R. Anandan · G. Suseendran ·
Pushpita Chatterjee ·
Noor Zaman Jhanjhi ·
Uttam Ghosh *Editors*

How COVID-19 is Accelerating the Digital Revolution

Challenges and Opportunities

Springer

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ISBN 978-3-030-98166-2 ISBN 978-3-030-98167-9 (eBook)
https://doi.org/10.1007/978-3-030-98167-9

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The registered company address is: Gewerbestrasse 11, 6330 Cham, Switzerland

Preface

It is our immense pleasure to put forth this book *How COVID-19 is Accelerating the Digital Revolution: Challenges and Opportunities*. The objective of this book is to adopt advancements of knowledge and help disseminate results concerning recent applications and case studies in the areas of digital revolution post COVID-19 among working professionals and professionals in education and research, covering a broad cross section of technical disciplines.

This book explores how digital technologies have proved to be a useful and necessary tool to help ensure that local and regional governments on the frontline of the emergency can continue to provide essential public services during the COVID-19 crisis. Indeed, as the demand for digital technologies grows, local and regional governments are increasingly committed to improving the lives of their citizens under the principles of privacy, freedom of expression, and democracy.

The digital revolution refers to the advancement of technology from analog electronic and mechanical devices to the digital technology available today. The era started during the 1980s and is ongoing. The digital revolution also marks the beginning of the Information Era. In 1980 started with the Internet and after with mobile devices, social networking, big data, and computing clouds, revolutionized to block chain Technology.

Due to the COVID-19 pandemic, Internet-based services are making up for the losses. E-commerce, web-based securities trade, viewership of videos and sports events, and videoconferences on social media are on the rise. In line with the government's push for more cashless transactions, most people urge smartphone electronic payment services. Smartphone-based payments are becoming popular among people, who do not want to touch cash because of the pandemic, and the tools to support teleworking, such as videoconference software, have seen their shares rise by nearly twofold since before the coronavirus outbreak.

These confronted with the COVID-19 crisis, are trying to radically change their business models and the ways their employees work. The COVID-19 outbreak has indeed given them a chance to put their teleworking plans into practice. Online services need to be expanded not just in business practices but in public areas such as healthcare, education, and administrative services—which were previously deemed to necessitate face-to-face interactions. It is a big step forward that, due to concern over mass COVID-19 infections at hospitals, doctors are now allowed to see first-time patients online. Universities have so far rigorously required their students to physically attend classes, but now they are conducting online classes more flexibly. Because of the COVID-19 pandemic, new-generation technology has huge potential to promote digitization. It features communications speed 10 times faster than the prevalent LTE standard, and delays will be reduced to one tenth.

That will enable the remote operation of machines and devices on a real-time basis, as well as rapid transmission of ultrahigh-resolution images. The new communications network will enhance and improve videoconferencing, remote education, and remote medical services. This book focuses on the digital revolution post COVID-19 pandemic.

We extend our appreciation to many of our colleagues. We extend our sincere thanks to all experts for giving preparatory comments in the book that will surely motivate the reader to study the topic. We also wish to thank the reviewers who dedicated time to review this book.

We are very much grateful to our family members for their patience, encouragement, and understanding. Special thanks are also due to many individuals at Springer who have contributed their talents and efforts in bringing out this book in present format.

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Acknowledgments

We would like to express our thanks to Almighty Allah SWT for all his blessings, and our great appreciation to all of those we have had the pleasure to work with during this project. The completion of this project could not have been accomplished without their support. First, the editors would like to express deep and sincere gratitude to all the authors who shared their ideas, expertise, and experience by submitting chapters to this book and adhering to its timeline. Second, the editors wish to acknowledge the extraordinary contributions of the reviewers for their valuable and constructive suggestions and recommendations to improve the quality, coherence, and content presentation of chapters. Most of the authors also served as referees. Their willingness to give time so generously is highly appreciated. Finally, our heartfelt gratitude goes to our family members and friends for their love, prayers, caring, and sacrifices in completing this project well in time.

We dedicate this book to our best friend, and one of the editors Late, Dr. G. Suseendran. We lost him recently during the current COVID-19 pandemic.

Taylor's University, Subang Jaya, Selangor Malaysia
Director Center for Smart Society 5.0 [CSS5.0]
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About the Editors

R. Anandan completed his UG, PG, and Doctorate in computer science and engineering.

He is IBMS/390 Mainframe professional and is recognized as Chartered Engineer from Institution of Engineers in India and has received fellowship from Bose Science Society, India. He has completed seven certification courses, mainly from CISCO. Dr. Anandan is currently working as a professor and head of the Department of Computer Science and Engineering, School of Engineering and Associate Director – Innovation and Incubation, Vels Institute of Science, Technology & Advanced Studies (VISTAS), Chennai, Tamil Nadu, India, which is a pioneer institution in engineering. He has vast experience in the corporate field and at all levels of academics in computer science and engineering. His interests are not limited to artificial intelligence, soft computing, machine learning, high performance computing, big data analytics, image processing, 3D printing, and knowledge engineering. Under his eminent guidance, eight PhD research scholars are pursuing their studies. Three PhD research scholars have been awarded under his guidance and supervision. He is a member of many reputed international and national societies, such as the International Association of Engineers (IAENG), Hong Kong; Computer Science Teacher Association (CSTA), New York; Universal Association of Computer and Electronics Engineers, USA; Association of Computer Sciences and Information Technology (IACSIT), Singapore; Institution of Engineers, India; Computer Society of India; and Indian Society of Technical

Education (I.S.T.E.). He serves as editorial board member/technical committee member/reviewer of international journals by publishers such as Springer, Thomson Reuters, SCI, and Elsevier. Dr. Anandan serves as international committee member for international conferences conducted in association with Springer and Scopus. He has published more than 130 research papers in various international journals covered by Scopus and SCI, and also in refereed journals. He has presented 76 papers at various international conferences. Dr. Anandan received best reviewer award for the year 2017–2018 from the *International Arab Journal of Information Technology* (SCI Journal) under Elsevier Publication, the Netherlands, and the reviewer of the year award 2018–2019 from Energy Review Elsevier Publication, Amsterdam, the Netherlands. He received an appreciation award on Teachers' Day towards publication of articles for the academic year 2017–2018. He is recipient of the awards Dr. APJ ABDUL KALAM Best Scientist Award for Computer Science Engineering from BOSE Science Society, Tamil Nadu, India; Distinguished Researcher in Artificial Intelligence Award by Research under Literal Access Awards, India; Outstanding Scientist award by International Research Awards on Engineering, Science and Management; Award for excellence in Young Researcher in Computer Science Engineering by Global Outreach Research, New Delhi, India; Distinguished Professor Award by Vedant Academics Bangkok Awards – 2019 during International Award Conference on Multi-Disciplinary Research and Application held in Kasetsart University, Chatuchak, Bangkok, Thailand; and the Achievers Icon Award 2020 in the category Innovative Educator in Computer Science and Engineering by Band Opus India Pvt. Ltd. He has authored and edited 16 books, and some of his leading books are *Software Engineering*, *Advanced Java Programming*, *Functions of Hardware and Internet*, *Bigdata and Hadoop Beginners Guide for OOPS Concepts in Java Programming*, *Web Technology*, *Statistics with R Programming*, *Information Security*, *Artificial Intelligence*, and *A Closer look at Bigdata Analytics*. He filed has 9 patents of his work. He is also associated as editor with Wiley, World Scientific Press, and Nova Publishers.

G. Suseendran received his MSc in information technology and MPhil from Annamalai University, Tamil Nadu, India, and PhD in information technology-mathematics from Presidency College, University of Madras, Tamil Nadu, India. As an additional qualification, he has obtained DOEACC "O" Level AICTE from the Ministry of Information Technology and Honors Diploma in Computer Programming. He was working as an assistant professor in the Department of Information Technology, School of Computing Sciences, Vels Institute of Science, Technology & Advanced Studies (VISTAS), Chennai, Tamil Nadu, India, which is a well-known university. Dr. Suseendran has 10 years of teaching experience in both UG and PG levels. His research interests include wireless senor network, ad-hoc networks, IoT, data mining, cloud computing, image processing, knowledge-based systems, and web information exploration. He has produced for MPhil scholars and 6 PhD research scholars.

He has published more than 90 research papers in various International Journal such in Science Citation Index, IEEE Access, Springer Book Chapter, Scopus, and UGC referred journals. Dr. Suseendran has presented 20 papers in various international conferences. He has authored or edited 14 books (CRC Press and Springer) and received 6 awards. He has been awarded globally as top reviewer by Publons (Web of Science).

Pushpita Chatterjee is a postdoctoral research consultant at Tennessee State University, Nashville, TN, USA, since 2021. Prior to joining TSU, she was a research associate with Old Dominion University, VA, from 2016 to 2018, and worked as a senior research lead at SRM Institute of Science and Technology (a Unit of SRM University, Chennai), Bangalore, India. Dr. Chatterjee received her PhD from the Indian Institute of Technology Kharagpur, India, in 2012. She received her MTech in computer engineering and MS in computer and information science from the University of Calcutta in 2004 and 2002, respectively. She has more than 50 papers with more than 400 citations to her credit in international journals, conferences, and books. She is actively reviewing papers of tier-1 conferences and IEEE Transactions and Elsevier journals. Her research interests include energy-aware computing, machine learning, distributed and trust computing, wireless networks, and software-defined networking.

She is co-editing two books with Springer and Elsevier in the field of cybersecurity and serving as a guest editor for special issues with Elsevier Computers & Electrical Engineering, Hindawi Wireless Communications and Mobile Computing, and TechScience Press.

Noor Zaman Jhanjhi [NZ Jhanjhi] is currently working as associate professor, director of the Center for Smart Society 5.0 [CSS5], and cluster head of the cybersecurity cluster in the School of Computer Science and Engineering, Faculty of Innovation and Technology, Taylor's University, Malaysia. He is supervising a great number of postgraduate students, mainly in cybersecurity for data science. The cybersecurity research cluster has extensive research collaborations globally with several institutions and professionals. Dr. Jhanjhi is associate editor and editorial assistant board for several reputable journals, including *IEEE Access Journal*, *PeerJ Computer Science*, and *PC*, member for several IEEE conferences worldwide, and guest editor for reputed indexed journals. Dr. Jhanjhi is active reviewer for a series of top-tier journals and has been recognized globally as a top 1% reviewer by Publons (Web of Science). He has been awarded as Outstanding Associate Editor by *IEEE Access* for the year 2020. Dr. Jhanjhi has high indexed publications in WoS/ISI/SCI/Scopus, and his collective research impact factor is more than 350 points as of the first half of 2021. He has international patents to his credit and has edited or authored more than 30 research books published by world-class publishers. He has great experience supervising and co-supervising postgraduate students. An ample number of PhD and master's students graduated under his supervision. He is an external PhD/master's thesis examiner/evaluator for several universities globally. He has completed more than 22 internationally funded research successfully. Dr. Jhanjhi has served as keynote speaker for several international conferences, presented several webinars worldwide, and chaired international conference sessions. His research areas include cybersecurity, IoT security, wireless security, data science, software engineering, and UAVs.

Uttam Ghosh joined Meharry Medical College as Associate Professor of Cybersecurity in the School of Applied Computational Sciences in January 2022. Earlier, he worked as an assistant professor of the practice in the Department of Computer Science at Vanderbilt University, where he was awarded the 2018–2019 Junior Faculty Teaching Fellow (JFTF). Dr. Ghosh obtained his Master of Science and doctorate in electronics and electrical communication engineering from the Indian Institute of Technology (IIT) Kharagpur, India, in 2009 and 2013, respectively. He has postdoctoral research experience at the University of Illinois in Urbana-Champaign, Fordham University, and Tennessee State University.

Dr. Ghosh has published more than 80 papers in reputed international journals by IEEE Transactions, Elsevier, Springer, IET, Wiley, InderScience, and IETE, and also in top international conferences sponsored by IEEE, ACM, and Springer. He has coedited and published three books: *Internet of Things and Secure Smart Environments*, *Machine Intelligence and Data Analytics for Sustainable Future Smart Cities*, and *Efficient Data Handling for Massive Internet of Medical Things*.

Dr. Ghosh has conducted several sessions and workshops related to cyberphysical systems (CPS), SDN, IoT, and smart cities as co-chair at top international conferences including IEEE GLOBECOM 2020-2021, IEEE MASS 2020, SECON 2019–20, CPSCOM 2019, and ICDCS 2017. He has also served as a technical program committee (TPC) member at renowned international conferences. Dr. Ghosh is associate editor of *Human-Centric Computing and Information Sciences* and the *International Journal of Computers and Applications*. He is also a reviewer for international journals by IEEE Transactions, Elsevier, Springer, and Wiley. He serves as a guest editor for special issues with *IEEE Sensors*, *IEEE Transaction on Industrial Informatics* (TII), *IEEE Journal of Health Informatics* (JBHI), *IEEE Transaction on Network Science and Engineering* (TNSE), *ACM Transactions on Internet Technology* (TOIT), *Elsevier Computers & Electrical Engineering*, *Computer Communications*, *Springer Cluster Computing*, *Multimedia Tools and Applications* (MTAP), *Wiley Internet Technology Letters* (ITL), *MDPI Sensors*, and *Future Internet*. Dr. Ghosh is co-editing five books on smart IoT, security, and data analysis with CRC Press and Springer. He is a senior member of IEEE and a member of ACM and Sigma-Xi.

Editorial Advisory Board

Chapter 1
Impact of Early Termination of Lockdown and Maintaining Social Distancing: COVID-19

Syed Muzamil Basha, J. Janet, S. Balakrishnan, Sajeev Ram, Somula Ramasubbareddy, and N. Ch. Sriman Narayana Iyengar

Abstract A novel corona-virus named COVID-19 has spread rapidly and has caused a global outbreak of respiratory illness. It has been confirmed that the bats are the source host of SARS, and camels act as a source for MERS. However, the source host of the COVID-19 remains unknown. All three kinds of pneumonia show human-to-human transmissions. Among which, COVID-19 shows a longer incubation period. The routes for the human to human transmission are common, respiratory droplets, contact, and aerosol. In which, the new form is Aerosol transmission. In which, integration of the air with droplets will occur during transmission that leads to the formation of Droplet Nucleus. It can lead to infection after inhalation. Because of this, the virus has already spread to South Korea, Japan, Iran, Italy, and other countries. The objective of this chapter is to address the impact and list the suggestion to handle COVID-19 safely. The methodology followed in drafting this chapter is to provide answers to the following questions: Q1: The clinical manifestation of COVID-19? Q2: How to prevent the transmission of this disease and protect themselves? Q3: The outcome of COVID-19 pneumonia. Q4: How to diagnose COVID-19? Q5: The effects of COVID-19 pneumonia on pregnancy: Q6: Coronavirus pneumonia in children. Q7: The response strategies against the COVID-19 in China. Q8: Therapeutic Strategy for COVID-19. Q9: Consequences

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_1

of COVID-19 in Human Daily Life. Q10: How to deal with the novel Coronavirus disease calmly? Q11: The COVID-19 prevention among students. Q12: Plan to return to the campus. Q13: Home-based self-care in climacteric women Q14: Strategies to climacteric women's psychological problems during COVID-19 pandemic. The outcome of the present research is to provide suggestions to the humankind towards handling the epidemic safely.

Keywords COVID-19 · SARS · MERS · Pregnancy · Climacteric woman

1.1 Introduction

Coronavirus consists of a core of genetic material surrounded by an envelope with protons spikes. It can cause severe Acute Respiratory Syndrome. The sudden attack of COVID-19 is related to people both in China and to the whole world. Before COVID-19, our human beings have suffered from SARS and MERS. Coronavirus is a kind of single and the positive strand RNA is coated by the envelope with the corolla-like spikes. All Coronavirus belong to the Beta genera. They are different in their diameters. The receptor of the SARS and the Novel Coronavirus are the same, which is ACE2, and to the MERS is CD26. The overall number of infected people around the world is 8427 for SARS, 1135 for MERS, and 105,335 for COVID-19. As for the death toll, it's 919 for SARS, 427 for MERS, and 3587 for COVID-19. Hubei province of China is the most serious province of the epidemic. The methodology followed in drafting this chapter is to provide answers to the following questions: Q1: The clinical manifestation of COVID-19? Q2: How to prevent the transmission of this disease and protect themselves? Q3: The outcome of COVID-19 pneumonia. Q4: How to diagnose COVID-19? Q5: The effects of COVID-19 pneumonia on pregnancy: Q6: Coronavirus pneumonia in children. Q7: The response strategies against the COVID-19 in China. Q8: Therapeutic Strategy for COVID-19. Q9: Consequences of COVID-19 in Human Daily Life. Q10: How to deal with the novel Coronavirus disease calmly? Q11: The COVID-19 prevention among students. Q12: Plan to return to the campus. Q13: Home-based self-care in climacteric women Q14: Strategies to climacteric women's psychological problems during COVID-19 pandemic. The outcome of the present research is to provide suggestions to the humankind towards handling the epidemic safely.

The organization of the paper is as follows: In methodology section, the questioner formed is answered from the literature review made on impact of COVID-19 on human life style. In conclusion section, the inference obtained from the study made is included along with the future scope.

1.2 Methodology

The diseases have spread from sick people to others in close contacts including family members, health workers staff, and the people who're living, studying, traveling together, etc. The COVID-19 is an infectious disease. It could spread from person to person through two main methods.

1. The droplets produced when an infected person speaks, cough, or sneeze.
2. Through Close contacts.

Q1: How about the clinical manifestation of COVID-19? [1]

Three kinds of pneumonia have quite similar in nature clinical importance. Fever at different degrees, fatigue, and dry cough. When SARS patients show the continuous high fever, severe and critical COVID-19 patients have moderate a lower fever, even not a fever at all. Severe patients usually can develop to an RTS rapidly. Laboratory test of these three kinds of pneumonia is almost the same, which is in line with the characteristic of the virus infection. Routine blood tests usually show normal or decreased white blood cells. Decrease the lymphocyte, increased the CRP, and also increased in creatinine, LDH, muscle enzyme, and the myoglobin. Nucleic acid testing is applied as the gold standard for diagnosis. Samples include the nasopharynx swab, sputum, lower respiratory secretions, blood, and the feces. In severe patients, doctors may also detect progressively decreased lymphocytes, increase the troponin, D-dimer and the inflammatory factors such as the Interleukin 6. The imaging features of these three kinds of pneumonia? This is the dynamic imaging of a SARS patient. At Day 3, things are onset, small Ground-Glass Opacity (GGO) image could be observed in the lung. At Day 9, multiple GGO images in both two lungs, together with the crazy paving sign. At Day 20, multiple large GGO images in both lungs, and on Day 25, we can see consolidation image, and it developed into a white lung in the end. Imaging of MERS shows the several features that lack the exudation GGO, and also consolidation imaging. Imaging features of COVID-19 can be divided into three stages; early-stage, progressing stage, and the severe stage. At the early stage, lesions are atypical, which makes it as easy to miss, thus we should pay more attention.

Treatment of three kinds of pneumonia is the same basically. The first is to determine the treatment site. Severe and critical patients will be automated by the intense care unit. Secondly, common treatment contains bed rest, support, biochemical monitoring, suitable oxygen therapy, antiviral treatment, and the anti-bacterial treatment. The third part is the treatment of severe and critical patients. Apart from treating basic disease and preventing complications, one should also pay attention to the prevention of the secondary infection organ support, which is partial to the respiratory and circulatory system. There is no specific medication for the virus and as a treatment is a supportive care. There is no vaccine to protect against this virus. Treatment and vaccines are still in development. The symptoms could range from mild to severe. There can be fewer respiratory symptoms such as cough and shortness of breath or diarrhea. In severe cases, there are difficulty breathing, kidney failure, hypoxemia, even cause death. COVID-19 can be diagnosed by a history of epidemiology, clinical manifestation, and the lab test. Common signs of COVID-19 include mild to severe respiratory illness with a fever, cough, and shortness of breath. In more severe cases, infections can cause pneumonia, severe acute respiratory syndrome, kidney failure, heart failure, central nervous problems, and even death. So far, the global number of the reported cases of COVID-19 has surpassed 100,000 more, including about 80,000 in China and over 28,000 outside of China, including 100 countries/areas.

