of highlights mustn't be legitimately utilized as a contribution for a classifier to yield an official choice [36] in-out technique. The planning test and testing phase both are planned in idle space, where these inert portions are relied upon the correlative data to encode from various kinds of highlights and the promise structure uncovering hidden class circulation. Figure-1 represents the work done in this model.

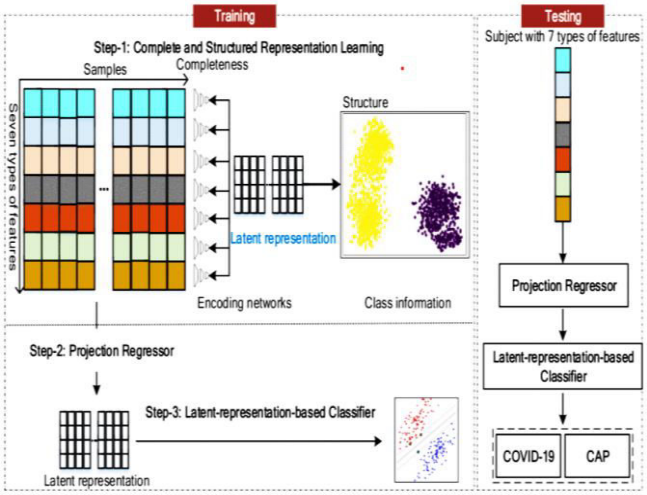

Fig1: Latent-representation-based diagnosis framework. For the input, different colors indicate different types of features, while for the class information yellow and purple indicate COVID-19 and CAP, respectively.

E. Prior Attention Residual Learning [37]

The best multi-task prior-attention model gaining knowledge of approach in the first stage of every COVID-19 scanning CT images. This will relate to some properties:

- A two folded 3D-ResNet based sub-networks are depending on to a mannequin for the detection of pneumonia and group sorting. For sorting purpose characterization is applied as a parallel classifier to find a corona from the interstitial lung detection (ILD) with the other infections. Furthermore, it is also planned for a

double classifier that can force to convey whether a given CT filter conveys pneumonia [38]. Compared with the division techniques or the object detection techniques, the present proposed approach which relies on exclusively order models is very less hard to actualize, because this model requires only the exclusively vulnerable picture level names and also less hyper-boundary in the instructing stage. These styles utilize only the picture level names to attain a secure discernibly sufficient example in a short time.

- Very well inspired with the aid of some current advances of deep interest mechanisms [39-41], basically, by utilizing the self-attention lingering reading for present-day pores and skin injury arrangement [42], Authors had planned a prior attention model from the proposed models. Very numerous works was done [43-45] to get the deep convolutional neural network (DCNN) model instructed in an order to undertake top-notch restriction ability which can highlight the discriminative arrears in a picture with exclusively level marks on a picture. Already there is a model of a sub network that was proposed earlier for recognizing a paired classifier and also for use of CT filters with and aside from pneumonia, for only concentrating on injury data. In this manner, they utilized the various leveled work guides and created a core mind full of delicate intrigue maps. So, at these points, they use these maps to compare layers of the sort characterization of sub-organization to make main focus on the injury parts.
- Compared with residual learning, the proposed model is dealing with the modular design. Prior attention mechanism deals with the residual blocks that are called as Prior-attention residual learning (PARL) blocks. Deep fashions were not a problem because these were built by the staking the PARL blocks and also were skilled end to end.
- Some more problems are like insufficiency in data, inter class similarity, non-lesion areas of images, interclass variation frequently appear in dealing with processing the entire areas of scientific picture [46]. Among these problems the very important problem was non-lesion zones, these are explicitly underneath circumstances in spotting the non-lesion zones in the clinical photographs which have many-sided tissue varieties. The proposed strategy can easily solve this problem by methods for becoming acquainted with fine lesion-mindful intrigue records from the lesion photographs and conventional photographs. In this way, the proposed approach can be moreover used in equivalent inevitabilities in logical practice, for example in pores and skin lesion grouping, chest issue order, glaucoma identification, pneumonic knob location, and their danger forecast [47-49] etc.

F. Weakly Supervised Lesion Localization Learning [50]

Weakly supervised injury localization was an imitation of the mixer of activation areas produced by using the extreme array community i.e., 3D deep convolutional neural network (DeCoVNet) and unsupervised lung segmentation. This technique was demonstrated in the below figure. The right side of the figure was postulant blow areas of DeCoVNet which was obtained by applying category activation mapping (CAM) technique [51]. These areas had already a good holding but still, it made much forged nice predictions. Coming to the left portion they had extracted corona affected regions from unsupervised results of lung segmentation. 3d connected aspect (3DCC) approach was applied to the CT scan [52], they discovered injury areas which had been touchy according to the 3DC algorithm and that could have utilized because of injury localization [53]. To reach the rejoinder map, he thought the variance within a 7 x 7 eyelet hole for every pixel, so the 3DCC activation. So then the 3DCC activation location method is chosen as comparably better and termed as the R3DCC. Finally, the CAM stimulation, which had the largest overlay including R3DCC were once elected as the last corona injury location results. Figure-2 represents walkthrough of weakly supervised lesion localization.

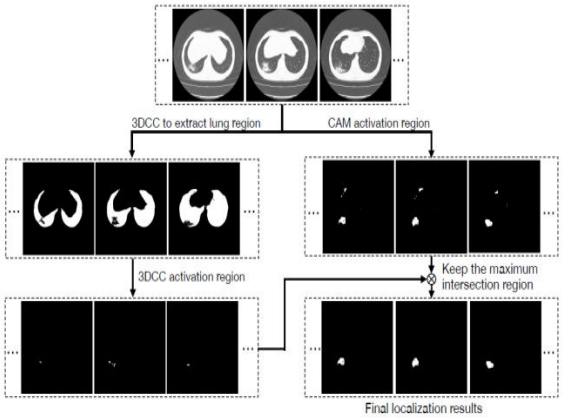

Fig 2: The walkthrough of weakly supervised lesion localization

G. The Regression Analysis Models [54]

The regression analysis model is developed using exponential, quadratic, 3rd, 4th, 5th, 6th degrees, and also exponential polynomials for corona prediction within the coming seven days. This method is based primarily on North American country and also our government for following the seven days plans. This analysis could be one of ML algorithms [55-56]. This analysis consists of a group of ML algorithm strategies that are enabled in North American countries to forecast a nonstop outcome variable (B) supported the worth of 1 or more variables (A), A is predicted variable [57]. There is a relation between the result and the predicted values, which had taken into the account equation where A and B variables are stated mathematically as

$$B=iA + j \quad (1)$$

Where, i= block on the A axis, j= slant on the line

Here i, j are the regression analysis constraints. The authors have proposed 6 regression analysis type models such as exponential, quadratic, 3rd, 4th, 5th, 6th degree polynomials. These models are equationaly declared below.

$$B=iA^2 + jA \quad (2)$$

$$B= iA^2+jA+ k \quad (3)$$

$$B= iA^3 + jA^2 + kA + l \quad (4)$$

$$B= iA^4 + jA^3 + kA^2 + lA + m \quad (5)$$

$$B= iA^5 + jA^4 + kA^3 + lA^2 + mA + n \quad (6)$$

$$B=iA^6 + jA^5 + kA^4 + lA^3 + mA^2 + n + o \quad (7)$$

Where, i, j, k, l, m, n and o are the regression analysis parameters.

Findings and drawbacks of different literatures pertaining to COVID-19 detection is elaborated in Table-1.

TABLE1: TAKEOUTS FROM VARIOUS LITERATURES CONCERNING DIFFERENT TECHNIQUES FOR COVID-19 DETECTION

Year of Publication	Journal/ Conference Name	Authors	Title of the Journal/ Conference	Methodology	Dataset Description	Findings	Drawbacks
2020	*IEEE Access*	Mohamed Elhoseny, Ripon K. Chakrabortty, Mohamed Abdel-Basset, Reda Mohamed and Michael Ryan	A Hybrid COVID-19 Detection Model Using an Improved Marine Predators Algorithm and a Ranking-Based Diversity Reduction Strategy [5]	(IMPA) for X-Ray image segmentation (RDR)	5 X-ray images	COVID-19 Detection using X-Ray images based on marine predators algorithm (IMPA) and also used Ranking-Based Diversity Reduction Technique (RDR) values are paralleled with five state-of-art algorithms	The proposed algorithm is applied for X-ray can be applied to color image segmentation.
2020	*IEEE Access*	Linhao Zhong, Jiaying Darong Liu, Lin Mu Jing Li, Wang, Zhe Yin,	Early Prediction of the 2019 Novel Coronavirus Outbreak in Mainland China Based on Simple Mathematical Model [18]	Simplified SIR model Suspected Infected Recovered (SIR)	Wuhan, Hubei, China infected data set	The author has collected data set from the differed data sets from the WHO and predicted the no of cases that will be increased in the coming months by using a simplified SIR model, by calculating the mean value with the data sets collected	Data was collected only from one country, and also less accuracy
2020	*IEEE Transactions On Medical Imaging,*	Fuhua Yan, Dinggang Shen, Feng Shi, Huan Yuan, Zhibin Wan, Huiting Jiang, Dijia Wu, He Sui, Hengyuan Kang, Liming Xia, Changqing Zhang.	Diagnosis of Coronavirus Disease 2019 (COVID-19) with Structured Latent Multi-View Representation Learning [31]	latent representation classifier, structured representation learning	2522 CT images from Chinese Centers for Disease Control and Prevention (CDC)	From the CT images, they had automatic diagnosed the disease by using the projection regression, latent representation classifier, structured representation learning. Also compared the results with the Gaussian-Naive-Bayes (GNB), SVM, Logistic Regression (LR), and Neural Networks (NN), K-Nearest Neighbors (KNN) in terms of accuracy, sensitivity and specificity, respectively.	Diagnosis performance is done with an accuracy of 95.5%. May be data collected from the clinical patients and has to use more classifications.
2020	*IEEE Transactions On Medical Imaging, 2020*	Yaofeng Wen, Hongbing Lu, Hu Luo, Yunfei Xiang, Xiaoming Li, Chen Liu, and Dahong Qian, Jun Wang, Yiming Bao,	Prior-Attention Residual Learning for More Discriminative COVID-19 Screening in CT Images [37]	(PARL) Prior-attention residual learning block		The author has developed a multi-tasking learning strategy of the CT scan images whether they are affected with corona or other lung diseases. Parl block model is a combination of two models.	In the future, more predictions to be done to find in early stages
2020	*IEEE Transactions On Medical Imaging, 2020*	Qing Fu, Qiang Zhou, Jiapei Feng, Hui Ma, Wenyu Liu, and Chuansheng Zheng, Xinggang Wang, Xianbo Deng,	A Weakly-supervised Framework for COVID-19 Classification and Lesion Localization from Chest CT [50]	Image Acquisition Weakly supervised Lesion Localization	CT scans from 540 patients of (Union Hospital, Tongji Medical College,	The excellent framework to find the real positive cases by using CT scan, for that they used 3D deep convolutional neural network to detect DeCoVNet from CT scans, and also results are compared with deep learning classifiers	Data was collected and calculated on very less patients.
2020	*Springer*	Ramjeet Singh Yadav	Data analysis of COVID-2019 epidemic using machine learning methods: a case study of India [54]	Regression Analysis	COVID_19 Data set	The author analyzed the data with creating the 6 different polynomials are exponential, quadratic, 3^{rd}, 4^{th}, 5^{th}, 6^{th} degree using the regression analysis model.	Data analysis can be done more effectively by using other models.
2020	*IEEE Transactions On Computational Social Systems,*	Xiao Wang, Jun Zhang , Tao Wang, Tian-Lu Gao, Wei Duan, Kelvin Kam-fai Tsoi, Lifang Li,	Characterizing the Propagation of Situational Information in Social Media During COVID-19 Epidemic	Weibo data and natural language processing techniques	Sina Weibo (the Chinese equivalent of Twitter)	Identify and categorize the data upon the situational information and predicting the different types of situational information from the weibo. They used	No drawbacks, but data can be collected with other keywords.