Different ways to deactivate the corona virus:

1. Thirty minutes in 56 centigrade can effectively deactivate viruses.
2. Using suitable disinfectants such as the Ether, 75 percentage, the ethanol can inactive the virus.

Different countries responded differently depending on whether they had zero cases, sporadic ones, clusters, or widespread transmission. Wuhan, the center of the coronavirus outbreak has been totally locked down to contain in the spread of COVID-19.

***Q2: How do we prevent the transmission of this disease and protect themselves?* [2, 3]**

1. Have to make the regular hand washing with soaped water or alcohol-based hand rub.
2. Covering mouth and nose when coughing and sneezing.
3. The choice and appropriate to use the mask.
4. Open your door, window to improve the air circulation.
5. To reduce out of the activities, and stay at home.
6. Having a fever, cough, and difficulty in breathing, please go to the hospital, seek medical care earlier, and share your previous travel history with your health provider.

Most of them even after contracted with virus have no clinical symptoms, due to their strong immune system [4]. In most of the cases, the immune system is not aware enough to keep the balance. To do so, everyone needs to cooperate with their immune system to protect themselves from the viral infection [5, 6]. To boost the strength of the immune system, healthy lifestyle is most important [7].

At present, according to the clinical features and the radiographic imaging, patients with COVID-19 pneumonia have three stages.

1. Early-stage, generally, patients have mild symptoms, and the radiographic features are simple. Include small patch GGO later and the nodule in the single lung or both lungs.
2. The disease progresses, the patient's symptoms have further gravitated. And the radiographic features a variety and follows multiple GGO or consolidation in bilateral mattery, halo sign, or reversed halo sign around the nodule. And we can say sub-segmental atelectasis, pulmonary fibrosis formation.

3. In the advanced stage, the patient's respiratory function decrease obviously and there can be a white lung. And there may be a lot of pulmonary fibrosis formation. All of these are typical imaging features of COVID-19 pneumonia.

Q3: The outcome of COVID-19 pneumonia. **[8]**

Lesion reduce, density decrease, GGO completely absorbed all within a short period of time, it developed into a fibrous cord shadow. The only way it develops for better and then that is the result of most patients. If the disease deteriorates it will turn into a white lung in only a very few patients.

Q4: How to diagnose Coronavirus disease in 2019 (COVID-19). **[9]**

There are four points we need to understand for this COVID-19:

1. The latent period for this COVID-19 is usually like 3–7 days. Need to pay attention for 14 days for one patient, whether the victim is infected with the disease (or) not.
2. Need to do a blood routine test to pay attention to white blood cell number and the lymphocytes number.
3. Clinical manifestation is imaging features. To do CT scanning to see whether the patient's lung has some change like Ground-Glass Opacity or patchy shadow.

To make a decision whether this patient is a suspected case or is completely not COVID-19. So there are two or three types of tests we needed to know.

1. First one is nucleic acid by RT-PCR to find whether she has or he has COVID-19 nucleic acids.
2. Get samples from throat swabs or blood to do a nucleic acid test. Use the same symbol to do genetic sequencing. To find some homologous with no COVID-19 sequence.
3. The antibody, either it is an IgM or IgG antibody. In early stage, it should be IgM, but in a recovery stage, natural stage, it should be IgG.

But compared with the nucleic acids or genetic sequencing, the antibody is not so acute. Sometimes it has high false-positive results. It's hard to make a final decision. There are four types of classes

1. The silent infection: The patient is infected with the COVID-19 but the symptoms are very slight or without any symptoms, imaging manifestation of his abnormal chest.
2. Mild pneumonia: That means the patient's condition is fine. Having a fever, respiratory symptoms, and also in lung, some imaging changes like the ground-glass opacity.
3. The third type is a severe one, which means the disease condition is slowly progressive to bad. So except the fever, except the blood tests that changed, except the CT scanning changes.

Either one of three types of these. The first one is you have increased respiratory rate, your respiratory rate is more than the 30 times per minute or you have hypoxia, without any oxygen therapy, the pulse oxygen sensuality should be less than 93%. The third one is the ratio of arterial oxygen pressure with inspiration oxygen less than 300-mm mercury.

4. Critical cases: Need to be transferred to ICU to get an enhanced treatment.

- Have respiratory failure, need to get mechanical ventilation.
- Blood pressure is very low.

Combined with multi-organ failure (heart, kidney, and some important organ)

Q5: The effects of COVID-19 pneumonia on pregnancy. **[10]**

Infective fever during the second trimester, it could lead to a two-fold increase in the incidence of autism in infants. COVID-19 is a newly discovered virus. So it is worth further exploration of what short-term and long term effects the infective fever could have on infants. Two, the effect of pregnancy on COVID-19 pneumonia.

1. In principle, the weight gain will slow down after the second trimester. It is recommended to work around at home.
2. Measure blood pressure twice a day and make a record. For diabetes and gestational diabetes, regular blood glucose monitoring can also do at home.
3. Count fetal movement.

Fetal movement is reduced under intrauterine hypoxia, counting fetal movement can help identify fetuses with intrauterine hypoxia. The fetal movement is not less than six times within two hours, otherwise, fetal movements are considered reduced. Reasonable medical consultation, seek medical attention having any simple terms of discomfort such as nausea, headache, fetal movement reducing. The principle of X-ray and CT examination is basically the same and their effects on the fetus are related to the gestational week. At the early embryonic development, high dose exposure above 1 gray is fatal to the embryo. Radiation doses received at 8 to 15 weeks of pregnancy have the greatest impact on the fetus's central nervous system.

Q6: Coronavirus pneumonia in children. **[11]**

From the clinical characteristics of the children, fever and the cough are common. Some children and neonatal cases may have typical symptoms, manifested as gastrointestinal symptoms such as vomiting and diarrhea, or only manifested as a poor response and shortness of breath. Most cases of children significantly milder recover faster, and the prognosis is good. Critical cases often have an underlying disease or multiple infections. From the lab test, blood routine and the CRP tests, observe children's leukocyte, and the absolute lymphocyte counts are mostly normal.

Children with underlying lung disease should pay attention to the identification of new lesions based on the original imaging. The stages of disease process are as follows:

1. Early-stage: Localized lesions, sub-segmental or segmental patchy shadows and ground glass shadows distributed under the pleura, with or without thickening of the lobular septum.

2. Progression stage: The lesions increase, the scope expands, multiple lung lobes are involved, and some lesions become consolidated, which can coexist with ground glass shadow or strip shadow.
3. Severe stage: It is a diffuse lesion of the lung, mainly with consolidation, and the few are "white lungs", the whole lung involve showing bronchial air signs. Pleural effusion and pneumothorax are rare.
4. During the recovery stage: The absorption of the original lesion improves for the diagnosis and the clinical typing.

The characteristics of existing childhood infection cases are as follows:

Type of Case	List of symptoms
Asymptomatic infection [12]	No clinical signs and symptoms
Mild infection [13]	Fever, Fatigue, Myalgia, Cough, Sore Throat, Runny nose, and Sneezing
Common infection [14]	Frequent fever or cough, mostly dry cough, followed by sputum cough, some may have wheezing
Severe infection[15]	fever and the cough

For the standard of severe infection, there are five points.

1. Shortness of breath: Different ages, have different Respirator Rate (RR), if the baby less than two months of age, RR is more than or equal to 60 per minute, 2–12 months of age, RR is more than or equal to 50 per minute. One to five years old, RR is more than or equal to 40 per minute. If the baby is more then five years old, the respiratory rate is more than or equal to 30 per minute, but you should remember, you must, except for the effects of fever and crying.
2. Oxygen saturation less or equal to 92% at rest.
3. Assisted breathing: Find the groaning, wing flaps, triple concave sign, cyanosis, intermittent apnea.
4. Lethargy and the convulsions.
5. Refuse to feed or feeding difficulties, with signs of dehydration.

Q7: The response strategies against the COVID-19 in China. **[16]**

Late in December 2019 several local health facilities reported a cluster of patients with pneumonia of unknown cause in which initially was linked to the seafood wholesale market in Wuhan Hubei Province, China. This disease named COVID-19 by WHO was declared as a global public health concern after spreading in China and outside of China. As of March 5th 2020, the total number of confirmed cases of COVID-19 in China has exceeded 80,000. And cumulative confirmed cases outside of China have reached more than 15,000.

While there was a downward trend in China, there has been a gradual increase outside of China with the majority of reports from Korea, Japan, and Italy. Starting from February 25th, the daily confirmed cases of COVID-19 outside of China have exceeded as a number of cases in China. This means that China is now under trip pressure control of the COVID-19 spread within China resumed production and control introduction or imported cases from outside of China.

There are three key components of an epidemic:

1. Source of infection
2. Transmission and
3. Susceptible cases

COVID-19 is neither SARS nor murmurs, no influence, it's a new virus with its own unique string characteristics. Unlike SARS, which only confirmed cases as a main source of infection. Asymptomatic individuals also play a role in the COVID-19 virus spread. Some studies have also confirmed that patients in the incubation period are infectious. These two distinctive features of transmission during the incubation period as well as during the asymptomatic stage greatly increase the risk of COVID-19 spread in a community.

The main route COVID-19 transmission where droplets and the format during unprotected close contacts between infectors and susceptible. The aerosol road is potential transmission way, in aerosol-generating procedures, which are conducted in healthcare facilities.

There have been reports of positive various testing in the faces of confirmed cases, and newborns or mother diagnosed with COVID in China. Therefore, focal-oral and mother-fetus routes also potential transmission ways, this means, transmission routes of COVID-19 may be more complex than that of SARS. So based on the epidemiology characteristics observed in China, everyone is susceptible as to the present no waxing for prevention and no specific antiviral agent available for COVID-19.

So, understanding this main features of COVID-19 epidemics non-pharmacologic public house measure applications should be the key strategies to contain the COVID-19 spread. The overall strategies of National Emergency Response against the COVID-19 in China were Target and control of the source of infection, block transmission, and prevent further spread and protect us acceptable. For the purpose of controlling the source of infection and management, a series of policies were made around five early. That means early identification, early report, early isolation, early diagnosis, and early treatment. Reason two months period, six editions of guideline for prevention under control seven editions of national clinical guidelines were released.

These guidelines provide a clear definition of confirmed cases, clinical diagnosis cases, suspected cases, and simple terms. And also optimized the procedures so case confirmation, in addition to this, the board action imposed on separating Wuhan and its surroundings starting January 23rd, 2020. Has effectively prevented further spread of the disease to the rest of the country.

The novel PCR diagnostic tools were developed for early and quick diagnosis of cases. Fewer clinics with men task early identification of suspected cases have made significant contributions. More hospitals were mainly designated for early as a relation of cases and the early treatment. On top of this Chinese integration of COVID-19 is a national infectious disease information system has helped the dissemination of up-to-date information.

And coordinate intervention throughout the country, besides the five early strategies other joint strategies were applied to interrupter the chains of transmission and protectors acceptable. Including suspension or public gathering, disinfection of public places with dense population and the strings and personal protection practice of the general public and healthcare provider. And also strong epidemiology investigations were being carried out for cases clusters and context to identify the source of infection and implement targeted control measures such as contact tracing.

Q8: Therapeutic Strategy for COVID-19. **[17]**

General treatment includes taking enough rest, having balanced nutrition, guaranteed calories, and staying hydrated, and so on. Vital signs especially blood pressure should be monitored. Stem Cell Transplantation, Convalescent Plasma Therapy and Lung Transplantation are the new strategies for dealing with COVID-19.

Q9: Consequences of COVID-19 in Human Daily Life. **[18]**

1. At the beginning of the epidemic, individuals hoarded a large amount of food in their houses in case of food shortage. As a spring festival came to an end, it is understandable that some people were afraid of returning to the workplace.
2. The medical staff has experienced excessive fatigue, anxiety, insomnia, decompression, and they may deeply blame themselves in the face of the death of patients infected with coronavirus.
3. Healthcare providers on the frontline of the fight against coronavirus are facing the risk of being infected, worrying about their families, and refusing to take a reasonable rest.

The fear and concern can be amplified by the pre-existing anxiety and depression disorders. The effect of outbreaks will cause high levels of paranoia and result in delusion. As stress increases, severe anxiety can also cause relapse and substance abuse in highly susceptible individuals. There is an interaction between immunity and mental symptoms. Worsening mental symptoms can render a person most susceptible to physical ailments.

When individuals face serious life events, this elevated, long-stayed stress can lead to poor decision-making, impair memory, and affect overall well-being. Now-a-days, insufficient and excessive stress caused by the epidemic is harmful to our mental and physical health, and the social stability as well. The feature of insufficient stress is a slow response. Example: people refused to wear a mask and wash their hands when they were infected with the coronavirus. They do not realize that they may spread the virus to others. When facing the coronavirus, people with excessive stress may have mental problems that should be treated urgently, such as resent or tend to hurt others, etc.

For an individual, we should know these temporary physiological reactions are normal. This is the human body's own warning response. Do not complain and be panic too much. Replacing with positive emotions like support and comfort in our daily life. Stay away from stressors. Stay at home and learn by the necessary news. Do not pay attention to and send rumors or unconfirmed negative reports to your friends. Change your behavior and lifestyle. Keep a healthy diet and exercise regularly. Make use of this opportunity to communicate with your family members or do some pleasant things together, such as cooking, playing the piano. Pay more attention to what we can do and focus on the good things around us.

The government also rented buses or planes to escort the migrant workers back to the factory. For a hospital, before entering the fever clinic, ward, or intensive care unit, the medical staff were well trained on how to protect themselves from being infected. The hospital arranges enough medical staff in the fight against coronavirus, so the doctors and nurses can take a rest and avoid excessive fatigue. The hospitals must ensure that the supply of medical protective equipment for their employees. For people who need psychological therapy, they can get help through the hotline or in the hospital.

Q10: How to deal with the novel Coronavirus disease calmly. **[19]**

The perspective of ordinary people are in the following three forms:

1. What is emotion and emotion response?
2. What is the neuro-endocrine-immune network?
3. How can we use this network to keep calm?

An emotion is a complex psychological state that involves three distinct components:

1. A subjective experience,
2. A physiological response, and
3. Behavioral or expressive response.

Angry, anxious, are the negative emotion, while love, happy, is a positive emotion. When we have emotions, our bodies will give some physiological responses. All the negative mood emotional responses are harmful to our bodies. So please do our best to be calm and to be positive when we feel stress.

The neuro-endocrine-immune network: It includes the nervous system, endocrine system, and the immune system. The nervous system regulates the endocrine and immune system through the neurotransmitters and the neuropeptides. The endocrine system interacts with the other two systems by the hormone, and the cytokinesis the main language of the immune system. The close interactions among these three systems help to maintain our body homeostasis, and the invasion of the Coronavirus brings great challenges to the nervous system, endocrine system, and the immune system.

Q11: COVID-19 prevention among students. **[20]**

The virus is said to spread mainly from person to person.

1. Between people who are in close contact through respiratory droplets produced when an infected person coughs, sneeze, or speak. These droplets can land in the mouth and nose of the people who are nearby or possibly be held in the lungs.

2. It may be possible that a person can get a virus by touching a surface or object that had the virus on it, and then touching their own mouth, nose, or possibly their eyes.
3. There is the possibility of aerosol transmission in the related closed environment for a long time exposure to a high concentration of aerosol.

The route of transmission in the digestive tracts remains determined. There is a lot of person on the campus. So, students should pay attention to their daily life, develop good personal hygiene habits, and the restrict way, prevent, and control it.

1. Avoid going to public space, especially in a crowded place with bad ventilation such as restaurants, Libraries, and the classroom, and keeping a distance of more than one meter.
2. When returning to the apartment, wash hands immediately after blowing nose or coughing, using running water and soap for at least 20 s before and after meals.
3. Make use of a disposable surgical mask when going out, seeking medical treatment, or taking public transportation. Do not spit. Spitting should be wrapped with paper towels, and disposed of in a covered trash bin.
4. Avoid being exposed, or in close contact with people who are sick.
5. Household spray cleaners and paper towels should be used to clean and disinfect the objects and surface that you frequently touch, such as door handle, mobile phone, toilet ring.

It is recommended to ventilate 2–3 times a day each time for more than 15 min. For medical students who participate in various treatment in the house program, there are few points to note here.

1. Minimize exposure to respiratory passaging that cause the virus.
2. Select appropriate personal protective equipment, maintain hand hygiene, and put on clean, new sterile gloves before entering the ward, or care area.
3. Replace gloves if they are torn or heavily contaminated.
4. Put on a clean isolation gown before entering. Change to the gown if it becomes soiled.
5. Use a medical protect mask.
6. Disposable respirators should be removed and discarded after leaving the ward or clean area.
7. Remember to close the door, put on google before entering, and remove it after leaving.

Q12: Plan to return to the campus. **[21]**

1. Ensure compliance with campus policy.
2. Inform counselors and mentors of your plan.
3. Avoid close contact with people who have symptoms of respiratory disease such as fever, cough, or sneeze. Inform the temperature before getting back to school. If you have any suspicious symptoms such as fever or cough, you should cancel or post your plan, and seek local medical advice immediately.
4. Customize a reasonable way to campus, and choose the right transportation.

5. Prepare personal protective equipment.
6. Get in touch with the counselors and mentors and obey the campus's arrangement.

Q13: Home-based self-care in climacteric women [22]

Due to the decreased ovarian function in the female hormone, climacteric women can appear some physiological and psychological as factors of symptoms. The presence of COVID-19 may increase climacteric women sustainability to develop menopausal symptoms. In the space period of the outbreak of COVID-19, psychological and somatic symptoms for climacteric women may arise due to your special physiological and psychological states.

1.2.1 Common Physiological and Psychological Symptoms in Climacteric Women and Their Impact on Women and Their Families

Climacteric is from age 40–60. From physiology, it is a transition from a reproductive to non-reproductive life. From endocrinology, it is from decreased ovarian function to failure of ovarian function. It means loss of ovarian hormone, particularly estrogen. So, menopausal related symptoms including irregular menstruation, hot flasher sweat, emotional fluctuations, depression, anxiety, sleep disorder, vaginal dryness, painful intercourse, fatigue, etc., are early signs. Osteoporosis, chronic conditions such as diabetes, cardiovascular disease, and long-term harm. All symptoms that can have an impact on the early part of a woman's life, creating life quality issues that lead to further problems. So menopausal symptoms are associated with a poorer quality of life.

1.2.2 Home-Based Self-Care in the Climacteric Women During the COVID-19 Pandemic

To keep a balanced diet, have a variety of different foods, choose whole grain food, plenty of vegetables and fruits. Intake 300 millimeters of milk or equivalent dairy products per day. Control sugar, less oil, limit salt and drink plenty of water. Generally, 1500–1700 mm per day. If you can diversify the diet to achieve the balance, try it out. You can select nutritional supplements in order to maintain the body's health under certain resistance to the virus. If you lack a fresh vegetable, maybe your lack of Vitamin C, minerals, and trace elements. If you lack fresh meat, maybe you lack protein and trace elements such as iron and zinc. You can either single and multi-vitamins and minerals, or milk powder.

1.2.3 Exercise or Physical Activities at Home Are Important

Eating and moving are the keys to maintain a healthy weight. Exercise can maintain energy balance and manage your weight. So it is important to exercise for at least 30 min a day.

A good enough sleep is necessary for high-quality life and health. It is best to go to bed no later than 11:30 PM and do not go to bed too late. Stop smoking and eliminate exposure to second-hand smoke. Limit your alcohol consumption.