		Qingpeng Zhang , and Fei-Yue Wang	[59]			cohen's kappa value calculator and SVM, NB, RF classifiers.	
2020	*IEEE OJEMB*	Tanya Talkar, and Jeffrey S. Palmer, Thomas F. Quatieri,	A Framework for Biomarkers of COVID-19 Based on Coordination of Speech-Production Subsystems [60]	Voice Frequency, time-varying loudness, phonation, aspiration	Audio data for 5 subjects was obtained from YouTube, Instagram, and Twitter sources:	The author has collected data from the audio files and computed the biomarkers from the vocal of corona patients through speech production involving respiration, phonation, and articulation. Justified that the corona will affect the respiratory function at the symptomatic stage.	Used only fewer data and not tested in real-time. There should be a diagnostic of the patents rather than this framework.
2020	*Springer*	Virginia Dignum, Paul Davidsson, Amineh Ghorbani, Mijke van der Hurk, Maarten Jensen, Christian Kammler, Frank Dignum, Fabian Lorig, Luis Gustavo Ludesche,	Analysing the Combined Health, Social and Economic Impacts of the Coronavirus Pandemic Using Agent-Based Social Simulation [61]	ASSOCC (Agent-based Social Simulation for the COVID-19 Crisis)	-	The author has analyzed the corona pandemic daily and also analyzed how it is spreading, what are measures to be taken by government, and also explained the tool like ASSOCC to predict the corona. The authors developed a NetLogo simulation for the agent movement.	Results are not calculated and the priority was not mentioned clearly
2020	*IEEE Access*	Rhys Leahy, Nicholas Johnson Restrepo, Sara El Oud, Nicholas Gabriel, Yonatan Lupu, And Neil F. Johnson, Richard F. Sear, Nicolás Velásquez,	Quantifying COVID-19 Content in the Online Health Opinion War Using Machine Learning [62]		Facebook	The online anti-vax community creating many disturbances about the COVID-19, so in this authors has created a model which predicts the unwanted and replace with the correct data step by step	More data should be tested in the other social community applications with large data set.
2020	*The New England Journal Of Medicine.*	Peng wu, Xuhua Guan, Xiaoye Wang.	Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia [63].	Laboratory Testing Statistical Analysis Ethics Approval	Covid-19 Data set from NICP	Collected information from the first effected people and analyzed the early transmission dynamics in Wuhan and china. Age of most effected people is 59 years.	--
2020	*JAMA Network 2020.*	Jennifer M McGoogan, Zunyou Wu,	Characteristics of and Important Lessons From the Coronavirus Disease 2019 (COVID-19) Outbreak in China [64]		WHO reports	It's a Report of 72 314 Cases From the china by age, fatality, spectrum, Also Evaluation of COVID-19 With SARS and MERS and given info to the government.	--
2020	*Proceedings Of The National Academy Of Sciences*	DowdJB, Andriano L, Brazel DM.	Demographic science aids in understanding the spread and fatality rates of COVID-19 [65]	Demographic Science and COVID-19 Policy	Itally population data,	Described the ages and fatality rate of the population affected by the corona virus. and also explained about the spread of the virus in ages. Population over 65 ages is more effected.	Data should be collected from all the ages and also from other countries also.
2017	*Computational And Structural Biotechnology Journal*	Konstantinos P Exarchos, Michalis V Karamouzis, Dimitrios I Fotiadis, Konstantina Kourou, Themis P Exarchos,	Machine Learning Applications in Cancer Prognosis and Prediction [66]	Holdout method, Random Sampling, Cross-Validation, Bootstrap	Cancer Dataset	Based at the analysis in their consequences, it is evident that the mixing of multidimensional heterogeneous statistics, mixed with the software of different strategies for function choice and class can provide promising gear	Result accuracy has to be increased

						for inference inside the most cancers area.	
2010	*International Journal Of Ayurveda Research*	Manish Kumar Goel, Praddep Khanna and Jugal Kishore	survival analysis: Kaplan-Meier estimate [67]	Kaplan Meier Estimator, Log-rank test, ox proportional hazard model	Survival Analysis	Kaplan-Meier method is a useful method that may play a significant role in generating evidence-based information on survival time.	The results should be compared with other survival analysis also.
2014	*Biostatistics*	Mittal Sushil, Madigan D,Burd RS, Suchard MA	High-dimensional, massive sample-size Cox proportional hazards regression for survival analysis. [68]	Cox survival analysis models	Dataset contains patient records of injured children aged <15	Through the experiments, they demonstrated that, with the advantage of becoming at once on HDMSS records, we are able to attain models that have higher predictive accuracy and calibration.	No Drawbacks
2013	*Computational And Mathematical Methods In Medicine*	Chen Y, Jia Z, Mercola D, Xie X.	A gradient boosting algorithm for survival analysis via direct optimization of Concordance index. [69]	(Stochastic) gradient boosting machine for concordance index learning (GBMCI).	Large breast cancer dataset	GBMCI consistently performs better than three state-of-the-art survival models (the Cox PH model, its boosting enlargement, and the random survival woodland) over several function representations.	This study also illustrates the importance of feature engineering of clinical and gene expression data in cancer prognosis studies.
2008	*8th IEEE International Conference On Data Mining*	Khan FM, Zubek VB	Support vector regression for censored data (SVRc): a novel tool for survival analysis. [70]	support vector regression, Cox proportional hazards		Compared with the conventional Cox model, SVRc achieves tremendous improvement in average accuracy in addition to within the capability to discover excessive-hazard and low-danger affected person populations.	Results are not accurate.
2020	*Nature Public Health Emergency Collection - Intensive Care Med*	Qiurong Ruan, Kun Yang, Wenxia Wang,Lingyu Jiang, Jianxin Son	Clinical predictors of mortality due to COVID-19 based on an analysis of data of 150 patients from Wuhan, China [71]	Means (SDs) or as medians (IQRs) or the Mann–Whitney–Wilcoxon test.	Covid-19 Data set	Predictors of a deadly outcome in COVID-19 instances covered age, the presence of underlying sicknesses, the presence of secondary infection, and improved inflammatory indicators inside the blood. The outcomes obtained from this have a look at also suggest that COVID-19 mortality might be due to virus-activated "cytokine hurricane syndrome" or fulminant myocarditis.	

III. PROPOSED MODEL

After reviewing all these models and theories, for detecting COVID-19 there should be the best model and that model will be used in the proposed model and also using statistical analysis of COVID-19 patients, we will get the Discharge summary time. This will be helpful for doctors and mankind. Figure-3 explains our proposed workflow of how we use the models to detect corona and also discharge time.

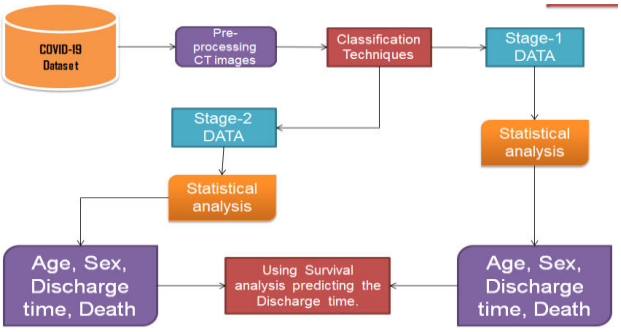

Fig 3: The walkthrough of COVID-19 Detection and Discharge time likelihood Stratagy

IV. CONCLUSION AND FUTURE DIRECTIONS

This paper explained different models and algorithms which are used to detect COVID-19 and also for the diagnosis of COVID-19. Different models are surveyed in this paper such as MPA, RDR, SIR model, regression analysis, PARL,[5,18,33,37,50,54] latent representation classifier, etc. Each model has its own advantage, but it is observed that latent representation classifier and structured representation learning model outperformed other models. It detects the coronavirus very efficiently as compared to other models in terms of efficiency and dynamic result.