Q14: Strategies to climacteric women's psychological problems during the COVID-19 pandemic. **[15]**

The climacteric are a crucial stage of female life and most of the women can achieve self-balance through neuro-endocrine self-regulation.

1. To know about the COVID-19 correctly, reduce exposure to the coronavirus, and take any measures for personal protection.
2. Enrich life, pay attention to information of COVID-19 in less time. Most time, read your favorite books, watch entertainment programs, listen to your music, and keep a normal life.
3. Keep lines of communication open and be honest in your relationships. It seems like staff, friends, and families could support and help each other.
4. Pay attention to the physical and mental health of your family members and create a positive home atmosphere. Clean your room, keep your room ventilated, try to improve your cooking skills, and prepare delicious meals for your family. Enhance the relationship with your husband and strengthen the parent-child relationship.
5. Mindfulness meditation means deliberately pay attention to your present moment without judging it. Sit comfortably and strengthen your upper body. Try to put aside all thoughts of the past and the future, and focus on the present. Remain in the present by paying attention to physical sensations, especially your breath. Attune to the sensation of air moving in and out of the body while taking a breath.

1.3 Conclusion

In this chapter, the question framed to address the impact of COVID-19 and suggestions provided are useful to the researcher in providing useful insights. The questioner was based on climacteric, pregnancy women with psychological problems (Q8, Q16, and Q17). The impact on children is discussed with the help of Q9. The measures that the human community should take to avoid the spread of COVID-19 is discussed with the help of Q10. The overall suggestions provided to prevent the transmission of COVID-19 are to avoid contact with the virus. To wear the mask, clean your hands, and stay home to keep away from the crowd. Also, to keep a healthy lifestyle is important for your healthy immunity and be optimistic. The outcome of the present research is to provide suggestions to the humankind towards handling the epidemic safely. In Future work, we would like to concentrate on Stem Cell Transplantation, Convalescent Plasma Therapy, and the Lung Transplantation strategies for dealing with COVID-19.

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Chapter 2
Health Care Digital Revolution During COVID-19

Imdad Ali Shah, N. Z. Jhanjhi, Mamoona Humayun, and Uttam Ghosh

Abstract The digital revolution has had both good and bad effects since the 1980s. COVID-19 was identified only a few weeks after the pandemic began. COVID-19's rapid spread over the world, combined with the virus's originality, necessitated novel solutions. Professional communication across numerous platforms is increasingly reliant on social media. The constant flow of new knowledge and novel methods of practice has led to the creation of new digital communication strategies. There are majority of health employee remained sick or self-isolation to physically face COVID-19's patents, clinical groups describe widespread use of messaging apps for communication, to organize service provision or manage staff rotations. The use of digital solutions has risen to previously unheard-of heights as a result of the lockdown, increasing the possibility of scaling up alternative social and economic methods. However, they provide new technological risks and concerns, placing new expectations on policymakers. Growth in COVID-19 is the digital and technological revolution that has shaped our world over the last century. As healthcare systems around the country prepare for an influx of COVID-19 patients, immediate action is needed to modernize healthcare delivery and scale up our systems by

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_2

leveraging digital technologies. The COVID-19 pandemic has brought to light the limitations of our current healthcare system's ability to serve all the world during a crisis. The main goal of this chapter is to concentrate on digital healthcare issues and challenges, as well as to provide limitations and recommendations.

Keywords Digital Healthcare · COVID-19 · Healthcare-system · Issues and challenges

2.1 Introduction

Dr. Eric Topol defines digital health as the potential to digitize human beings using several methods while completely utilizing our ever-expanding development of connectivity, social networking, and health information systems. Dr. Topol feels that the era of medical information asymmetry is coming to an end, with the majority of data now in the hands of doctors. Many elements of our lives are being impacted and changed by the digital revolution. It has already revolutionized several parts of our lives, from healthcare to education. The aging population and rising medical expenditures will necessitate changes in how we approach healthcare in the future. To address the needs of rising and aging populations, as well as to increase geographical reach, health systems will need to expand their digital alternatives if they wish to service these patients. The rapidity, scale, and systemic influence of the Fourth Industrial Revolution set it apart from earlier industrial revolutions. He predicted that the Fourth Industrial Revolution would unfold in an exponential rather than a logical way, significantly altering how we live, work, and interact [1]. As time goes on, this will become more prevalent in numerous facets of healthcare [2]. It is expected that in ten years, supercomputers will aid in the development of a functioning computational model of the human body, using data that is replenished regularly by internal organ measurements, collected by nano-sensors, and transmitted by smartphones. The software will generate nutrition advice and therapy for individuals based on data from millions of people [3]. However, this vast amount of electronic health data is largely underutilized, and there is a pressing need to transform it into relevant, expressible, and time-limited information [4]. As a developing paradigm of intelligent computing approaches, cognitive computing contains major brain characteristics of natural intelligence, such as perception, attention, thought, and so on, as well as the ability to integrate past experiences into itself [5]. Advanced image processing and predictive analysis are the most prevalent applications in healthcare. The digital system, on the other hand, may provide considerably more. As health-care systems around the country prepare for an influx of COVID-19 patients, immediate action is needed to modernize health-care delivery and scale up our systems by leveraging digital technologies [6]. Despite the fact that some digital technologies, such as those used in telemedicine, have been around for decades, they have had limited market penetration due to extensive regulation and a lack of supportive payment structures [7] (Fig. 2.1).

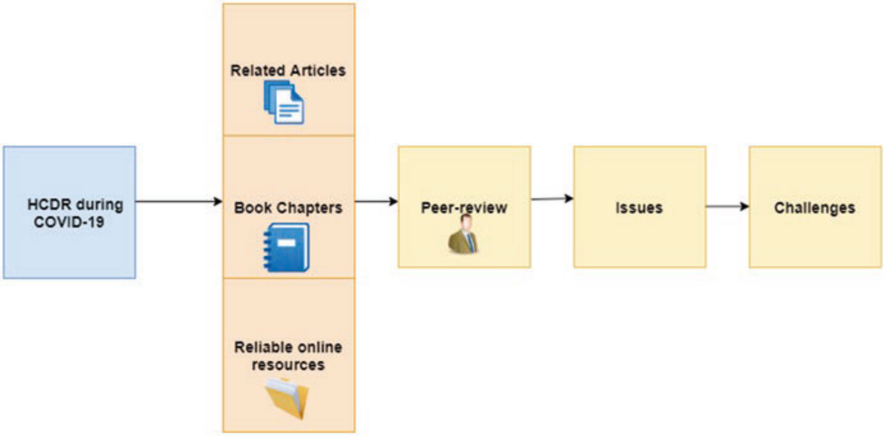

Fig. 2.1 Overview of chapter

This chapter will focus on the following points:

1. To peer-review related articles, book chapters, and reliable online resources about the healthcare digital revolution and COVID-19
2. To focus on issues of the health care digital revolution during COVID-19
3. To find out the challenges of the health care digital revolution during COVID-19

2.2 Literature Review

This paradigm has given rise to new realities and difficulties, calling into question the ability of healthcare institutions to deal with new commercial and economic models, data governance, and regulation. Countries must respond appropriately so that digital health, which is increasingly based on disruptive technology, can benefit everyone [8]. Nature issued a supplement on the revolution in digital technology, acknowledging that the online revolution has transformed [9]. The application of digital technologies to improve COVID-19's impact on the healthcare system in different parts of the world was highlighted [10]. Artificial intelligence tools can help diagnose and treat diseases more effectively if they are detected and analyzed earlier. The healthcare business can better serve remote, rural, and unreachable locations by providing faster and higher-quality treatments, lowering the cost of hospitalization [11]. Digital healthcare has transformed quickly [12]. Early detection and analysis of any disease can aid in better diagnosis and treatment via artificial intelligence approaches. The healthcare business can better serve remote, rural, and unreachable locations with speedier and higher-quality services, lowering hospitalisation costs [13, 14]. Due to a shortage of data analysts and two scientists, it is unable to meet the demand [15, 16]. To promote patient engagement [17, 18]. There have only been a few literature evaluations on the application of cognitive computing in healthcare, and none of them have produced any essential insights on this burgeoning topic [19, 20]. Clinical diagnoses are usually reliant on statistics, and major scientific breakthroughs have been made by recursively analyzing large amounts of unstructured data. Consider the challenge of DNA sequence classification, which is complicated by the infinite [21, 22]. To facilitate healthcare delivery without physical interactions, many countries have adopted digital-first initiatives, remote monitoring, and telehealth systems. Only a few months ago, this would have been beyond the realm of possibility [23]. This quick transformation was feasible due to three factors. First, rather than starting from scratch, many organizations might provide solutions by customizing existing software. When COVID-19 struck, the technology had reached a point where it could be used at scale. Second, amid the crisis, many countries loosened privacy and data protection requirements for video and other communications technologies [24]. Many patients are seen in primary care and hospital outpatient clinics can benefit from remote management [25]. This includes COVID-19 patients who can be handled remotely with symptomatic management and self-isolation instruction Table 2.1 summary of research studies and Fig. 2.2 overview of targeted health care system in literature review.

2.3 HealthCare Paradigm Evaluation

The goal is to locate the most appropriate new technology to address the current healthcare challenge. We can keep track of medical information, develop medical knowledge, assist in treatment processes, and communicate with patients [31]. In comparison to physics, biology has always been difficult to model using mathematics [32]. The enormous difficulty and diversity of biology defy merely rational formulations, and only statistics come close to a satisfying description [31]. A growing number of mobile health Healthcare tools are being developed to collect patient-generated data, including over 250 million mobile health apps available for download and over 300 million wearable devices in public usage [33]. Patients can be monitored and treated directly using mobile health software [34]. Healthcare innovations have the potential to expand healthcare admittance around the world, increase clinical information collection, and advance healthcare information distribution. New viruses are being detected using nanotechnology (Fig. 2.3).

2.4 Health Care Digital Evaluation in COVID-19

The combination of persons and workstations to construct distributed systems on object of completing inventive activities with precision is known as open innovation. Humans and machines both have advantages and disadvantages. The COVID-19 epidemic has posed numerous obstacles for healthcare providers around the world,

Table 2.1 Summary of research study

References	Technique	Algorithms	Applications	Limitations
[22]	In an intelligent home scenario, IoT sensors gather patient voice and visual signals, and the scores from the signals are integrated to give a final score for emotional decision-making.	Algorithms for feature extraction, ML, DL, and AI	Youngsters, the elderly, and persons with mental illnesses are all at risk.	The time required of the proposed system
[26]	Several design patterns, as well as the design and development of smart IoT systems, were discussed.	Blackboard pattern, Recommendations algorithm	Using wearable technology to manage patient comorbidity	Managing response time and scalability during the discovery process
[27]	For healthcare, different body sensors were used, and features were derived from the sensor data.	DCN is a type of NN	Sensor-enabled individual	The implementation of a true smart home environment is insufficient. A distributed cloud-based infrastructure was used.
[28]	To monitor and analyze users' health, a combination of cognitive and edge calculations was used.	Algorithm for supervised learning	In case of a patient emergency	Users' "emotions" are not acknowledged by the proposed system, and no appropriate care is provided.
[29]	Development of smart IoT systems	ML, DL, and AI	Sensor-enabled individual	A distributed cloud-based infrastructure was used.
[30]	Sensor Data	AI	Elderly heart diseases	Needs to more on AI application

as well as resulting in one of the most serious societal catastrophes of the twentieth century. It has also served as a litmus test for the maturity of digital health technology, whether used for primary care, surveillance, or the development of new initiatives. In this editorial, we consider recent changes in service delivery [35]. Primary care and outpatient hospital care have long held the potential of being mostly supplied digitally, but the digital transformation has been slow until lately. The reality of system inertia and delayed adoption rates due to a variety of hurdles relating to reimbursement, accreditation, and human factors have to temper aspirations around digital transformation. Only 20% of states in the United States, for example, enforce payment parity between telemedicine and in-person services [36]. In a couple of

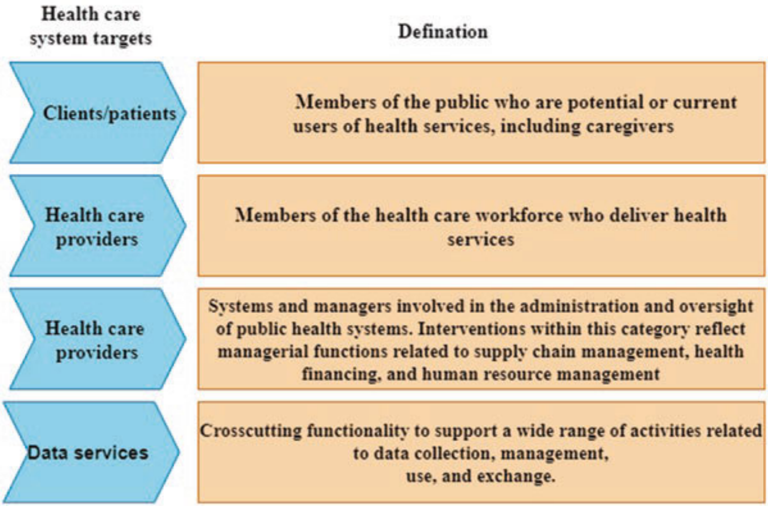

Fig. 2.2 Overview of targeted Health care system in literature review

weeks, the COVID-19 epidemic has drastically altered everything. The ability of digital health technologies to safeguard patients, professionals, and the general public from exposure has been widely recognized, which has accelerated the adoption of these technologies in ways never seen before. 2 To facilitate healthcare delivery without physical interactions, many countries have adopted digital-first initiatives, remote monitoring, and health systems. In the UK, general practitioners has taken a big step forward in terms of health, implementing a new electronic pathway to manage the delivery of services to the right place [37]. In a couple of weeks, the COVID-19 epidemic has drastically altered everything [38]. The ability of digital health technologies to safeguard patients, professionals which has accelerated the usage of these technologies in previously unseen ways.

2.5 Transition from Hospital to Home

When we were sick, the doctor used to come to our house and check on us but that is difficult to conceive in today's world. Hospitals and institutional-based medical services have dominated instead. Globally, aging is the most pressing issue in the healthcare sector [23]. Korea has the world's quickest-aging population. By 2050, the ratio of people aged 65 and more in Korea is predicted to reach 41% [24]. It is not acceptable to spend one's old age in hospitals or long-term care facilities owing to illness, and to die in a hospital, if one's objective is to pursue happiness. As a result, future medical care will be led by a medical system and culture capable of providing treatment and medical care in the location where one has lived their latter life and death [25]. With the rise of telemedicine and the Internet of Things in

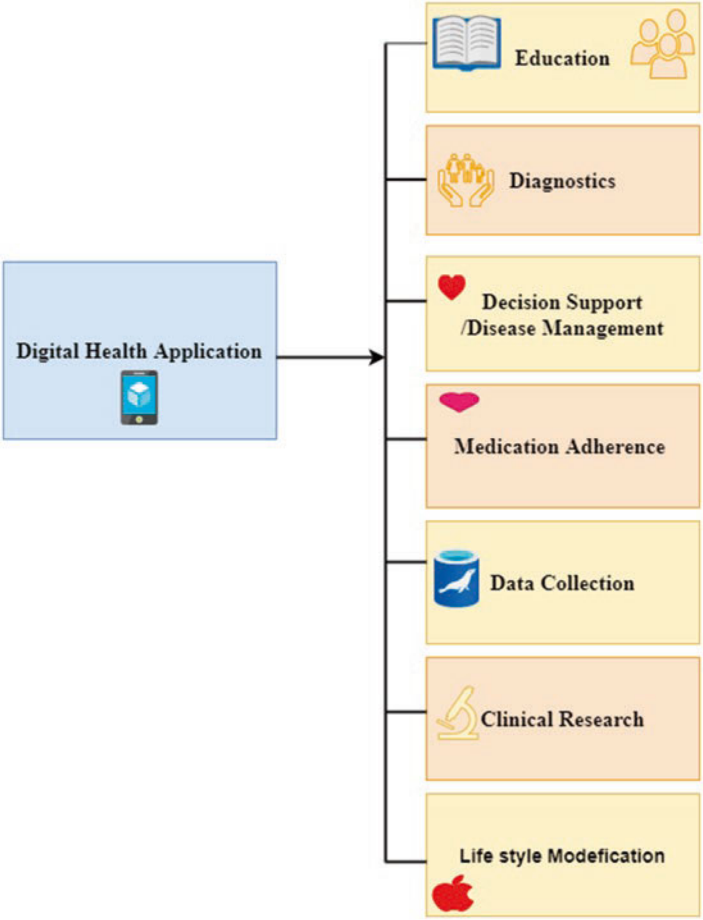

Fig. 2.3 Overview of health application

healthcare, it's growing more conceivable that "house" will be considered as the hospital [39]. Smart card technologies are currently in development and are expected to become widely used in the near future. For instance, using wearable's and computerized coaching for chronic diseases [40]. As a result, individual health management becomes easier, and a person can become more involved in his or her own health concerns. Smart care services, such as telemedicine, have been shown in recent study to improve the efficacy and effectiveness of hypertension, diabetes, and metabolic syndrome management [41]. Korea's medical care delivery system now consists of primary medical care, secondary midsized hospitals, and tertiary care hospitals; however, home healthcare may be recognized as a separate medical unit in the next ten years [42]. To put it another way, the idea of a home hospital will evolve into a new medical care paradigm figure overview of transition from hospital to home (Fig. 2.4).

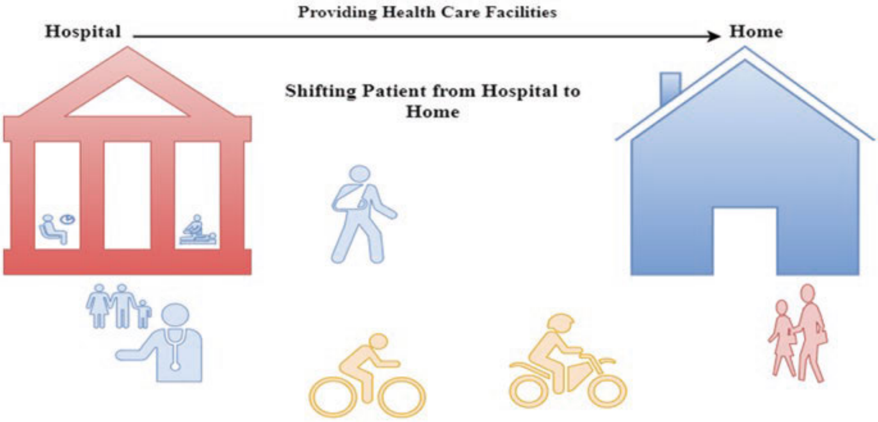

Fig. 2.4 Overview of transition from hospital to home

2.6 Treatment for Patients with Evaluation Digital Health

The quick creation and deployment of new care models, aided by digital health innovation, is perhaps the most significant digital health shift. These digital alternatives arose from a need to protect fragile patients from the risks of visiting the hospital, while also promoting social distances and safeguarding employees [43]. The usage of telemedicine consultation methodologies has facilitated this in both primary and secondary care in the United Kingdom [44, 45]. Multidisciplinary team meetings have shifted away from in-person attendance and toward Zoom and other platforms to allow for complex care choices to be made without putting big groups of healthcare workers in danger. The rapid navigation of governance and digital integration required by the introduction of these digital care processes was aided by the pressing necessity generated by the COVID-19 epidemic. Without it, implementation could have taken a long time.

2.7 COVID-19: Digital Healthcare Model

During the 'COVID-19' pandemic, new healthcare paradigms are required. COVID-19 transmission is at an all-time high, the majority of countries have implemented strict detentions, making communication and meetings between patients and doctors difficult. In the era of digital health technology, the focus has shifted to telehealth mobile apps, websites, and chatbots [46]. Highlights the basic shareholders at the center of the 'COVID-19' crisis (Fig. 2.5).