In the area of machine learning, many models were already implemented to detect and analyze the corona virus. It will be very useful if we embed two or more models with proper compatibility to the dataset and other clinical parameters to get even better results while detecting COVID 19. Ultimately it will be very helpful for the human race. [64] We can develop a model with a generic strategy that can detect, expect and also guess the state of COVID 19 in a short span of time during this pandemic situation.

REFERENCES

[1] Hosseini M. S. and Zekri M., "Review of medical image classification using the adaptive neuro-fuzzy inference system", in Journal of medical signals and sensors, vol. 2, p. 49, 2012. pmid:23493054.

[2] Quek C., Irawan W., and Ng E., "A novel brain-inspired neural cognitive approach to SARS thermal image analysis", in Expert Systems with Applications, vol. 37, pp. 3040–3054, 2010.

[3] Narasinga Rao, M. R., Sajana, T., Bhavana, N., Sai Ram, M., & Nikhil Krishna, C. (2018). "Prediction of chronic kidney disease using machine learning technique", in Journal of Advanced Research in Dynamical and Control Systems, 10, 328-332. Retrieved from www.scopus.com

[4] Siva Kumar, P., Sarvani, V., Prudhvi Raj, P., Suma, K., & Nandu, D. (2017). "Prediction of heart disease using multiple regression analysis and support vector machines" in Journal of Advanced Research in Dynamical and Control Systems, 9(18 Special Issue), 675-682. Retrieved from *www.scopus.com*

[5] Mohamed Abdel-Basset, Reda Mohamed , Mohamed Elhoseny, Ripon K. Chakrabortty, And Michael Ryan "A Hybrid COVID-19 Detection Model Using an Improved Marine Predators Algorithm and a Ranking-Based Diversity Reduction Strategy" in IEEE access April 28, 2020.

[6] Faramarzi, M. Heidarinejad, S. Mirjalili, and A. H. Gandomi, "Marine predators algorithm: A nature-inspired Metaheuristic", in Expert Syst. Appl., vol. 152, Aug. 2020, Art. no. 113377.

[7] S. Guan, Z. B. Lv, S. Yan, Y. N. Du, H. Chen, L. G.Wei, R. M. Xie, and B. D. Chen, "Imaging features of coronavirus disease 2019 (COVID-19): Evaluation on thin-section CT", in Acad. Radiol., vol. 27, no. 5, pp. 609_613, May 2020.

[8] Aksac, T. Ozyer, and R. Alhajj, "Complex networks driven salient region detection based on superpixel segmentation", in Pattern Recognit, vol. 66, pp. 268_279, Jun. 2017.

[9] P. Prathusha and S. Jyothi, "A Novel edge detection algorithm for fast and efficient image segmentation", in Data Engineering and Intelligent Computing. Singapore: Springer, 2018, pp. 283_291.

[10] N. Narayanan, R. C. Hardie, T. M. Kebede, and M. J. Sprague, "Optimized feature selection-based clustering approach for computer-aided detection of lung nodules in different modalities", in Pattern Anal. Appl., vol. 22, no. 2, pp. 559_571, Oct. 2017.

[11] J. Han, C. Yang, X. Zhou, and W. Gui, "A new multi-threshold image segmentation approach using state transition algorithm", in Appl. Math. Model., vol. 44, pp. 588_601, Apr. 2017.

[12] J. Kuruvilla, D. Sukumaran, A. Sankar, and S. P Joy, "A review on image processing and image segmentation", in Proc. Int. Conf. Data Mining Adv. Comput. (SAPIENCE), Mar. 2016, pp. 198_203.

[13] Oliva, E. Cuevas, G. Pajares, D. Zaldivar, and V. Osuna, "A multilevel thresholding algorithm using electromagnetism optimization, in Neurocomputing, vol. 139, pp. 357_381, Sep. 2014.

[14] S. Arora, J. Acharya, A. Verma, and P. K. Panigrahi, "Multilevel thresholding for image segmentation through a fast statistical recursive algorithm", in Pattern Recognit.Lett.,vol.29,no.2, pp.119_125,Jan. 2008.

[15] J. N. Kapur, P. K. Sahoo, and A. K. C. Wong, "A new method for gray-level picture thresholding using the entropy of the histogram, in Comput". Vis., Graph., Image Process., vol. 29, no.1,p. 140, Jan. 1985.

[16] Rajesh, N., Maneesha, T., Hafeez, S., & Krishna, H. (2018). "Prediction of heart disease using machine learning algorithms". International Journal of Engineering and Technology(UAE), 7(2.32 Special Issue 32), 363-366. Retrieved from www.scopus.com

[17] Razia, S., & Narasingarao, M. R. (2017). "A neuro computing frame work for thyroid disease diagnosis using machine learning techniques." in Journal of Theoretical and Applied Information Technology, 95(9), 1996-2005. Retrieved from www.scopus.com

[18] Linhao Zhong, Lin Mu Jing Li, Jiaying Wang, Zhe Yin And Darong Liu, "Early Prediction of the 2019 Novel Coronavirus Outbreak in Mainland China Based on Simple Mathematical Model", in IEEE ACCESS Digital Object Identifier 10.1109/ACCESS.2020.