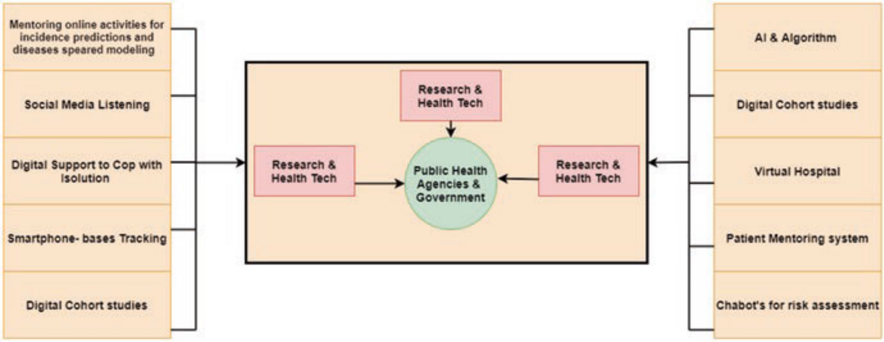

Fig. 2.5 Overview of models Health care needed in COVID-19

2.8 Discussion

Healthcare Enterprise is a collaborative effort between healthcare professionals and big corporations to enhance the way healthcare computer systems communicate data. IHE encourages the coordinated application of established standards to specific clinical demands in order to provide the best possible patient care. (Health Level 7 2020) were established to provide standards for radiological imaging and electronic medical information. Despite the widespread adoption of these standards, infrastructures for sharing healthcare information among hospitals, clinics, and laboratories did not begin to be developed until 2001.

2.8.1 Digital Healthcare and Implementation

The COVID-19 situation is a good pattern of how difficult it is to come up with global technology answer to a problem. The varied traditional, ethical, and to increase the acceptance of digital technology, consumers' spiritual perspectives should be acknowledged. During the current situation, the collective advantage of public health and the maintenance of local social order are prioritized [47]. Digital measurements might be inconvenient, damage separate liberties. A significant digital divide exists in several nations now, and Disadvantaged people may be overlooked when digital technologies are implemented [48]. Trace Together, a Singapore-based program has been used to track COVID-19-infected patients [49]. This patient monitoring system could be valuable in disease surveillance and outbreak control, but individual data privacy standards prevent it from being used, it would not be able to deploy it in European countries. The Corona App was created in France and is founded on comparable specifications [50]. Persons must register on the app and enter data about their well-being, and whether or not they are experiencing signs [51]. This information is tracked using a relocation system that is updated every hour. The COVID Symptom Tracker app was created at King's College London to assist patients in tracking their own symptoms [49, 52]. Finally, some developing countries face significant challenges in delivering digital health solutions in rural and remote areas, including inadequate or missing basic digital infrastructure.

2.8.2 Overview of Chapter

Our contributed of this chapter on following points:

- Inadequate risk evaluation: While unstructured data is chastised for its lack of order and difficulty in being converted into electronic health records, cognitive computing solutions fail to consider the risk that such data poses.
- Thorough training approach: To effectively comprehend and optimise the process, cognitive computer systems require training data at initially. The slow adoption of cognitive computing systems is likely due to the lengthy process of training them.

In France, where the COVID-19 outbreak is spreading quickly, the health technology ecosystem has stepped in to help tackle the issue quickly and generously. In hospitals and general clinics, a variety of telemedicine and telemonitoring technologies have been installed. However, a lack of cooperation among operators has resulted in challenges such as a lack of agreement on which symptoms to monitor and which alert systems to implement [53]. The German health ministry even states that they now want to help translate new regulations into real solutions to speed ups to take step for healthcare digitalization [54–56]. COVID-19 digital efforts should be relevant to both hospital and public health systems, tailored to the population, quickly deployable, and ready to evolve as the body of information about COVID-19 grows. It needs take steps in light of ISARIC initiatives.

2.9 Future Research Directions

Cognitive computing has the ability to alter the entire healthcare value chain, from drug discovery to patient personalization, improved clinical results, and more effective public health management.

- Recover the strategy and study of clinical studies and the accuracy of the outcomes.
- IoT-based systems that implement real-world applications are always changing and producing new necessities.
- To learn from people's intelligence and present more exact analytics, management processes must be coordinated and people must be interacted with. As a result, a new IoT age known as Cognitive IoTs has emerged.

2.10 Conclusion

The digital revolution has had both good and bad effects since the 1980s. COVID-19 was identified only a few weeks after the pandemic began. COVID-19's rapid spread over the world, combined with the virus's originality, necessitated novel solutions. Professional communication across numerous platforms is increasingly reliant on social media. The constant flow of new knowledge and novel methods of practice has led to the creation of new digital communication strategies. There are majority of health employee remained sick or self-isolation to physically face COVID-19's patents, clinical groups describe widespread use of messaging apps for communication, to organize service provision or manage staff rotations. The use of digital solutions has risen to previously unheard-of heights as a result of the lockdown, increasing the possibility of scaling up alternative social and economic methods. However, they provide new technological risks and concerns, placing new expectations on policymakers. Growth in COVID-19 is the digital and technological revolution that has shaped our world over the last century. As healthcare systems around the country prepare for an influx of COVID-19 patients, immediate action is needed to modernize healthcare delivery and scale up our systems by leveraging digital technologies. The COVID-19 pandemic has brought to light the limitations of our current healthcare system's ability to serve all the world during a crisis.

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Chapter 3
Impact of Internet of Health Things (IoHT) on COVID-19 Disease Detection and Its Treatment Using Single Hidden Layer Feed Forward Neural Networks (SIFN)

S. Murugan, K. Vijayakumar, V. Sivakumar, R. Manikandan, Ambeshwar Kumar, and K. Saikumar

Abstract COVID-19 endemic has made the entire world face an extraordinary challenging situation which has made life in this world a fearsome halt and demanding numerous lives. As it has spread across 212 nations and territories and the infected cases and deaths are increased to 5,212,172 and 334,915 (as of May 22 2020). Still, it is a real hazard to human health. Severe Acute Respiratory Syndrome cause vast negative impacts economy and health populations. Professionals involved in COVID test can commit mistakes when testing for identifying the disease. Evaluating and diagnosing the disease by medical experts are the significant key factor. Technologies like machine learning and data mining helps substantially to increase the accuracy of identifying COVID. Artificial Neural Networks (ANN) has been extensively used for diagnosis. Proposed Single Hidden Layer Feedforward Neural Networks (SLFN)-COVID approach is used to detect COVID-19 for disease

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_3

detection on creating the social impacts and its used for treatment. The experimental results of the proposed method outperforms well when compared to existing methods which achieves 83% of accuracy, 73% of precision, 68% of Recall, 82% of F1-Score.

Keywords COVID-19 · Machine learning · Single Hidden Layer Feed forward Neural Networks

3.1 Disease Detection Using IoHT

The IoT has changed the way we live, work and take choices. In several industries, including health care, it has already had a substantial and positive influence. A huge revolution has begun in the health sector with the impact of IoT. A new layer in health care infrastructure, Internet of Health Things (IoHT), has been created by rapid developments in sensor-based applications and Internet technologies [1]. IoHT is a term that represents internet-connected identifiable devices and which can be employed in the medical sector. Through medical attention and detection errors, these technologies promote safety. The data collected by gadgets are analysed and medical consultations are remotely conducted. The Web of Things has changed the world already. The life and work of people has been influenced.

In big data, essential source is healthcare. There is a strong need for early identification of disease for accurate review of healthcare data. Viruses are small organisms that only reproduce within an organism's living cells. In living species, coronaviruses are one of most common families of viruses that cause different respiratory diseases. In Wuhan, China, an increasing number of rare cases of pneumonia were recorded in December of 2019. A novel coronavirus, known as COVID-19, was quickly determined to be cause of this epidemic.

Coronaviruses, a kind of viruses, causes severe sickness and disorders in human health. This sickness was burst only at the end of December 2019. This new virus which has spread worldwide is very infectious. WHO (World Health Organization), on 30th January 2020, declared this as a PHEIC (Public Health Emergency of International Concern) because it spread around eighteen nations. On 11th of February 2020, WHO named this outbreak as "COVID-19".Apart from China, , as there was a tremendous increase in COVID-19 cases which was about thirteen times than earlier, which was more than 118,000 in 114 countries and caused 4000 deaths, on March 11th 2020, WHO announced this a pandemic [2].

COVID-19 along with ARDS, SARS (Severe Acute Respiratory Syndrome) is a family of viruses. WHO mentions that this virus which is transmitted through the respiratory tract affects an individual who is in contact with the infected individual [3]. The symptoms are observed from the 2nd day till 14th day, which is the development duration of MERS, and SARS. Specialist face fundamental difficulties while sharing the information during disorder recognizing and to give treatment [4]. Individual with COVID symptoms are keenly observed. Specifically, no treatment

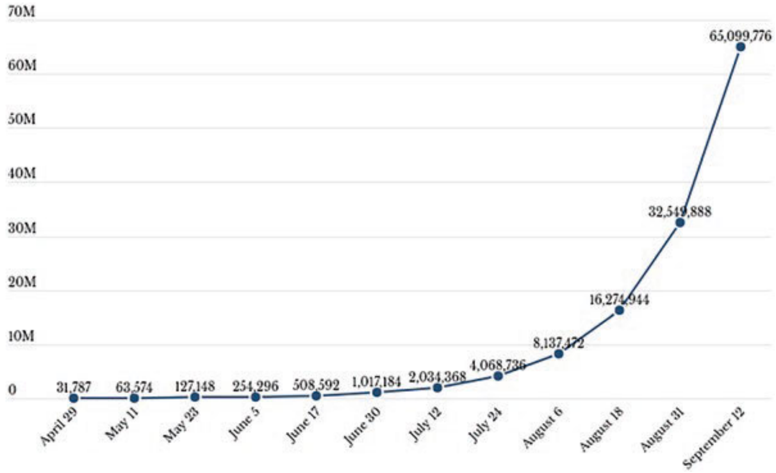

Fig. 3.1 Growth of COVID-19 in India

has been yet found as on April 10th 2020 to prevent this dreadful virus, and thus patients are given treatment based on their symptoms. Medicines, namely hydroxychloriquine, anti-virals, antipyretic are used for treatment. But some preventive measures are being followed like frequently washing hands with soap for a minimum of 20 seconds, avoiding very closer contact among individuals thereby maintaining a distance of about 1 meter, wearing mask which covers nose and mouth which is believed that there are chances to reduce the infection being spread [5]. In brief, reliable and fast early detection of confirmed COVID-19 cases plays vital role in prompt quarantine and medical care, which is also of great significance for patient prognosis, disease prevention, and public health protection. If this continuous, India could possibly face more than 65 million cases by the end of September 2020. COVID-19 has rapidly grown in India as illustrated in Fig. 3.1.

Apart from the procedures followed by clinics, machine learning offers more support to recognize the disease by processing textual and image information of individuals but requires enormous data. Moreover, the nature of the virus can also be predicted and classified. Supervised machine learning approaches requires annotated data to classify text or image data. Algorithms based on this approach are used in various critical projects. Outbreak of pandemic of COVID-19 has brought many countries to a halt. Based on number of affected nations, cases and applied digital measures around world, COVID-19 pandemic can be distinguished. Restricted information is also accessible about how digital interventions can help to contain a global pandemic. Current pandemic situation has kindled several researchers worldwide to overcome this problem. Internet of Things (IoT) is a networked device/operation system that complies with all network aspects, for example hardware, software and network connectivity, as well as all other essential electronic/computer systems. If we talk a little more about IoT, it goes beyond a notion which builds the entire architectural context that allows data to be integrated and exchanged effectively between the data subjects and providers. Most of the problems arise in current typical situation as the non-effective reachability of patients, which after concern about vaccine development is second most significant difficulty. Utilisation of IoT concept makes it quite valuable for patients to be accessible, which ultimately helps them to receive considerable care to get out of sickness. This work is arranged as: Sect. 3.2 describes the background study, Sect. 3.3 discusses methodology, Sect. 3.4 depicts performance analysis and concludes with Sect. 3.5.

3.2 State of Art Methods

Iwendi Celestine et al. 2020 introduced improved Random Forest approach enhanced by the AdaBoost approach. This model used travel, geographical, demographic, and health information of the persons infected by COVID-19 virus for predicting the severity and recovery [6].

Tuli et al. 2020 designed a better mathematical model for predicting and analyzing development and threat of COVID-19 in nations globally. When iterative weighting to fit Generalized Inverse Weibull distribution was involved, a best fit was achieved for developing a prediction model which was deployed on a cloud platform in order to obtain more precise and real-time prediction results [7].

Sujath et al. 2020 developed useful method for forecasting spread of COVID virus. For additional processing in the future, details of the patients should be persistently maintained [8]. Jiang et al. 2020 implemented a machine learning approach which predicted an individual who was infected by COVID virus and there was a possibility for developing ARDS. An accuracy of 80% was obtained [9].

Abdani et al. 2020 suggested and implemented a lightweight deep learning approach to accurately detect the risk of COVID-19 [10]. This model was designed such that it can be deployed on different platforms like tablets, mobiles, and normal computers with no distress of memory capacity. This approach was developed by integrating modified spatial pyramid pooling (SPP) model [11] with convolutional neural network (CNN). Through the use of modified SPP called SPP-COVID-Net, numerous inputs were processed simultaneously [12] with a total parameters of 862,331with not more than 4 MB of storage. The multi-scale facility of this model paved way for identifying COVID patients with different severity levels. This SPP-COVID-Net achieved the average accuracy of about 0.946. In [13], an online healthcare surveillance model is proposed that is capable of evaluating patient health data in order to negotiate occurrence of death. This collects associated patient information required by sensing and healthcare instruments for investigation.

Olivera et al. 2019 [14] model based on the probabilistic principle of Bayesian Monte Carlo to forecast distribution of infectious diseases is suggested. Big downside to this strategy is that it is impacted by collection of past as well as subsequent probabilities. Aayush Jaiswal et al. [15] use of pre-trained deep learning architectures to classify and diagnose COVID-19 in chest CT as an automated tool. By utilizing its own trained weights on ImageNet dataset along with a convolutionary neural structure, proposed model is used to extract functions.

Tushaar Gangavarapu et al. [16] To achieve most discriminative and instructive function subspace, developed novel filter-wrapper hybrid ensemble feature selection technique depends on weighted incidence frequency and penalty method. Longxi Zhou et al. [17] propose fully automated, fast, precise, and machine-agnostic system that can segment and calculate CT scans from various sources to the infection regions.

Shreyas Setlur Arun et al. [18] prediction of spread of COVID19 disease is presented and scale of pandemic, recovery rate and fatality rate are expected. Yujin Oh et al. [19] patch-based method with a comparatively small number of trainable COVID-19 diagnostic parameters for CNN is proposed. Our statistical analysis of possible imaging biomarkers of CXR radiographs inspires suggested method.

Vasilis Z. Marmarelis [20] A novel method, each defined by a Riccati equation with adaptively approximate parameters, was proposed based on data-guided identification and concatenation of infection waves. Barabas J et al. [21] presents a device that encapsulates all of above features through readily accessible components (both hardware as well as software) and is again improved with preliminary acquisition of RTLS data, enabling identification of person-to-person communication detected after symptoms to identify potential vectors of infection and mitigate their further spread via smart quarantine.

Deng-Ping Fan et al. [22] to automatically classify contaminated regions from chest CT slices, a novel COVID-19 Inf-Net (Lung Infection Segmentation Deep Network) was proposed. Yanfang Ye et al. [23] propose and develop an AI-driven system called alpha-satellite) to include as an initial providing a dynamic COVID-19 risk assessment in United States. More precisely, device would automatically have risk indices associated with it in a hierarchical way (e.g., state, county, POI) provided a point of interest (POI) to encourage citizens to pick acceptable safeguard actions while mitigating everyday life disturbances. Loveleen Gaur et al. [24] is a realistic method for detection of COVID-19 from chest radiographs and for differentiating from normal and Viral Pneumonia affected by DCNN. In this work, transfer learning evaluates three pretrained models of CNN (EfficientNetB0, VGG16 and InceptionV3). A balance of precision and efficiency with fewer parameters ideal for mobile applications justifies adopting this specific models. Data collection utilised for study is accessible to public and compiled from many sources.

3.3 System Model

The proposed method is used to detect the COVID and diagnoses the disease. The original data is collected from the database, the data is preprocessed by using smoothing method. Once the data is preprocessed then it can be forwarded to feature extraction process. GLCM based feature extraction is used, the classifier input

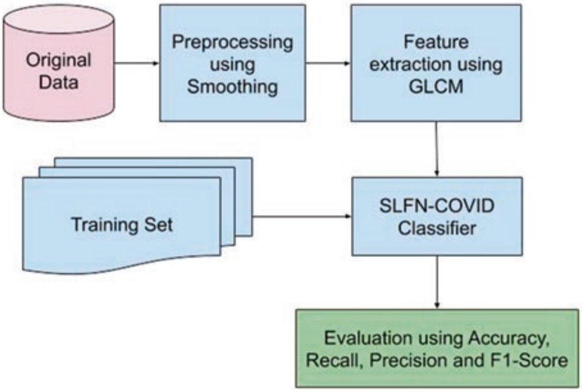

Fig. 3.2 Flow of proposed method

is extracted features that can be SLFN COVID evaluate system. Parameters used to evaluate system is accuracy, recall, F1-Score and precision. Flow of method proposed is depicted in Fig. 3.2.

3.3.1 Preprocessing Using Smoothing

It is tedious to process a raw image. Hence, prior to processing, some operations has to be performed like noise removal and ignoring unnecessary portions of the image. This process is termed as preprocessing which further helps to process the image successfully. Moreover, the image quality is improved by smoothing. After this process, noise is reduced, enhanced and the image is reconstructed for extracting salient features to process further. This process is necessary before feature extraction and analysis.

3.3.2 Grey Level Co-occurrence Matrix (GLCM) Based Feature Extraction

GLCM is formed with several statistical features obtained from a grey scale image. It is a square matrix given as G(i, j) which involves four directions namely horizontal, vertical, left and right cross directions for partitioning G into the normalized typical matrices. For every adjacent direction, evaluation is performed. These texture features are described as correlation, angular secondary moment, inverse difference moment, contrast, sum of squares, sum average, variance, sum and difference variance, auto correlation, entropy, sum and difference entropy, information measures of correlation 1 and correlation 2, inverse difference, cluster shade and prominence, dissimilarity, and maximum probability.

3.3.3 Classification

The classification using artificial neural network that can be discussed below.

3.3.4 Back Propagation Artificial Neural Network (BPANN)

Currently most common NN model in use is BP neural network [25]. In 1986, Rumelhart and Mcllelland proposed BP algorithm that solved weight adjustment issues of nonlinear continuous function in multilayer FFNN area well. It is a standard error algorithm for back propagation [26, 27]. After advent of BP neural network, a lot of research has been performed on activation function selection, structure parameter design, and network defect improvement. Grossberg discovered in 1973 that sigmoid function is very analogous to working conditions of biological neurons, so he began researching relationship between properties of sigmoid function and integrity of NN. He marketed feature to become most commonly deployed BP-NN activation feature.

Core principle of BP method is to break learning process into two steps i.e. constructive signal signalling and error back-propagation. Data is collected from input layer to output layer via hidden layer at point of constructive communication [28]. In output side, output signal forms. In course of sending signal forward network weights are fixed. State of neurons of every layer only influences state of next layer neurons. If it is not feasible to produce desired output in output layer, so error signal can spread again. In back propagation process, step by step, error signal that failed to fulfil accuracy criterion spreads forward and all units of each layer share error. Based on error signal, connection weights are adjusted dynamically. In loop of forward and back change, weight attribute of neurons keeps correcting. Learning ceases until the output signal error meets the precision requirement [29].