[19] R. M. Anderson, "The pandemic of antibiotic resistance", in Nature Med.,vol. 5, pp. 147_149, Feb. 1999.

[20] J. Koopman, "Modeling infection transmission", in Annu. Rev. PublicHealth, vol. 25, pp. 303_326, Apr. 2004.

[21] S. A. Levin, B. Grenfell, A. Hastings, and A. S. Perelson, "Mathematical and computational challenges in population biology and ecosystems science", in Science, vol. 275, pp. 334-343, Jan. 1997.

[22] T. W. Ng, G. Turinici, and A. Danchin, "A double epidemic model for the SARS propagation", in BMC Infectious Diseases, vol. 3, p. 19, Sep. 2003.

[23] W. O. Kermack and G. Anderson McKendrick, "Contributions to the mathematical theory of epidemics 1927", in Bull. Math. Biol., vol. 53, pp. 33_55, Jan. 1991.

[24] N. T. J. Baily, "The Mathematical Theory of Infectious Disease", in 2nd ed. New York, NY, USA: Hafner, 1975.

[25] R. R. Tang, "The singularly perturbed boundary value problem of the non-linear integro differential system", in Ann. Differ. Equ., vol. 4, pp. 407_412,Dec. 2004.

[26] M. Iannelli, M. Martcheva, and X. Z. Li, "Strain replacement in an epidemic model with super-infection and perfect vaccination", in Math. Biosci.,vol. 195, no. 1, pp. 23_46, 2005.

[27] J. Liu, Y. Tang, and Z. R. Yang, "The spread of disease with birth and death on networks", in J. Stat. Mech., Theory Exp., vol. 2004, no. 8, 2004, Art. no. P08008.

[28] Pradeepini, G., Pradeepa, G., Tejanagasri, B., & Gorrepati, S. H. (2018). "Data classification and personal care management system by machine learning approach." In International Journal of Engineering and Technology(UAE), 7(2.32 Special Issue 32), 219-223. doi:10.22444/IBVS.6227_old

[29] Benvenuto D, Marta G, Lazzaro V, Silvia A, Massimo C (2020) "Application of the ARIMA model on the COVID-2019 epidemic dataset". Data in brief 105340. MedRxiv. https://www.medrxiv.org/content/ 10.1101/2020.03.26.20044511v1

[30] Dye., C. Epidemiology: Modeling the SARS Epidemic. Science, 2003, vol. 300, no. 5627, pp. 1884_1885.

[31] Hengyuan Kang, Liming Xia, Fuhua Yan, Zhibin Wan, Feng Shi, Huan Yuan, Huiting Jiang, Dijia Wu, He Sui, Changqing Zhang, and Dinggang Shen, "Diagnosis of Coronavirus Disease 2019 (COVID-19) with Structured Latent Multi-View Representation Learning, in IEEE transactions on medical imaging", 2020 VOLUME 8, 2020, Page no 5176, Digital Object Identifier 10.1109/ACCESS.2020.2979599

[32] Ayushree; Arora, Sandeep Kumar, "Comparative Analysis Of Aodv And Dsdv Using Machine Learning Approach In Manet", in Journal Of Engineering Science And Technology, published on December 2017, Volume no 12, Issue no 12, Page no 3315-3328.

[33] Yingming Li, Ming Yang, Zhongfei (Mark) Zhang, Senior Member, IEEE "A Survey of Multi-View Representation Learning", in Journal Of Latex Class Files, Vol. 14, NO. 8, AUGUST 2015

[34] Watts and S. H. Strogatz, "Collective dynamics of `small-world' networks", in Nature, vol. 393, no. 6684 pp. 440_442, 1998.

[35] R. Pastor-Satorras and A. Vespignani, "Epidemic spreading in scale-free networks", in Phys. Rev. Lett., vol. 86, pp. 3200_3203, Apr. 2001.

[36] R. Zhang, Y. Zheng, T. W. C. Mak, R. Yu, S. H. Wong, J. Y. Lau, and C. C. Poon, "Automatic detection and classification of colorectal

polyps by transferring low-level CNN features from nonmedical domain", in IEEE journal of biomedical and health informatics, vol. 21, no. 1, pp. 41–47, 2016.

[37] Jun Wang, Yiming Bao, Yaofeng Wen, Hongbing Lu, Hu Luo, Yunfei Xiang, Xiaoming Li, Chen Liu, and Dahong Qian, "Prior-Attention Residual Learning for More Discriminative COVID-19 Screening in CT Images", IEEE Transactions On Medical Imaging 2020, VOL. 39, NO. 8, AUGUST 2020.