3.3.4.1 Topology Structure of BP Neutral Network

As is seen in Fig. 3.3, simplest BPNN has three layers. Input layers, Hidden layers and output layers are used. Number of nodes in input layer is equal to n-input vector dimension. In output layer, number of nodes is proportional to form of output module q. In hidden layer p, number of nodes is correlated with a particular programme that is normally chosen by best.

W1, which is defined as a formula (3.1), is relation weight matrix between input layer nodes and hidden layer nodes. Similar to this relation weight matrix can be specified as W2 between hidden layer nodes and output nodes. For hidden layer and output layer nodes, threshold matrix is θ_1 and θ_2, respectively:

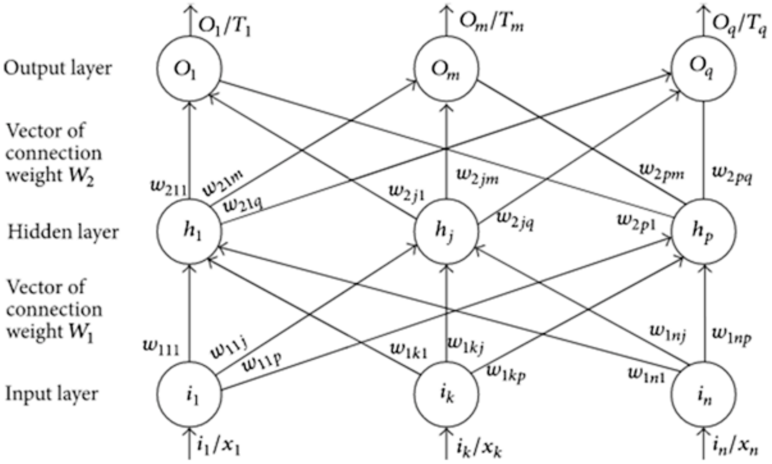

Fig. 3.3 Topology structure of BPNN

$$W_1 = \left\{ \begin{matrix} w_{111} & \cdots & w_{11j} & \cdots & w_{11p} \\ \vdots & & \vdots & & \vdots \\ w_{1k1} & \cdots & w_{1kj} & \cdots & w_{1kp} \\ \vdots & & \vdots & & \vdots \\ w_{1n1} & \cdots & w_{1nj} & \cdots & w_{1np} \end{matrix} \right. \tag{3.1}$$

3.3.4.2 Learning Algorithm of BP Network

BP network learning method is split into 2 steps which are propagated forward and back. It is a gradient descent method which can make error of per connection weights of NN reduce. Assign random numbers in [−1,+1] set to relation weight matrices W1−, W2 and threshold matrices of hidden layer and output layer nodes θ_1 and θ_2 at beginning of learning.

3.3.4.3 Forward Operation

Next, enter {X, T} learning samples, where X is learning samples' input vector and T is corresponding output vector:

$$X = \left(x_1, x_2 \ldots x_k \ldots x_n\right), 1 \le k \le n \tag{3.2}$$

$$T = \left(T_1, T_2 \ldots T_m \ldots T_q\right), 1 \le m \le q \tag{3.3}$$

N is number of input layer nodes; q is number of output layer nodes.

Forward data propagates through input layer and hidden layer to output layer. Created weight value is learning outcome of classification of performance patterns. They primarily contain following measure.

Step 1: (Output value estimation of hidden layer nodes). Nodes value in hidden layer is

$$i_{1j} = \sum_{k=1}^{n} w_{1kj} x_k, 1 \le j \le p \tag{3.4}$$

If n is number of nodes of input layer, p is number of nodes of hidden layer, w 1kj is relationship weight, and x k is input vector component.

Nodes output value is

$$h_j = f\left(i_{1j} + \theta_{1j}\right) \tag{3.5}$$

Where threshold of node j is θ_{1j} .

Sigmoid function given by Rumelhart is activation function f used:

$$f\left(i_{1j}\right) = \frac{1}{1 + e^{-i_{1j}}} \tag{3.6}$$

Step 2: (Calculating output value of output layer nodes). Input values for output layer nodes m are

$$i_{2m} = \sum_{j=1}^{p} w_{2jm} h_j, 1 \le m \le j \tag{3.7}$$

Node m output value is

$$O_m = f\left(i_{2m} + \theta_{2m}\right) \tag{3.8}$$

Where θ_{2m} is output layer node threshold m and f is activation function specified by sort (3.5).

3.3.4.4 Back Operation

Evaluate output value error and predicted output layer value error. From output layer, back propagation error via hidden to input layer. Values of connection weight are adjusted. Steps are as follows.

Step 1: (Calculation of output error of output layer nodes). Error between O_m learning value of output layer m node and output value of T_m learning samples is

$$\varepsilon_m = \left| O_m - T_m \right| \tag{3.9}$$

Step 2: (learning error testing). ε_0 is maximum learning error, which is set by user in [0,1] interval.

When $\max(\varepsilon_m) \le \varepsilon_0$, enter next learning sample. Network weights are adjusted and original learning samples are reentered. When all learning samples fulfill above criteria, learning process is terminated.

Step 3: (evaluate learning error in output layer nodes). Nodes output layer m, learning error is

$$d_{2m} = O_m \left(1 - O_m\right)\left(O_m - T_m\right) \tag{3.10}$$

Step 4: (evaluate learning error of hidden layer nodes). Hidden layer j learning error is

$$d_{1j} = h_j \left(1 - h_j\right) \sum_{m=1}^{q} w_{2jm} d_{2m} \tag{3.11}$$

Step 5 (revise value of connection weights matrix w_2). Set weight value as modified current weight value at time t+1; then set new weight value.

$$w_{2jm}\left(t+1\right) = w_{2jm}\left(t\right) + \eta d_{2m} h_j + \alpha\left[w_{2jm}\left(t\right) - w_{2jm}\left(t-1\right)\right] \tag{3.12}$$

where learning rate is η and momentum factor is α. In scope [0,1], both α and η exists. Using alpha will speed up learning speed and help to solve common BP algorithm's local minimum problem.

Step 6: (revise value of connection weight matrix w_2). Consider,

$$w_{1kj}\left(t+1\right) = w_{1kj}\left(t\right) + \eta d_{1j} x_k + \alpha\left[w_{1kj}\left(t\right) - w_{1kj}\left(t-1\right)\right] \tag{3.13}$$

Step 7: (revise threshold θ_2). Output node layer threshold is

$$\theta_{2m}\left(t+1\right) = \theta_{2m}\left(t\right) + \eta d_{2m} h_j + \alpha\left[w_{2jm}\left(t\right) - w_{2jm}\left(t-1\right)\right] \tag{3.14}$$

Step 8: (revise threshold θ_1). Hidden layer threshold layer is

$$\theta_{1j}\left(t+1\right) = \theta_{1j}\left(t\right) + \eta d_{1j} + \alpha\left[\theta_{1j}\left(t\right) - \theta_{1j}\left(t-1\right)\right] \tag{3.15}$$

3.3.4.5 Run the BP Neural Network

Following learning, run BPNN and carry out pattern recognition for input vector I. BP learning algorithm's forward operation is used. Steps are as follows.

Step 1: Assign BP learning algorithm's updated value to relation weight matrices w_1 and w_2 and threshold matrices θ_1 and θ_2.
Step 2: Input input vector I that requires recognized.
Step 3: To measure output of hidden layer, apply formulas (3.3), (3.4), and (3.5).
Step 4: To measure output of output layer, that is, classification result of input vector I, use formulas (3.5), (3.6), and (3.7).

3.3.5 Proposed Classification Using SLFN-COVID

Several attempts are made to overcome the flaws of Back Propagation Artificial Neural Network (BPANN). It revealed that SLFN with a maximum of hidden nodes was able to evaluate function for *m* various vectors present in the dataset used for training.

For *m* samples in $\mathbf{D} = \{(\mathbf{x}^{(k)}, \mathbf{t}^{(k)}) \mid \mathbf{x}^{(k)} \in \mathbf{R}^n, \mathbf{t}^{(k)} \in \mathbf{R}^p, k = 1,.., m\}$ where $\mathbf{x}^{(k)} = [x_1^{(k)}, x_2^{(k)}, \ldots., x_n^{(k)}]^T$ and $\mathbf{t}^{(k)} = [t_1^{(k)}, t_2^{(k)}, \ldots., t_p^{(k)}]^T$ represents features and target respectively in the training dataset. SLFN having *M* hidden nodes with activation function $g(x)$ as well as linear activation function in output nodes it is shown in Eq. 3.16 as:

$$\sum_{i=1}^{M} \beta_i g_i\left(x^{(k)}\right) = \sum_{i=1}^{M} \beta_i g\left(w_i . x^{(k)} + b_i\right) = o^{(k)}, K = 1, \ldots, m \tag{3.16}$$

Where, $\mathbf{w}_i \in \mathbf{R}^n$ gives the weights of input and *i*th hidden nodes in Eq. 3.17

$$\mathbf{w}_i = \left[w_{i1}, w_{i2}, \ldots, w_{in}\right]^T, \tag{3.17}$$

$\boldsymbol{\beta}_i \in \mathbf{R}^p$ is the weights of i^{th} hidden and output nodes in Eq. 3.18

$$\beta_i = \left[\beta_{i1}, \beta_{i2}, \ldots, \beta_{ip}\right]^T, \tag{3.18}$$

$\mathbf{w}_i \bullet \mathbf{x}^{(k)}$, b_i, $\mathbf{o}^{(k)} \in \mathbf{R}^p$ represents the inner product of $\mathbf{w}_i$ and $\mathbf{x}^{(k)}$, bias of *i*th hidden node and output of NN for *k*th vector respectively.SLFN estimates *m* vectors i.e., $\mathbf{w}_i$, $\boldsymbol{\beta}_i$, and b_i exists such that in Eqs. 3.19 and 3.20:

$$o^{(k)} - t^{(k)} = 0 \tag{3.19}$$

$$\sum_{i=1}^{M} \beta_i g\left(w_i . x^{(k)} + b_i\right) = t^{(k)}, k = 1, \ldots, m \tag{3.20}$$

This equation can also be represented as: $H\beta = T$

where, $H \in R_m xM$ is hidden layer output matrix of NNs.

$$H = \begin{bmatrix} g\left(w_1 \cdot x^{(1)} + b_1\right) & \cdots & g\left(w_M \cdot x^{(1)} + b_M\right) \\ \vdots & \ddots & \vdots \\ g\left(w_1 \cdot x^{(m)} + b_1\right) & \dots & g\left(w_M \cdot x^{(m)} + b_M\right) \end{bmatrix} \tag{3.21}$$

$\boldsymbol{\beta} \in \mathbf{R}_M xp$ specifies weights of output and hidden layers.

$$\beta = \begin{bmatrix} \beta_1^T \\ . \\ . \\ . \\ \beta_M^T \end{bmatrix} \tag{3.22}$$

$T \in R_m xp$ represents target values of m vectors in training dataset

$$T = \begin{bmatrix} t^{(1)^T} \\ . \\ . \\ . \\ t^{(m)^T} \end{bmatrix} \tag{3.23}$$

In each iteration of conventional gradient descent based learning approach, the weights $\mathbf{w}_i$ that connected input and hidden layers and biases b_i has to be initialized and adjusted. This was the main reason for making the training process often time consuming and hence the training model at times fails to obtain global minima. But, the minimum norm least-squares used in SLFN avoided tuning those parameters. In the training process in Eq. 3.24, SLFN with fixed $\mathbf{w}_i$ and bi was identical for estimating the least square solution $\hat{\beta}$ of $H\beta = T$

$$H\left(w_1, \dots, w_M, b_1, \dots, b_M\right)\hat{\beta} - T = \min_\beta H\left(w_1, \dots, w_M, b_1, \dots, b_M\right), \beta - T \tag{3.24}$$

with the smallest value $\hat{\beta} = H \dagger T$

where, $H\dagger$ was Moore-Penrose generalized inverse of matrix H. Basic significant properties of this solution are less training error, unique solution and smallest weight norms. Less norm least-square solution provided for SLFN is termed as ELM which involves the following steps during training process:

- $\mathbf{w}_\mathrm{i}$ and bi, for i= 1,…,M were set randomly.
- H, the matrix of the hidden layer output, was computed
- $\hat{\beta}$ was determined

To conclude, three major differences between BPANN and ELM-ANN were identified which are as follows:

- BP-ANN has to tune parameters like learning rates, momentum, number of hidden nodes, and terminating norm. But, ELM-ANN avoid these operations and defines only the number of hidden nodes.
- It is operated on differentiable activation functions only whereas ELM-ANN uses both type of functions.
- Both BP-ANN and ELM-ANN obtain their trained model with minimum training error. The difference is that the former possibly reaches local minima while the latter additionally obtains smallest norm of weight thereby providing better improved generalized model and reaches global minima.

3.3.5.1 Dataset

COVID-19was declared as Health Emergency by WHO and thus hospitals and researchers gave open access to the data related to this virus. The dataset employed for an analysis in this study was developed by Hannah Ritchie [30] which is regularly updated with the reports of WHO [31]. The additional information related to this dataset can be obtained from https://ourworldindata.org/coronavirus-source-data.

3.4 Experimental Analysis

The parameters used for analysis are Accuracy, F1 score, recall and precision, Notations TP, FN TN and FP represented in equations denote True Positive, False Negative, True Negative and False Positive.

Accuracy This is ratio of true predictions to total data predicted by the classifier. This significant measure is used to evaluate the classification model is given by in Eq. 3.25:

$$Accuracy = \frac{\mathrm{TP} + \mathrm{TN}}{\mathrm{TP} + \mathrm{TN} + \mathrm{FP} + \mathrm{FN}} \tag{3.25}$$

Precision This is ratio of samples that are aptly identified to the sum of identified samples which is given below in Eq. 3.26:

$$Precision = \frac{TP}{TP + FP} \tag{3.26}$$

Recall This is ratio of correctly identified samples to sum of samples that are TP and FN which is shown in Eq. 3.27:

$$Recall = \frac{TP}{TP + FN} \tag{3.27}$$

F1 Score It provides a perfect evaluation of classifying model which is computed in Eq. 3.28:

$$F1\,Score = 2 \times \frac{\text{Precision} \times \text{Recall}}{\text{Precision} + \text{Recall}} \tag{3.28}$$

The Table 3.1 analyzes the accuracy of existing and proposed methods.

Figure 3.4 illustrates the comparative analysis of accuracy for existing and proposed methods. X axis and Y axis provides number of samples and Accuracy in

Table 3.1 Accuracy analysis

No. of samples	ML based improved model [7]	SPP-COVID-Net classifier [10]	SLFN-COVID classifier
100	54	60	67
200	61	69	78
300	67	76	84
400	78	84	89
500	86	89	95

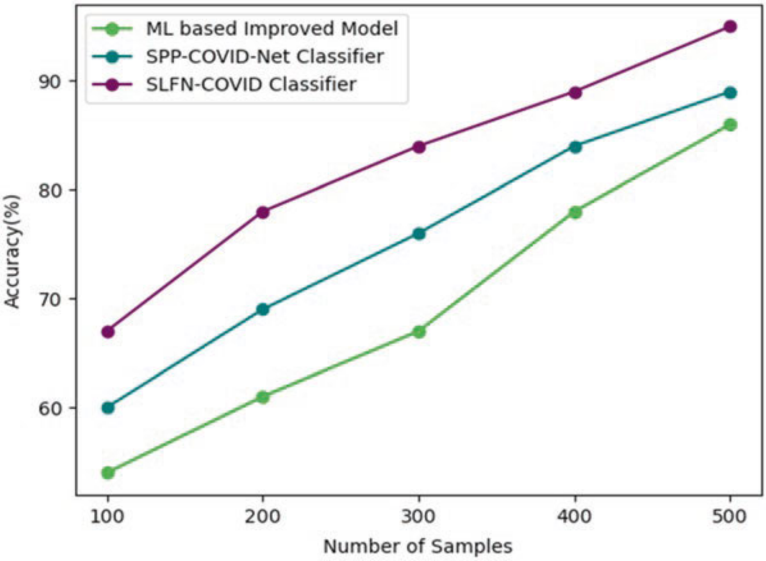

Fig. 3.4 Comparison of accuracy

percentage respectively. Green, teal and violet color indicates ML based Improved Model, SPP-COVID-Net classifier and SLFN-COVID Classifier respectively. The proposed method achieves 83% of accuracy. The Table 3.2 shows analysis of precision with existing and proposed techniques.

Figure 3.5 presents comparative analysis of precision for existing and proposed methods. X axis and Y axis provides number of samples and precision in percentage respectively. Green, teal and violet color indicates ML based Improved Model, SPP-COVID-Net classifier and SLFN-COVID Classifier respectively. The proposed method achieves 73% of precision. Table 3.3 analyzes recall of the existing and proposed methods.

Figure 3.6 illustrates comparative analysis of recall for existing and proposed methods. X axis and Y axis provides number of samples and recall in percentage respectively. Green, teal and violet color indicates ML based Improved Model, SPP-COVID-Net classifier and SLFN-COVID Classifier respectively. When compared to existing methods, proposed method achieves 68% of recall. The Table 3.4 shows analysis of F1-Score with existing and proposed techniques.

Table 3.2 Precision analysis

No. of samples	ML based improved model [7]	SPP-COVID-Net classifier [10]	SLFN-COVID classifier
100	47	51	59
200	51	62	68
300	58	68	71
400	65	70	79
500	71	75	89

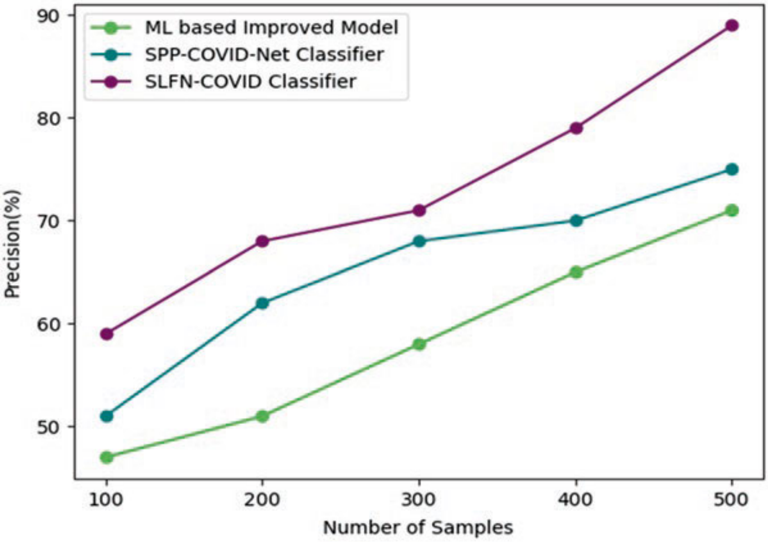

Fig. 3.5 Comparison of precision

Table 3.3 Recall analysis

No. of samples	ML based improved model [7]	SPP-COVID-Net classifier [10]	SLFN-COVID classifier
100	38	39	56
200	41	47	65
300	49	51	69
400	56	60	72
500	61	68	78

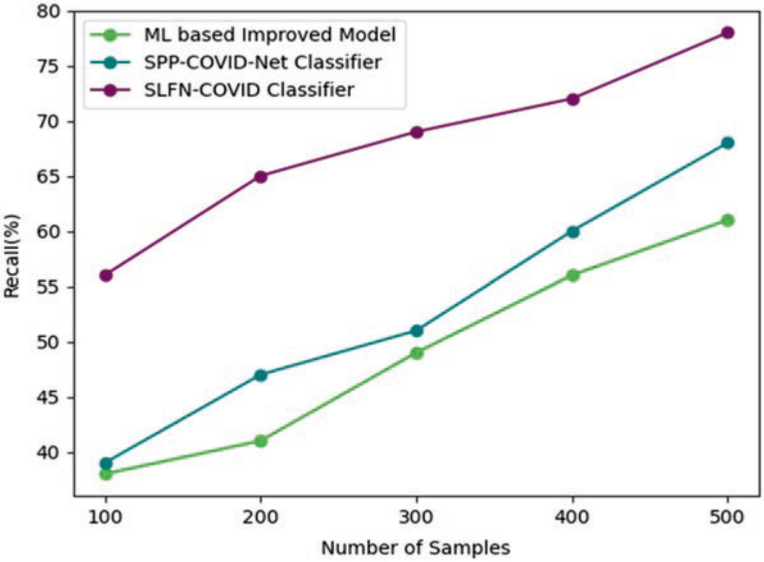

Fig. 3.6 Comparison of recall

Figure 3.7 compares F1 score obtained for existing and proposed methods. X axis and Y axis provides number of samples and F1-Score in percentage respectively. Green, teal and violet color indicates ML based Improved Model, SPP-COVID-Net classifier and SLFN-COVID Classifier respectively. Proposed method achieves 82% of F1-Score. Table 3.5 presents overall performance of existing and proposed techniques.

Figure 3.8 compares overall performance of existing and proposed methods. X axis provides parameters used for analysis and their corresponding values in percentage in Y axis. The pink, lavender and violet color indicates ML based Improved Model, SPP-COVID-Net classifier and SLFN-COVID Classifier respectively. When compared to the existing methods, proposed method achieves good results.

Table 3.4 F1-score analysis

No. of samples	ML based improved model [7]	SPP-COVID-Net classifier [10]	SLFN-COVID classifier
100	54	56	69
200	62	67	75
300	68	71	86
400	72	78	89
500	79	83	92

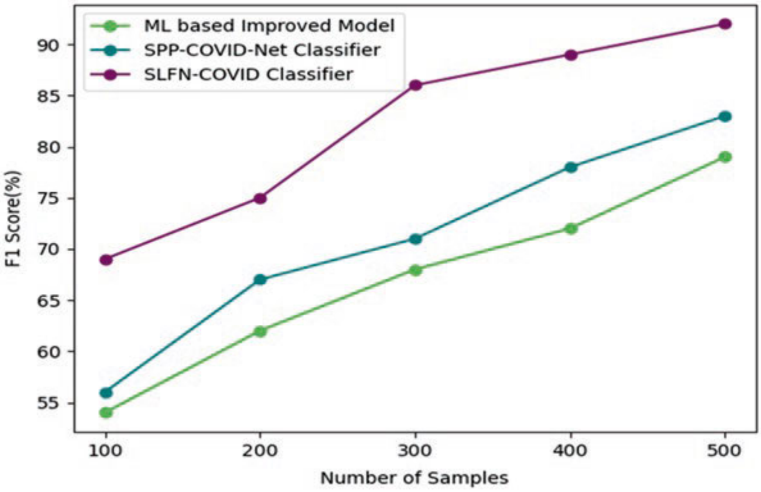

Fig. 3.7 Comparison of F1-score

Table 3.5 Overall Performance of the existing and proposed methods

Parameters	ML based improved model [7]	SPP-COVID-Net classifier [10]	SLFN-COVID classifier
Accuracy	69%	76%	83%
Precision	58%	65%	73%
Recall	49%	53%	68%
F1-Score	67%	71%	82%

3.5 Conclusion

Several approaches like GAN, RNN, LSTM, and ELM are developed for diagnosing COVID-19. The major issues related to COVID-19 are high-risk people, geographical issues, and radiology and recognizing which have been analyzed and described in this work. The proposed SLFN-COVID Classification method is used

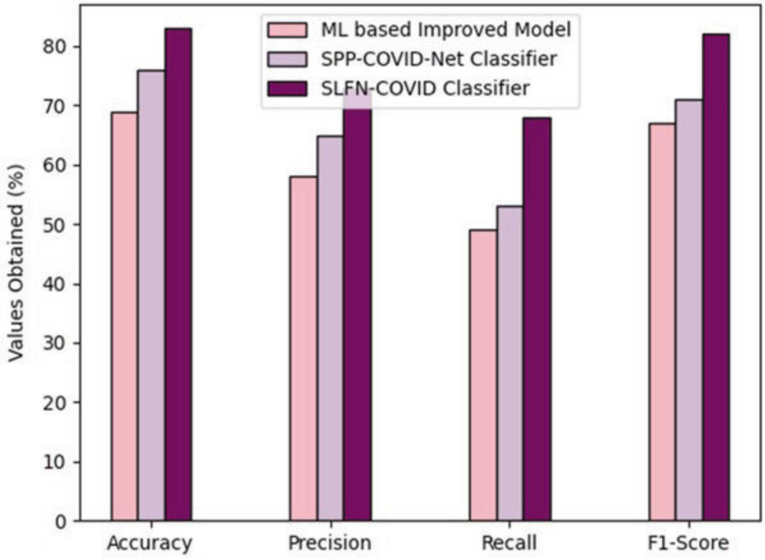

Fig. 3.8 Overall comparison of existing and proposed methods

for detection and diagnosing the disease based on the patient COVID-19 dataset which create the social impacts and its helps for treatment. The experimental results achieved are 83% of accuracy, 73% of precision, 68% of recall, and 82% of F1-Score. The SLFN-COVID classifier exceeds prior approaches. It is concluded that the the future effort is to focus on the growth of health services which led to an increase in data generation causing problems in the design of data access and data structures. An additional effort must therefore be undertaken to address the complexity and diversity of healthcare system data. In addition, a uniform standard of heterogeneous data management is necessary because of the diversity of data sources; for the diversity of the data content, a single programing interface is required for several data analytics modules.

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Chapter 4
Intelligent Approach to Combat COVID-19: An Insight Analysis

Pranati Rakshit, Soumen Kumar, and Moumita Kumar Roy

Abstract COVID-19 – the utmost global crisis and the major global pandemic is literally changing our life. Every person is observing at the everyday rise of the death toll and the fast, exponential growth of this novel and dynamic strain of the virus. To find the effective treatment, the virus source prediction, infection classifications are important issues to be addressed. As we are waiting to get rid of this situation and waiting to know the peak and down fall timing of this pandemic, forecasting of epidemic development is also important issue to be addressed. In this present chapter we have used some mathematical modeling and Artificial Intelligence based or more specifically Machine learning based approaches to combat this pandemic.

Keywords COVID-19 · Machine learning · Artificial intelligence · SIR model

4.1 Introduction

COVID-19 is one of the deadliest disease we ever had in last 100 years. As we all know in this era of fast moving world and growth in modern medical field still there is no perfect solution for this deadliest and infectious and fast growing germs. After entering into body through nose and mouth it stays up to three days in a throat where

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_4

persons starts feeling throat pain and high fever then it slowly and gradually attacks human lungs and problem is converted into mild pneumonia, if precautions will not be taken then person will become a perfect patient and at last may be he has to suffer and face death. Previously the version of COVID-19 we faced so called SARS but this version of deadliest germs is even more powerful. Sometimes it is astonished to know that such virus which is almost span all over the globe and peoples are dying as per report and NEWS we had from different sources and the origin of such virus is Hubei which is a province of China and together we are trying to combat with it, but still it is just unbeatable.

As with the arrival of this pandemic COVID-19 the world has faced a different time which not only came and took the life of several persons but also ruin the different sectors of human life and it also left a negative impact all corner of the world. As it spread with sneezing and one infected person may covered ten people in radius of 6 feet. People are getting infected and the case of infected people and dead one increasing day by day & on other side the world scientist and Doctors have no clue about it at the same time people are dying in lack of proper drugs. So by observing all these situations all countries supremo and accordingly Prime Minister of India Sri Narendra Damodar Das Modi Ji decided to close all private, Govt. sectors including college and school as because COVID-19 was spreading fast as we all know this period by LOCKDOWN due to this there is no work and people are facing problem to collect their daily and basic needs because COVID-19 impact all sectors including manufacturing unit/IT-sector/medical/Educational/Coaching. So, there is no job, but a good initiative by Govt. of India was taken to provide meal at free of cost at ration shop. This somehow gives relief. Now we are in 2nd year of this period and things started getting normal but again we are observing the second strain and after that also 3rd strain of Corona which is even more deadlier and in few of the state, lockdown is initiated and in remaining state date will be announced soon. The general people may follow some precautions like:

I. Wearing Mask when going outside and in place where gathering is more and also in hospitals.
II. Use hand sanitizer to kills germs.
III. Take healthy diet.
IV. Complete six hours of sleep.
V. Take part in activities and do breathing stuffs.
VI. Take vegetables and fruits.
VII. Drink more water.
VIII. Keep social distancing at least of 6 ft.

In this chapter we are going to overview how Mathematical modeling and AI (artificial intelligence) can efficiently speed up the steps of different strategies of prediction of the outbreak and combating COVID-19 starting from early detection of the virus, up to development of the vaccine. Besides that AI can be a major support for the health workers as they are severely overloaded with work pressure during these days.

4.2 Effect of COVID-19 in Our Daily Life

COVID-19 pandemic is the most devastating pandemic mankind has ever gone through. None of the previous pandemics had affected 213 countries in all 5 continents together. It has affected human life in all aspects either directly or indirectly.

COVID-19 affects different people in different ways. The most common symptoms include fever, dry cough, tiredness whereas some person also develop mild symptoms like aches and pains, sore throat and diarrhea. But serious symptoms like difficulty breathing or breathing shortness or pain in chest needs immediate medical treatment.

The health care system all over the world is facing the biggest challenge ever, specifically in developing and highly populated countries like India, the scenario is much worse.

The healthcare system is being challenged for diagnosis, quarantine or isolation of the suspected cases and treatment of the confirmed cases.

Most of the time, the infected people and their families are facing social avoidance apart from isolation. Sometimes the health workers and other administrative persons who are being exposed to COVID cases while performing their duties, are also facing social avoidance which is very unfortunate.

Doctors and other medical staff are working under huge pressure accompanying with the high risk of getting infected every moment. Sometimes they are facing a very unfortunate social avoidance which is much painful.

Another major problem is that people with other illness are getting neglected. Specially, the elderly persons, people having other major diseases (like cancer diabetes etc.) who needs regular medical supervision are helpless now a days.

The other challenge the Healthcare system is facing to keep the supply chain of medicine uninterrupted. The medicine production is slower so the supply chain of medicine is disrupted. This is another burden in Health Care system.

Apart from other aspects there are huge psychological effects in people’s life. A sense of panic has overwhelmed the society affecting all ages of people.

The increasing number of positive cases day by day and rumors about COVID-19 circulating in social media platforms are triggering the panic among the mass population.

Social distancing is a must to prevent or slow down the rate of transmission of the disease. Social distancing and lockdown have adverse psychological effects on people of different age groups. In present time people are being confined to a virtual world.

People are working from home on online platforms, classes of schools, colleges and other academic institutions are also being online. The children are restless being confined at home missing the warmth of playing with friends, going to schools, playing in the parks are visiting to a relative’s house or any other place where they were used to enjoy themselves. Now the adverse effect is that they are developing an affinity towards television, mobile phones, and video games. This scenario is making the situation worse. In joint families where many people are present inside the house, the situation is somewhat soothing for the children as they have elderly persons like grandparents or cousins who can spend some time with them. But in current time most of the families are nuclear. In nuclear families where both parents are working the situation is harder. It is very hard to find quality time for the children as in most of the cases domestic helps are also not being allowed.

The situation is not better for the teenagers as they accustomed with busy schedule outside home before the covid situation. They used to attend colleges or schools, tuition classes and other activities or merely spending time with friends and peers in different places outside home, and now they are totally confined in a online virtual world. It is very hard for them to cope up with the changed situation.

The adults are also facing challenges to balance between work and family needs. Majority of the adults are in anxiety and uncertainty about the future sometime there are job related and financial issues too.

A recent survey on 507 adults, people has shown that 71.8% of them are worried about the situation, 24.7% are depressed, 37.1% people become more irritable during the lockdown period, 21.1% of them are repeatedly thinking about testing themselves for covid out of phobia despite of having no symptoms at all.

Overall 64.9% of the respondents of the survey have found that their mental health has been affected. Some of them have found that the situation had threatened their existence and some having difficulties in adjustment with the new routine. Social distancing is restricting people from visiting or meeting their friends and relatives and it is still not known when everything is going to be normal again. There are restrictions in social gathering celebration of religious and festive events. Most of the time, life is confined between four walls. Life is monotonous accompanying with the anxiety for the future uncertainty about getting back the unrestricted life outside four walls.

The covid situation has adverse effect on economy all over the world in all aspects. After being recovered from the covid situation the next biggest challenge for mankind has to face is to recover the economy.

There is an established methodology for the natural progression of any epidemic disease. Infection and contamination are the root causes of any disease spread. After the initial contamination of infected person, common people exposes to their infection and got infected, thus infectious hosts are generated. When any people comes in contact with such infected host then disease spreading starts (Fig. 4.1).

The acquired disease like COVID-19, spread through virus or bacteria or any microorganism (these are called pathogenic agents) plays a vital role in disease spreading along with the other factors like environmental, carrier, infected hosts,

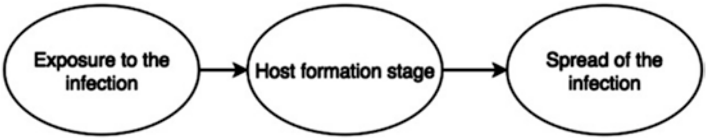


Fig. 4.1 Depicts the host formation and spread [1]

social economic condition etc. COVID-19, evolved as a pandemic spread over 200 countries in the world claiming a death of 738,965 and infected 20,258,229 people [2]. Stage 3 of this pandemic has started early in several European countries and in US, but India encountered an delayed outbreak, and entered peak transition after a couple of months. The characteristics & behavior of the epidemic is different in nature within the same country and in other countries and it is due to several interrelated factors, hence an interesting field of study for the researchers.

4.3 Mathematical Modeling

We know that, Mathematical epidemiology is a well-developed field. Ross pioneered the investigation of infectious disease by malaria modeling [3] and Kermack and McKendrick's general epidemic models [4] has also inspired researchers to use mathematical tool in this domain. Mathematical models help to simulate the behavior of these complex system dynamics which in turn helps to better control/prevent the problems. Quick analysis of epidemiological data is critical for the development of effective containment, viral spread control and preventive interventions. When the data related to the disease growth characteristics and parameters related to a disease spread are correctly measured and available, for example, the infected person count, hospitalized person count and confirmed numbers of recovered and dead individuals, then the calibration of any mathematical model becomes more accurate.

To interpret the real-time data like number of infected people, fatality numbers, time to get treatment and hospitalization is difficult. Lack of clarity and inconsistency in data interpretation has impact on interventions and suppression techniques, eventually changing the behaviour of transmission dynamics. Mathematical and statistical techniques can improve the intervention methodology by minimizing the data interpretation challenges. These mathematical/statistical models can examine the epidemiological data to calibrate the transmission model more accurately to test the aftermath of adopted intervention strategies and predict the risk associated with society and readiness of healthcare systems [5] to combat the spread.

In different studies, the time parameters of covid spread have been evaluated: In [6, 7], incubation period is calculated as 2–14 days, whereas the latency between infection and hospitalization has been reported as 10 days for the cases. According to the World Health Organization (WHO), the time difference between the reveal of symptoms in an infected person and his unfortunate death varies from 2 to 8 weeks [8]. Viral shedding time is estimated as 8–37 days [9]. Multiple factors drive the effectiveness and contribute to the calculation of period in intervention implementation [10]. The work [11] suggests that at room temperature, this virus can survive on non-living objects like paper, glass, metal, wood, , and cloth for 4–5 days. However, as per WHO guideline, 14 days of quarantine or isolation period is being considered as a standard time period in most of the countries to prevent the outbreak of this pandemic. Therefore, to implement the effective social guidelines and measure the effective lockdown period to minimize the transmission, it is important to predict/estimate the duration mathematically and statistically. As the population density varies across the countries and each population carry unique transmission patterns of the disease, the mathematical model also becomes dynamic with respect to geographical ethnicity. After a person gets infected, the onset of symptoms happen after 10 days and peak viral load occurs when virus attacks the respiratory track. The ill and symptomatic patient plays a key role in transmission spread [12, 13].

The categorization and the techniques used for the analysis of disease dynamics is based on different data sources used which includes social media, big data and clinical data. Along with various statistical & analytical parameters, medical characteristics of both symptomatic and asymptomatic patients are considered for mathematical model structuring which includes numerous factors and biases.

- **Incubation period**: To model the incubation period, the period between the individual was infected and the onset of covid symptoms in him. An approximate potential exposure timeframe is considered to measure the infection time. Incubation periods, and many other distributions is best fitted in gamma distribution.
- **Basic Reproduction Number (R0)**: It is defined as reproduction number Rt, at time t, a typical infective person can contaminate these many average number of cases. High R0, symbolizes fast growth, and that indicates possible asymptomatic infection spread, helps to find out any potential interventions. Large R0 values mean a sharp rise in infection spread and substantial amount of management required for transmission control; which in turn causes the rapid growth of number of cases in the absence of effective interventions or suppression.
- **COVID Awareness:** Social distancing, quarantine, isolation also socialize people to reduce spread.
- **Demographic population**: Age, Gender and their average health condition, specially the co morbidity of people due to socio economic condition.
- **Statistical factors impacting data collection:** like report time, bed facilities for treatment, death count etc.
- **Environmental** factors like temperature, humidity, Geographical location.
- **Governmental Strategy:** Lockdown period and strictness to follow the same, Transportation and communication rules modeling, Healthcare system Support and improvement to serve the infected people.

4.4 Stochastic Theory/Mathematical Models

Several traditional approach of the stochastic theory and mathematical model is followed in the below studies [14–19], which analyze and predict the death rate, infected count and probable end date of this pandemic period.

The SIR model is one of the simplest compartmental models consisting three compartments: Susceptible (S), Infectious (I) and Removed (R)[20]. Here

Susceptible(S) represents those persons who prone to be infected, but they are yet to be infected by the disease. These persons are not infectious and are not responsible for disease spread at this moment. Initially the entire population is considered in this group, Infectious(I) are those persons who have already been contaminated by the disease, reveals the disease symptoms and hence are infectious, they have the ability to spread the disease by infecting others and the Recovered(R) represents the people who got well after treatment or died. Also this model assumes same birth rate and death rate in this pandemic period, so the total population remains constant within a region (ignoring the very less significant population change), N = S + I + R = Constant. The SIR model can be expressed by the following set of ordinary differential equations [21]:

$$\frac{dS}{dt} = -\frac{\beta IS}{N}$$
$$\frac{dI}{dt} = -\frac{\beta IS}{N} - \gamma I$$
$$\frac{dR}{dt} = -\gamma I$$

Where, t is time and at time t, the number of susceptible persons is represented as S(t), whereas I(t) and R(t) are the number of infected persons and the number of recovered persons respectively at time t, β is the contact rate, and 1/γ is the average infectious period.

Based on the basic epidemiological model **SIR** (susceptible-Infected-Recovered) model, several modified compartmental model has been proposed to simulate the pandemic behavior, and the newly added compartments are mainly Exposed (E), Quarantined (Q), D (Death), Hospitalized (H) etc in different research journals.