[38] Bashir, AK; Arul, R; Basheer, S; Raja, G; Jayaraman, R; Qureshi, NMF, "An optimal multitier resource allocation of cloud RAN in 5G using machine learning", in Transactions On Emerging Telecommunications Technologies, Aug 2019, D.o.i: 10.1002/ett.3627

[39] Wang, M. Jiang, C. Qian, S. Yang, and C. Li. "Residual attention network for image classification", in Proc. IEEE Conf. Comput. Vis. Pattern Recognition, Honolulu, HI, USA, 2017, pp. 6450-6458.

[40] J. Hu, L. Shen, S. Albanie, G. Sun, and E. Wu. "Squeeze-and-excitation networks", [Online]. Available: arXiv:1709.01507v4

[41] L. Chen, H. zhang, J. Xiao, L. Nie, J. Shao, W. Liu, and T. Chua. "SCA-CNN: spatial and channel-wise attention in convolutional networks for image captioning", in Proc. IEEE Conf. Comput. Vis. Pattern Recognition, Honolulu, HI, USA, 2017, pp. 6298-6306.

[42] J. Zhang, Y. Xie, Y. Xia, and C. Shen. "Attention residual learning for skin lesion classification", in IEEE Trans. Med. Imag., vol 38, no. 9, pp. 2092-2103, 2019.

[43] B. Zhou, A. Khosla, A. Lapedriza, A. Oliva, and A. Torralba. "Learning Deep Features for Discriminative Localization". in Proc. IEEE Conf. Comput. Vis. Pattern Recognit., 2016, pp. 2921-2929.

[44] R. R. Selvaraju, M. Cogswell, A. Das, R. Vedantam, D. Parikh, and D. batra. "Grad-CAM: Visual explanations from deep networks via gradient-based localization", in Proc. IEEE Int. Conf. Comput. Vis., 2017, pp. 618-626.

[45] R. Tripathy, R.K. Nayak, P. Das and D. Mishra , "Cellular cholesterol prediction of mammalian ATP-binding cassette (ABC) proteins based on Fuzzy C-Means with Support Vector Machine algorithms" in Journal of Intelligent & Fuzzy Systems, Vol. 38:3, No. 12, pp.1-8, IOS Press Publication, ISSN: 1064-1246 (Print), ISSN: 1875-8967 (Electronic), 2020, DOI: 10.3233/JIFS-179934.

[46] Q. Guan, Y. Huang, Z. Zhong, Z. Zheng, L. Zheng, and Y. Yang. "Diagnose like a radiologist: attention guided convolutional neural network for thorax disease classification", in [Online]. Available: arXiv:1801.09927v1.

[47] L. Li, H. Liu, Y. Li, X. Wang, L. Jiang, Z. Wang, X. Fan, and N. Wang. "A large-scale database and a CNN model for attention-based glaucoma detection", in IEEE Trans. Med. Imag., vol 39, no. 2, pp. 413-424, 2020.

[48] J. Wang, J. Wang, Y. Wen, H. Lu, T. Niu, J. Pan, and D. Qian. "Pulmonary nodule detection in volumetric chest CT scans using CNNs-based nodule-size-adaptive detection and classification", in IEEE Access Deep Learning for Computer-aided Medical Diagnosis , Pg no 46033 – 46044, DOI: 10.1109/ACCESS.2019.2908195

[49] J. Wang, X. Chen, H. Lu, L. Zhang, J. Pan, Y. Bao, J. Su, and D. Qian. "Feature-shared adaptive-boost deep learning for invasiveness classification of pulmonary subsolid nodules in CT images", in Med. Phys., 2020. [Online]. Available: https://aapm.onlinelibrary.wiley.com/doi/10.1002/mp.14068.

[50] Xinggang Wang, Xianbo Deng, Qing Fu, Qiang Zhou, Jiapei Feng, Hui Ma, Wenyu Liu, and Chuansheng Zheng, "A Weakly-supervised Framework for COVID-19 Classification and Lesion Localization from Chest CT," Ieee Transactions On Medical Imaging, 2017, Page(s): 2615 – 2625, DOI: 10.1109/TMI.2020.2995965.

[51] B. Zhou, A. Khosla, L. A., A. Oliva, and A. Torralba, "Learning Deep Features for Discriminative Localization." in CVPR, IEEE Access 2016.

[52] Liao, M. Liang, Z. Li, X. Hu, and S. Song, "Evaluate the malignancy of pulmonary nodules using the 3-d deep leaky noisy-or network", in IEEE transactions on neural networks and learning systems, vol. 30, no. 11, pp. 3484–3495, 2019.

[53] Sajana, T., & Narasingarao, M. R. (2018). "A comparative study on imbalanced malaria disease diagnosis using machine learning techniques". Journal of Advanced Research in Dynamical and Control Systems, 10, 552-561. *Retrieved from www.scopus.com.*

[54] Ramjeet Singh Yadav, "Data analysis of COVID-2019 epidemic using machine learning methods: a case study of India", Springer, *https://doi.org/10.1007/s41870-020-00484-y*, 19 May 2020.