The epidemic trend in Wuhan, China is estimated applying the modified SIR model: **SEIR** (Susceptible, Exposed, Infectious, and Removed) model [22, 23]. The differential equations of the SEIR model are given as:

$$ds / dt = -\beta SI / N,$$
$$dE / dt = \beta SI / N - \sigma E,$$
$$dI / dt = \sigma E - \gamma I,$$
$$dR / dt = \gamma I,$$
$$\beta = R_0 \gamma,$$

where transmission rate is β, σ symbolizes the infection rate and γ is the recovery rate. There are differences between forecasted and actual data. The number of infections estimated as on Feb 29 using this model was 81,393 whereas the actual number of infection was 79,500. Using a similar model [24], forecasted 39,000 infections and the actual number was 67,760 in Hubei for Mar. 10, 2020.The **SLIAR** (consideration of stages like susceptible, latently infected people with symptoms and asymptomatic infectious people and removed/recovered individuals) epidemic model [25], introduced a little variation in the classic original SIR model, which considers different metric during incubation, spread and recovery: in every phase of disease propagation. The SL1L2I1I2A1A2R epidemic model implements an Erlang distribution in different compartments.

SEIQDR-based method for estimation [26], adopted the degree of infection of COVID-19 in susceptible populations. β_E and β_I are the infection rate coefficients of latent and freely infected people in susceptible populations a. They arrived at a formula:

$$f(t) = (\beta_E CE + \beta_I CI)\frac{S}{S+E+I+R} = \frac{\beta_I CS}{S+E+T+R}(kE+I),$$
$$k = \frac{\beta_E}{\beta_I}.$$

Another **8 compartments mathematical model** [27], has included two more compartments those have contribution to the disease dynamics: super-spreaders class (P) who have more contamination compared to other infected individuals and asymptomatic class (A) who are infectious, but not showing any disease symptoms. Here the basic reproduction number is evaluated for a qualitative analysis of the model, also local stability calculated and sensitivity analysis also performed. Eight epidemiological classes of the total population size N are described as follows: susceptible (S), exposed (E), symptomatic and infectious (I), super-spreaders (P), asymptomatic (A), hospitalized (H), recovery (R), and fatality (F). According to this model β, ρ1 and δi (β is the transmission coefficient of infected individuals, ρ1 Rate at which exposed people become infected I and δ is Disease induced death rate due to infected class) are the most important contributing and sensitive factors in determining the basic reproduction number R0 of the COVID-19 modelling. In concrete, it has been observed that an increase of the value of transmission rate i.e., the increase β will impact and increase the R0 sharply and parameter ρ1 also behaves in the same manner. On the contrary, death rate (δi) increase will eventually decrease R0.

To measure the real-time forecast, **hybrid autoregressive integrated moving average model** [28] have implemented a wavelet-based forecasting model (ARIMAWBF). They have predicted critical risk factor also. Both ARIMA and WBF models are used to forecast the spread of the epidemic.

Using the statistical data in Italy, Spain, and France, **ARIMA** time series model [29] was implemented to evaluate the COVID-19 prevalence.

Using the counts of confirmed infected persons, **The discrete-time SIR** model [30] has predicted death count, also the prediction was near to the actual number.

The **control-oriented SEIR model** [31] emphasizes the effects of delays in disease spread and analyses how different containment policies can impact the model dynamics. Here the objective is to minimize the reproduction number Rt,.

Dowd et al. [32] showed the impact of factors like age, gender on the count of death toll. It has been observed that the elderly population is severely affected by this virus infection and the mortality rate is also high among co morbid people. In Italy, the population had a greater percentage of elderly persons and hence faced worst impact. So the countries having similar age structure has may have a maximized threat.

He et al. [33] has considered the effect of pre-symptomatic transmission. From the observation, it was inferred that though the disease symptoms are yet to onset among all people, but the rate of transmission in the disease was at its peak before that. It calculates that the 44% of transmission can be detected even before the first symptoms become evident in the physique of the infected. Hence they flags concerns to the disease control authorities so that they can consider the pre-symptomatic transmission as an prevailing factor while implementing different preventive and curative measure to curb the spread.

In our mathematical study, it has been observed that the infection spread may be modelled as below graphical representation while studying the case of India. The spread has a Gaussian distribution.

India's spread of the disease:

Different available models [34] from recognized World Universities like MIT, Columbia University, John Hopkins University, University of California University of Arizona and other organizations have been elaborated with their model name along with the intervention assumptions & method. Figure 4.2 depicts COVID-19 size estimation for India with different probable state. Figure 4.3 is forecasting COVID-19 size for India with final casualty size.

Different mathematical models not only analyzed the rate or count of Infectious and Recovered individuals, but also focused on other aspects like a large number of population who are asymptomatically infected and hence playing key role in disease spread, the range of population who got false positive

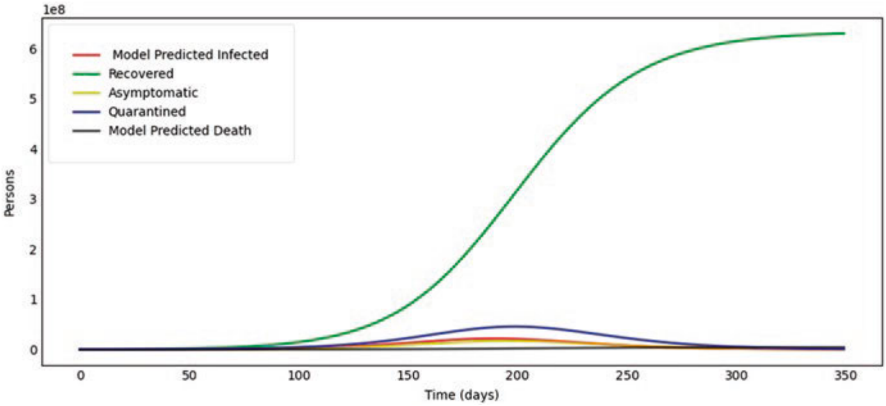


Fig. 4.2 COVID-19 size estimation for India with different probable state of disease

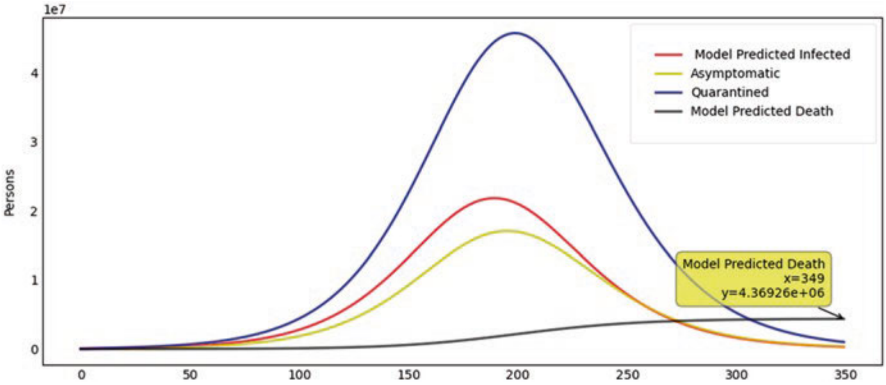


Fig. 4.3 Forecasting COVID-19 size for India with final casualty size

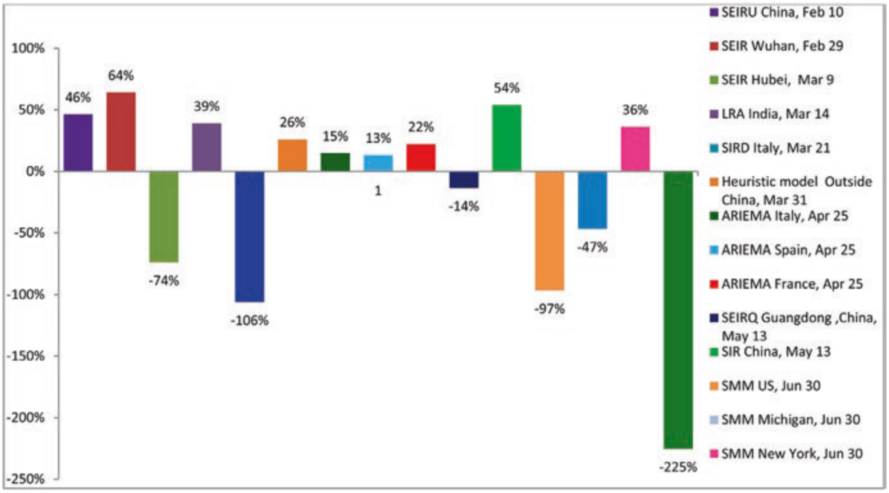


Fig. 4.4 Graphical representation of the anomalies in predictions

result or wrongly diagnosed etc. Thus the models developed several hypothesis in multiple directions representing various possible threats, hence providing a direction to future footsteps.

Most of the models are the derived and more extensive version of the basic SIR model, but they have thrown light on several un-accounted parameters. Since they have implemented different prediction methodology depending upon those parameters, their outcome also differs in numbers.

The graphical representation of these models' outcome is presented in Fig. 4.4 and the difference in prediction in Table 4.1 [35].

Table 4.1 Difference in predictions of COVID-19 pandemic

Model	Country	% (±) Deviation
SEIRU	China. February 10	46
SEIR	Wuhan. February 29	64
SEIR	Hubei. March 09	74
LRA	India. March 14	39
SIRD	Italy. March 21	106
Heuristic Model	Outside China. March 31	74
ARIMA	Italy. April 25	15
ARIMA	Spain. April 25	13
ARIMA	France. April 25	22
SEIRQ	Guangdong. China. May 13	14
SIR	China. May 13	54
SSM	US. June 30	97
SSM	Michigan	47
SSM	New York	26
SSM	California	225

4.5 AI: An Intelligent and Efficient Hand to Combat Covid

AI can put real hand in COVID-19 application, where the steps include undergoing a training process/learning mechanism from the information extracted from medical sources like screening diagnosis, virus analysis, treatment works etc. Then, they can utilize the gathered domain knowledge to establish comparable features of objects' behaviors, the relationship between objects, then, their trend analysis and output the optimum.

We know to combat against the virus, the main things which are needed to be done is-

- Identifying and reducing or locking the possible gateways or means of spread of the virus.
- Identifying or testing the infected ones rapidly and isolating the infected and non infected fast.
- Treatment of the infected with proper medical care & supervision.

Fortunately AI can be used to manipulate all the above means of combating the virus in effective way.

Now let us take a look how AI is making things possible-

- From the analysis of patient data AI can predict the high risk or susceptible community who are needed to be taken special care while they are being exposed to the virus.
- AI also can predict the possible ways of spreading the virus.
- AI can be used to identify the hotspot zones where rate of infection is high.
- By analyzing data, AI can also suggest the possible means of controlling the spread of the virus.

- AI can figure out the mortality risk of infected persons by analyzing previous data & point out the risk factors triggering mortality rate.
- The images from CT scan and other electronic images from the infected and non infected persons are collected and then analysed using various ways employing AI and then used for primary screening and detection of the virus.
- The other major aspect is that AI can be effectively and efficiently employed in infodemic control, awareness creation, planning, notification, suggestion among the mass population, employing social media and other Mass Communication mediums. AI potentially and efficiently helps in improvement and implementation of the plans to control the disease.
- AI can help the health workers by reducing the stress and workload on them.

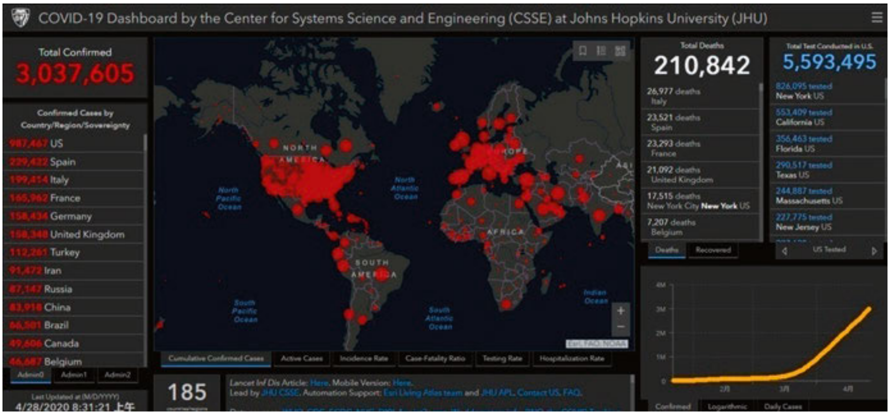
So AI is growing to be an indispensable weapon to combat against the Coronavirus disease in multiple ways. More specifically Machine learning is doing a great job in this regards.

4.5.1 Some Applications on COVID-19 Issues Addressed Using Machine Learning

4.5.1.1 Virus Source Prediction

The outburst of special type of pneumonia which is instigated by COVID-19 has a severe risk to human healthiness worldwide. To get the prevention from this deadly disease and to control the spread, it is noteworthy to discover the origin of this virus. Several studies have been done in different country which is related to get the source of this virus. The following section highlights some AI related techniques.

Randhawa et al. [36] has performed some genome analysis with the aid of machine learning (ML) techniques and Hill et al.[37] has also used genome analysis by means of machine learning (ML) along with digital signal processing (DSP) to classify COVID-19. They used more than 5000 genomes and test the relationship at the taxonomical level of the species and domain. With the Chaos Game Representation (CGR), with the representation in digital form, each and every genomic sequence has been mapped to its genomic signal. Here they have used 6 supervised learning classification models which have been used for training and for that, required feature vectors are obtained by the digital interpretation and can be taken as input to train. Here, 2D genomic feature set has been used to do classification taxonomically of the COVID-19 virus which can be accomplished by different machine learning based technique. This alignment-free technique can also precisely forecast the new sequences.



COVID-19 Dashboard by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University (JHU)

Total Confirmed
3,037,605

Confirmed Cases by Country/Region/Sovereignty

987,467	US
229,422	Spain
199,414	Italy
165,962	France
158,434	Germany
158,348	United Kingdom
112,261	Turkey
91,472	Iran
87,147	Russia
83,918	China
66,501	Brazil
49,606	Canada
46,687	Belgium

Last Updated at (M/D/YYYY)
4/28/2020 8:31:21 上午

185

Lancet Inf Dis Article: Here. Mobile Version: Here.
Lead by JHU CSSE. Automation Support: Esri Living Atlas team and JHU APL. Contact US. FAQ.

Total Deaths
210,842

26,977 deaths	Italy
23,521 deaths	Spain
23,293 deaths	France
21,092 deaths	United Kingdom
17,515 deaths	New York City New York US
7,207 deaths	Belgium

Total Test Conducted in U.S.
5,593,495

826,095 tested	New York US
553,409 tested	California US
356,463 tested	Florida US
290,517 tested	Texas US
244,887 tested	Massachusetts US
227,775 tested	New Jersey US

Fig. 4.5 Online dashboard to visualize the reported COVID-19 [2]

4.5.1.2 Epidemic Development Forecasting

As we know COVID-19 is a quickly propagating epidemic and impending people's lives. So, as a health emergency, different forecasting methods have been developed. Dong et al. [37] developed a real-time dashboard to envisage and track the testified COVID-19. On January 22, 2020, this dashboard was first opened for public. It basically shows the location and count of confirmed COVID-19 cases, growths, deaths, and rehabilitations in all distressed countries (Fig. 4.5).

In the very early stage, the lack of characteristic information and knowledge of new disease and due to probable uncertainty, the virus widened enormously. At the starting time of an epidemic, data were so less and it was very difficult to get a suitable forecasting model with very less training samples. It's a really a great challenge due to few data for training using machine learning. Fong et al. [38] predicted the outbreak of corona virus which was originated at Wuhan with the help of polynomial neural network through corrective feedback (PNN + cf). To improve accuracy, only statistically and mathematically significant and relevant information should be added.

4.5.1.3 Infection Classification

In present days the detection of COVID-19 using CT images is a growing and useful technique. With the help of image classification methods, one can detect whether the patient has this disease or not. Research on this type of medical images are very popular and going on for many years. This medical image analysis and through classification, detection of COVID-19 is also a challenging task. To distinguish COVID-19, Narin et al. [39] developed a deep convolutional neural network (CNN) based models to classify chest X-ray images into COVID-19 and normal categories.

Insufficient data problems and training time problem have been mitigated by implementing transfer learning techniques with the help of ImageNet data.

4.5.1.4 Contact-Tracing Apps

These are getting developed and widely used to determine the proximity of infected persons. If a Covid infected person updates his positive result in his/her Smartphone app, other users who are not infected but gets closer physical distance with the infected person, will get a risk alert in Smart phone. Thus AI algorithms can then determine the risk of cross infection and detect the whereabouts of the infected person. This is crucially important because this type of contact-tracing application can help to stop this pandemic. But in 80% persons who are using smart phone need to make use of this app. This statistics is stated according to the University of Oxford's Big Data Institute.

4.5.1.5 Drones and Robots

Drones and robots are nowadays a very useful media for delivery and which is contactless also to spray disinfectants in the populated area to curtail the menace of cross-infection. Some other robots are inspecting people for fever as well as other COVID-19 indications and distributing hand sanitizer spray and gel, in a word replacing the part of health workers. Several hospitals are using Robots to attend patients by serving food and medicine. And by this way, it is disinfecting rooms as well as minimizing contact with individuals.

4.5.2 Some ML Algorithms Used to Address COVID-19

4.5.2.1 Classification Using SVM

In some primary studies, patients were diagnosed to have some abnormal characteristics in chest X-Ray images. Barstugan et al. [40] proposed a system which will early detect coronavirus (COVID-19) with the help of machine learning techniques. Feature extraction techniques has been used to detect COVID-19 infection and to improve performance of classification. Subsequently, SVM is also used to classify with the extracted features. 99.68% is the highest classification accuracy that is obtained, shows the enormous capacity of the algorithm in detecting infection. A deep convolutional neural network (COVID-Net) is developed by Wang et al. [41] and applied to detect COVID-19 cases from chest X-ray images. The COVID-Net architecture makes widespread use of projection-expansion-projection-extension

(PEPX) design patterns. Besides, how to predict, COVID-Net also helps to interpret the disease and that is also the emphasis of the study. Interpretability can intensify the insight of the key factors related to COVID cases, that can help medical practitioner to perform improved screening.

4.5.2.2 Classification Using Deep Learning

Deep learning is an emerging and most used leaning methods nowadays. Along with detection jobs, the diagnosis of uncertainty occurred, is a very challenging but unavoidable job for radiologists. With the help of the publicly available COVID-19 dataset of chest X-ray, Ghoshal et al. [42] experimented on the drop weights-based Bayesian convolutional neural network (BCNN) to approximate the uncertainty in deep learning solutions. It expands human-machine amalgamation and try to attest that the accuracy of uncertainty prediction and the accuracy of prediction are closely related. It is supposed that this appearance of uncertain deep learning solutions will lead to broader medical applications of AI.

Similarly, Wang et al. [43] proposed a new indicative algorithm which is based on the radiographic deviations in CT images. The results establish that the mining of radiographic features by means of deep learning approaches is of excessive value for diagnosis of COVID-19.

4.5.3 Incorporating Cloud Computing

The growing coronavirus crisis has challenged online applications and due to huge improvement in cloud computing it has been intensely, securely, consistently scale up to a notable feat. It is only likely for the reason of our public clouds and their related technologies. All jobs related to office, shopping, entertainment solutions wherever it is and which needs social distancing and have caused in a enormous and sustained surge in users of cooperation, adapts personal exchanges to virtual ones. Along with supporting the sustainability of our world socio economic flow, the cloud architecture is also serving analysts to carry with huge amounts of computations in the research of disease transmission dynamics, bioinformatics.

Virtual frameworks provide a scalable end to end service virtualization through reliable virtual servers, virtual networks and above all unlimited virtual storage facilities. Cutting edge technologies and AI advancement is playing a vital role to accelerate viral condition sequencing, forecasting, protein-screening as well as other different researches in treating or hindering the Coronavirus. The centralized control optimizes the cost of working and leverages the control and program of distributed infrastructure in more effective manner.

4.6 Conclusion

We discussed about the predictive modelling to forecast the pandemic spread through mathematical and AI means, the time series data will enrich the future AI working. In short span of this literature, various forecasting models are analyzed and discussed in context with their approach towards prediction of different parameters considering different assumptions and challenges & often concluded with the probable recommendations to restrict this disease spread. Several parameters considered includes quarantine time span, death toll count, lockdown period, environmental parameters, available medical capabilities & facilities, mobility of population. Apart from the prediction methodologies, we admit that there are various challenges like tracking the infected people, right and accurate data gathering, measuring the parameters like incubation period, transmission coefficient etc.