[55] Ting DSW, Lawrence C, Victor D, Wong TY (2020) "Digital technology and COVID-19", in Nat Med 26:459–461. *https://doi.org/10.1038/s41591-020-0824-5*

[56] Benvenuto D, Marta G, Lazzaro V, Silvia A, Massimo C (2020) "Application of the ARIMA model on the COVID-2019 epidemic dataset" in Data in brief 105340.MedRxiv. *https://www.medrxiv.org/content/10.1101/2020.03.26.20044511v1*

[57] Bommadevara, H. S. A., Sowmya, Y., & Pradeepini, G. (2019). "Heart disease prediction using machine learning algorithms", in International Journal of Innovative Technology and Exploring Engineering, 8(5), 270-272. Retrieved from *www.scopus.com*

[58] Anila, M., & Pradeepini, G. (2018). "Least square regression for prediction problems in machine learning using R", in International Journal of Engineering and Technology(UAE), 7(3.12 Special Issue 12), 960-962. doi:10.14419/ijet.v7i3.12305

[59] Lifang Li, Qingpeng Zhang , Xiao Wang, Jun Zhang , Tao Wang, Tian-Lu Gao, Wei Duan, Kelvin Kam-fai Tsoi, and Fei-Yue Wang, "Characterizing the Propagation of Situational Information in Social Media During COVID-19 Epidemic", in IEEE Transactions On Computational Social Systems, Volume: 7 , Issue: 2 , April 2020, Page(s): 556 – 562, DOI: 10.1109/TCSS.2020.2980007

[60] Tanya Talkar, and Jeffrey S. Palmer, Thomas F. Quatieri, "A Framework for Biomarkers of COVID-19 Based on Coordination of Speech-Production Subsystems", in IEEE Open Journal of Engineering in Medicine and Biology (Volume: 1), Page(s): 203 – 206.

[61] Frank Dignum, Virginia Dignum, Paul Davidsson, Amineh Ghorbani, Mijke van der Hurk, Maarten Jensen, Christian Kammler, Fabian Lorig, Luis Gustavo Ludesche, Alexander Melchior, René Mellema, Cezara Pastrav, Loïs Vanhee, "Harko Verhagen Analysing the Combined Health, Social and Economic Impacts of the Corovanvirus Pandemic Using Agent-Based Social Simulation", in Springer, Pg no 177-194(2020).

[62] Richard F. Sear, Nicolás Velásquez, Rhys Leahy, Nicholas Johnson Restrepo, Sara El Oud, Nicholas Gabriel, Yonatan Lupu, And Neil F. Johnson, "Quantifying COVID-19 Content in the Online Health Opinion War Using Machine Learning", in IEEE Access Digital Object Identifier 10.1109/Access.2020, Page(s): 91886 – 91893

[63] Peng wu, Xuhua Guan, Xiaoye Wang, "Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia", in The New England Journal Of Medicine, 382:1199-1207 DOI: 10.1056/NEJMoa2001316.

[64] Zunyou Wu, Jennifer M McGoogan, "Characteristics of and Important Lessons from the Coronavirus Disease 2019 (COVID-19) Outbreak in China", JAMA Network 2020, Pg no; 323(13):1239-1242. doi:10.1001/jama.2020.2648.

[65] DowdJB, Andriano L, Brazel DM, "Demographic science aids in understanding the spread and fatality rates of COVID-19", Proceedings Of The National Academy Of Sciences, 117 (18) 9696-9698, *https://doi.org/10.1073/pnas.2004911117*.

[66] Konstantina Kourou, Themis P Exarchos, Konstantinos P Exarchos, Michalis V Karamouzis, Dimitrios I Fotiadis, "Machine Learning Applications in Cancer Prognosis and Prediction" in Computational And Structural Biotechnology Journal, Volume 13, 2015, Pages 8-17.

[67] Manish Kumar Goel, Praddep Khanna and Jugal Kishore, "survival analysis: Kaplan-Meier estimate", in International Journal Of Ayurveda Research, pg 274–278, doi: 10.4103/0974-7788.76794.

[68] Mittal Sushil, Madigan D,Burd RS, Suchard MA, "High-dimensional, massive sample-size Cox proportional hazards regression for survival analysis", in Biostatistics Volume 15, Issue 2, April 2014, Pages 207–221, *https://doi.org/10.1093/biostatistics/kxt043*

[69] Chen Y, Jia Z, Mercola D, Xie X. "A gradient boosting algorithm for survival analysis via direct optimization of Concordance index in Computational And Mathematical Methods In Medicine",Volume 2013 |Article D 873595 | *https://doi.org/10.1155/2013/873595*

[70] Khan FM, Zubek VB "Support vector regression for censored data (SVRc): a novel tool for survival analysis", in 8th IEEE International Conference On Data Mining, December 2008, DOI: 10.1109/ICDM.2008.50

[71] Qiurong Ruan, Kun Yang, Wenxia Wang,Lingyu Jiang, Jianxin Son, "Clinical predictors of mortality due to COVID-19 based on an analysis of data of 150 patients from Wuhan, China", in Nature Public Health Emergency Collection - Intensive Care Med, 2020 May;46(5):846-848, doi: 10.1007/s00134-020-05991-x.