In this virtual working environment, cloud computing plays a vital role & responsibility in survival of human civilization. We talk about diverse areas where cloud computing can be of assistance in fighting with this existing outbreak. Simulated intelligence in computing domain can assist in generating proper treatment protocols, neutralization methodologies, and implementation of improved medication and advanced immunization procedures. Advanced research works should be considered to go after the crisis of COVID-19 at different scales, for example, consideration of aftermath of medical situation of this epidemiological pandemic. The accessible and available information can be utilized to the examination of this infection. Likewise, in framing appropriate treatment protocol, taking preventive and protective measures in medication, and advancement in immune systems, at the same time people awareness and Government steps are also necessary to adapt the advancement of technology. More researches and surveys needs to be carried out with the help of the big data gathered from different patients and utilization of this data can diminish the spread or an effective solution to this pandemic. Though the several vaccination have started their efficacy throughout the world, but emergence of new strain of this virus has triggered a new challenge to the researchers.

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Chapter 5
Impact of COVID-19 on Higher and Post-secondary Education Systems

Imdad Ali Shah, N. Z. Jhanjhi, Mamoona Humayun, and Uttam Ghosh

Abstract Education has a critical role in societal progress. A strong educational system produces good citizens. Countries that scrimp on education fall behind in the drive for progress. The advancement of ICT has resulted in major and positive advancements in the educational system, allowing knowledge to be accessed from anywhere. Numerous of people are unable to be present traditional the advantages of classes in the e-learning system, which has been embraced by most modern civilizations. However, technology cannot be utilized to replace face-to-face communication learning. The combination of traditional education and eLearning is extremely beneficial, and many industrialized civilizations are reaping the benefits. COVID-19's rapid global expansion has recently brought the old educational system to a halt. Lockdown and seclusion have kept billions of children out of school. The majority of countries have declared school closures. Distance learning is the only way to keep the educational system moving in such a situation. The current eLearning infrastructure, on the other hand, was not prepared for such a quick change from traditional education to eLearning. The object of this chapter is to give focus to the higher and post-secondary education systems and to compare the results

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_5

to determine which system is more effective. Further, every day, lots of new problems are reported, such as internet access, conducting evaluations, etc.

Keywords COVID-19 · ELearning · Distance learning · ICT · Digital learning

5.1 Introduction

UNESCO is monitoring the pandemic's influence on education. The majority of these pupils are in elementary and secondary schools, but millions of students in pre-primary and postsecondary education are also affected. Over 180 countries have closed their schools across the board, while others have instituted localized closures. Over time, 500 million children and teenagers have been threatened with being unable to attend school or university due to nationwide lockdowns. The document Education Response in Crises and Emergencies has gotten a lot of attention from international organizations. The most prevalent technique used by governments to combat COVID-19 transmission has been to minimize physical contact [1]. Schools and families had to quickly transition to a new teaching and learning environment without the advantage of prior planning [2]. Similarly, inequalities in learning possibilities for children from diverse socioeconomic backgrounds were caused by different cases Fig. 5.1 Overview effect of Covid-19 on educational systems Fig. 5.1 Shows the Impact of Covid-19 education sector.

Figure 5.1 Country-wide closures have kept 1,389,345,915 pupils out of educational institutions, accounting for 80% of the world's students. Closures at a municipal level, such as those witnessed in California and Virginia in the United States, affect another 284 million students in some way. 140 governments have now ordered the closure of all of their schools and institutions across the country

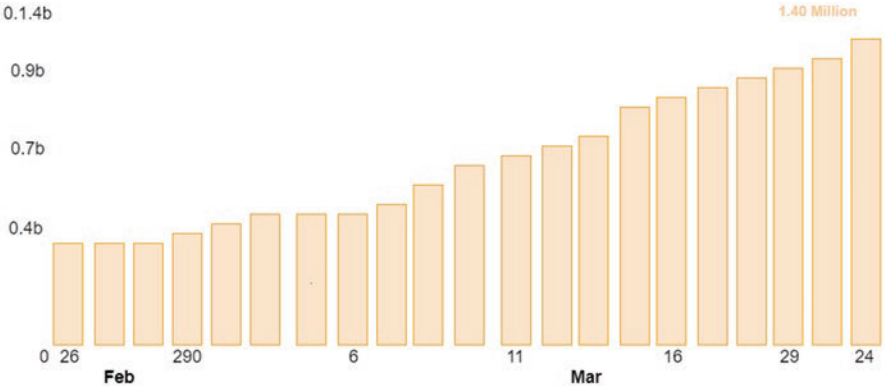


Fig. 5.1 Impact of Covid-19 on educational system

The main object of this chapter is to deeply peer-review the impact on higher and post-secondary education during COVID-19. Furthermore, this chapter will be consistent with the following objectives.

1. To provide an in-depth examination of the higher and postsecondary education systems during COVID-19
2. We will concentrate role of e-learning
3. We will give focus on internet connectivity issues.
4. To compare the affective outcomes of higher and postsecondary education systems.

5.2 Literature Review

Several universities in Nigeria had begun their first semester examinations before the COVID-19 outbreak, which forced the closure of all educational institutions across the country [3]. Students also had varying levels of internet connectivity and unequal access to electronic gadgets to complete their assignments. Around 56,000 schoolchildren currently do not have access to the internet [4]. The majority of the households in our poll had high-bandwidth internet access. However, there were significant differences in terms of technology's "possibilities of usage." For example, 15.3% of those polled said they only had access to a single device at home or only possessed a mobile phone [5]. The internet can also be described in terms of device access based on family composition [5]. Only one device was available in 12 percent of homes with two children, 32 percent of households. The primary difference between prior studies' school closures and the present lockdown is that schools have managed to keep some touch with pupils this time, primarily through online education. Despite the efforts to facilitate remote learning, many students have not been able to make use of it [6]. That teachers were unable to contact a significant percentage of students, owing to a lack of an internet connection or appropriate gadgets for remote learning [7]. People all over the world are facing a major challenge now. On the other hand, is igniting a desire to go deeper into the possibilities of virtual education [8]. Meanwhile, the Ministry of Education (MOE) in Saudi Arabia uses television and social media to deliver education to students of all ages [9]. It has nominated around 128 administrators and instructors to provide regular instruction in 112 educational courses via 19 television channels [6]. The government offers learners five options for online education [10]. Furthermore, e-learning is divided into two categories: complete learning and blended learning, depending on whether the approach is used as an addition to or a supplement to face-to-face education [11]. Face-to-face contact is not required in the case of total e-learning. In the case of blended e-learning, however, face-to-face contact is necessary. When it comes to mixed e-learning, both face-to-face and online learning are used on occasion, [6]. E-learning will not succeed if technology is used alone. Teachers that are comfortable with technology are critical to the success of e-learning [12]. Teachers

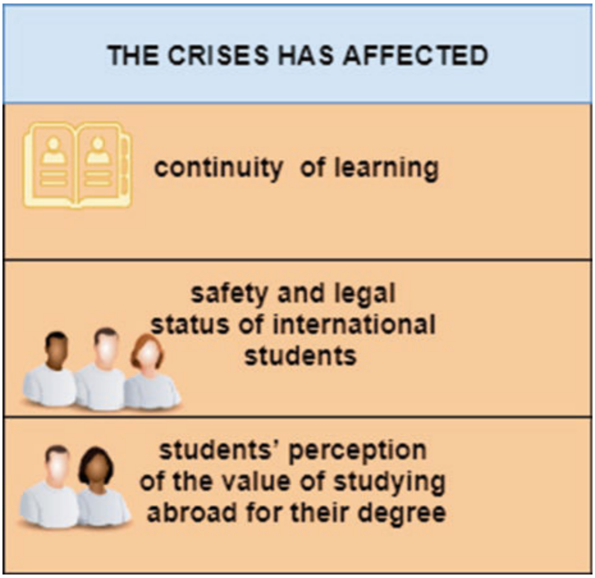


Fig. 5.2 overview affected crises

are required to take on new responsibilities as well as nurture a variety of inventive skills as a result of new technology. Several studies have identified the varied responsibilities that instructors are expected to accept when using new technology in the classroom Fig. 5.2 show affected crises [13, 14].

5.3 COVID-19 Evaluation of the Higher Education System

Going to school is the best public policy tool available for improving abilities. School is a place where kids can have fun while also improving their social awareness and skills. The primary goal of attending school or staying in school is to improve a child's abilities. Schooling for a relatively short amount of time improves skills and abilities. On the other hand, missing school or failing to attend school will have a detrimental impact on skill development. The structure of learning and schooling has been changed by the closing of schools.

- All educational activities were impacted: The government initially declared the suspension of schools for a month, but the time frame was steadily extended, and it is unclear when they will return. Various activities that are very important take place during this period, such as competitive exams and entrance tests for various universities, board examinations and semester examinations at universities, nursery school admissions, and university admissions [15, 16]. No immediate solution has been identified to stop the COVID-19 outbreak. The closing of schools and universities in India would not only have a short-term impact on the continuity of learning for young learners, but it would also have a significant influence on the country's economic growth as well as a society [17]. The institutions were forced to close, posing a slew of problems for stakeholders [18, 19]. To begin with, it had an impact on teaching and assessment methods. Only a few private schools employ online teaching methods and even fewer enroll in online courses. Children at those schools take classes online [20]. Low-income private and public schools, on the other hand, have been closed down and do not have access to an eLearning solution. It is interfering with kids' ability to learn. The change in teaching approach has caused a slew of problems for parents [21].

5.4 COVID-19 Evaluation of the Post-secondary Education Systems

Universities and other post-secondary education institutions have also seen substantial transitions to remote learning, though this is not as dramatic as it has been in schools because universities have been offering online instruction for several years [22]. However, the trend to more online teaching has lasted longer in universities than in schools [23]. Furthermore, Australian higher education providers are particularly vulnerable to income losses from international students, with many reporting employment losses and service reductions, both of which are likely to have negative consequences for current and future students. In the United States, the pandemic's effects on institutions and students have varied. 'The pandemic was universally disruptive to students, while also demonstrating that this disruption was substantially bigger for lower-income students [24, 25]. The fact that lower-income students were more likely to have been financially harmed by COVID-19 and were more concerned about the virus's direct health hazards appears to be the primary reason for this second conclusion [26, 27].

5.5 COVID-19 Evaluation of the E-learning

The concept of "internet" and "technology" as a support system is highly intertwined with the conduct of an e-learning system. Teachers must know the internet and technology in order to teach in the 4.0 era. E-learning will be used to merge traditional face-to-face meetings with the blended learning system. Because this pandemic requires study from home, the e-learning system is to be held to accommodate the teaching and learning process from home, especially in the face of the COVID-19 outbreak. Some information and technology items can be used to support the online classroom when performing e-learning. Whatsapp is the first e-learning application to be supported. It is a free chatting programme that is widely used. Whatsapp is efficient at increasing learning success and developing good attitudes toward the usage of Whatsapp in classes [28]. Whatsapp can also be used to increase pupils' enthusiasm to learn [29]. Whatsapp is recognized as a reliable tool in terms of peer evaluation [30]. The Google Classroom is the second eLearning assistance programme. It's also free software that allows students and teachers to chat and conduct online classroom activities. According to, teachers may manage classroom activities effectively and efficiently using Google Classroom [31]. Some teachers, on the other hand, believe that Whatsapp is merely a tool for managing documents and basic classroom functions, with no significant impact on teaching approaches [32]. Some drawbacks to using Google Classroom should be considered, such as the requirement for a smartphone and the availability of mobile data when using this service [44]. Youtube is another social media platform that can be used in the teaching and learning process. The incorporation of Youtube videos into the classroom contributes significantly to instructional flexibility. The usage of Youtube in the classroom serves a critical function in assisting students in comprehending lessons, having a significant impact on students' comprehension and also providing useful teaching resources [33]. Many additional programmes, such as ZOOM, Google Meet, Facebook, and soon, could be used as a useful tool to support online classrooms. The proper learning tools must be selected with care, taking into account the teachers' abilities to use technology, the students' needs, and other support systems. The purpose of using a supportive tool is to assist both teachers and students in using an e-learning system to perform teaching and learning Table 5.1 shows participation of line classes [34].

5.5.1 Distance Learning and Online Classes Design

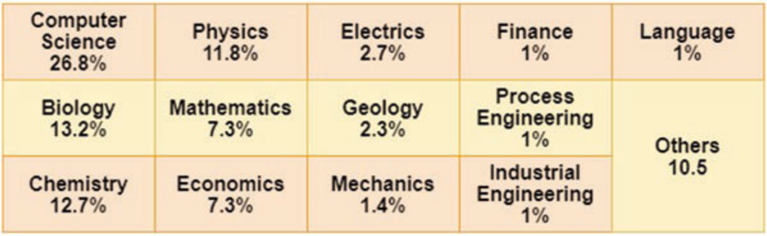
Faced with the Covid-19 outbreak, the government implemented an online learning strategy that tries to break the virus's chain of transmission. This regulation is unquestionably beneficial to apply, especially because some virus-affected countries follow suit. However, online learning is difficult since the learning objectives, such as the existence of perception, the distribution of material, the question and answer procedure, and evaluation activities, must all be carried out wholly through online media [35]. The school, teachers, students, and parents must all work together to ensure that this online learning design is successful. Over the last 10 years, online learning has been studied. Smartphones are chosen by consumers over other devices since they are easier to carry and offer a lower price than other gadgets. Online learning is a technique that allows students to perform more diverse and extensive studying [36]. Learning using online media can include a variety of formats, such as video or audio, in addition to written information figure Table 5.2 Show number student's age and percentage [37].

Table 5.1 Overview participations

Participations	Female	Male
Professors	74.70%	25.30%
Students	46.5%	53.5%

Table 5.2 Overview of number student's age and percentage

Age	Percentage
20–30	14.6%
30–40	28.1%
40–50	19.2%
50–60	28.3%
>60	18.1%



Computer Science 26.8%	Physics 11.8%	Electrics 2.7%	Finance 1%	Language 1%
Biology 13.2%	Mathematics 7.3%	Geology 2.3%	Process Engineering 1%	Others 10.5
Chemistry 12.7%	Economics 7.3%	Mechanics 1.4%	Industrial Engineering 1%	

Fig. 5.3 Participation's subjects name

5.6 Discussion

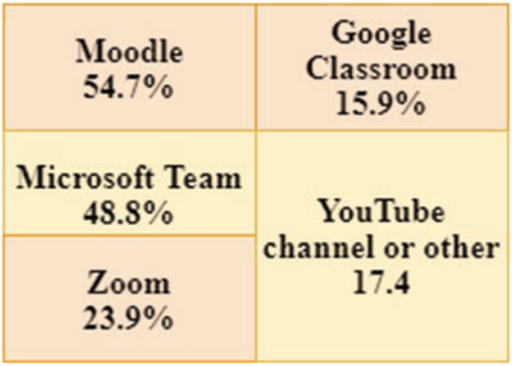
From the perspective of parents compelled to stay at home due to the lockdown, this study emphasizes the difficult effects of COVID-19 school shutdown on children's education. Despite all respondents having a TV/radio device and the vast majority having a computer device with internet access, it shows a significant absence of continuing learning engagement among children and young adults Fig. 5.3 participation's subjects name [38].

5.6.1 Current Situation

As of Sept 2021, 27% of countries were still restricted completely or partially. There are still regional disparities, with full school closures occurring in four of the nine regions. In two regions, a greater proportion of countries keep their schools completely closed. Overall, no region has all of its countries' schools fully reopened Fig. 5.4 overview percentage of people who use distance learning platforms [39].

5.7 Overview of Parents' Experiences of Their Students

Given the diversity of education frameworks among Australia's eight States and Territories, the naming of different levels of education and early learning is a bit hazy. Infants refers to early childhood education prior to the start of full-time



Moodle 54.7%

Google Classroom 15.9%

Microsoft Team 48.8%

Zoom 23.9%

YouTube channel or other 17.4

Fig. 5.4 Overview percentage of people who use distance learning platforms

schooling, with most children attending 1 year of preschool [39]. However some countries offer 2 years. An Infants/Primary school was the most prevalent type of education or care that their children received [40]. The most frequent form of education or care that their children were receiving was an Infants/Primary school student at a government school (11.7%), with the remaining education types reported by 5.2–6.8% of those who responded to the study, [41]. Fewer than four out of 10 high school graduates will attend college immediately after graduating, and half will never attend college [42]. The percentage of college graduates is 30.9%, once again falling the national average of 32.6%. For those who are able to attend a 4-year institution, the average college student graduates with more than $37,000 in debt. Unfortunately, many young people are left without the means or opportunities to acquire a postsecondary education [43, 45].

5.8 Critical Overview of Chapter

Online assessment tools have their own set of constraints [41]. In comparison to traditional measuring, several measurement mistakes have been identified in online assessment systems [42]. Due to the sheer increased disruptions in applicants' signals, new graduates' matching efficiency is dwindling, resulting in higher job separation rates and slower earnings growth. These include instructor, student, course, and staff expectations. There is no way to judge the effectiveness of these online courses without defined standards and expectations for faculty members [43].

From March 2020 to September 2021, 131 million students in pre-primary to upper secondary education in 11 countries lost at least three-quarters of their classroom teaching time. The majority of governments where students have completely missed three quarters of classroom instruction has decreased compared to prior projections. Since February 2021, countries have transitioned from complete school closure to partial school closure, resulting in this reduction (Fig. 5.5).

Students from pre-primary through upper secondary are included in the study. The statistics for enrolment in 2020 are extrapolated from the most recent number of students enrolled. Schools have gradually restored beginning May 31, 2021, with

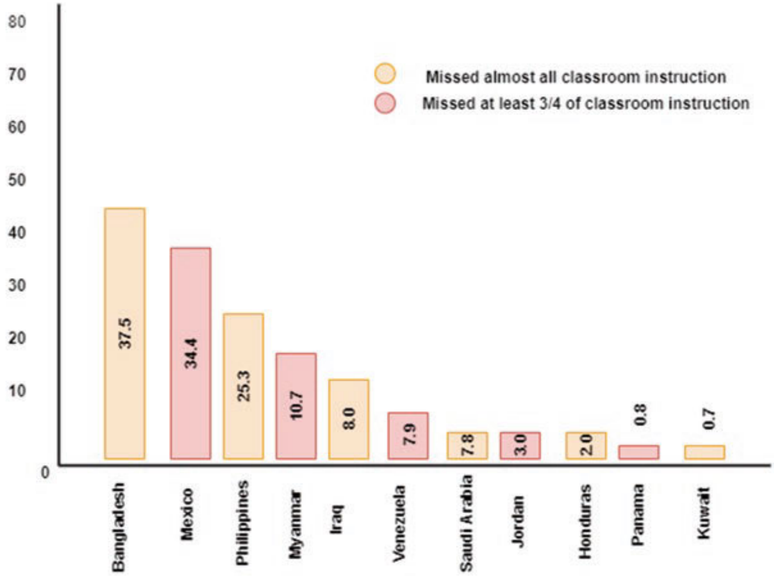


Fig. 5.5 Number of students (in millions)

schools for 0.7 million children remaining closed by August 2021. Updates on the COVID-19 education response.

5.9 Suggestions

1. Governments and educational institutions should make it a policy to offer free internet access.
2. To mitigate the effects of the pandemic on employment offers, internship programs, and research initiatives, immediate action is essential.
3. It provides online learning programs with quality promise mechanisms and quality criteria.
4. To give more focus to virtual education activities and their use on another online platform.

5.10 Conclusion and Future Work

Education has a critical role in societal progress. A strong educational system produces good citizens. Countries that scrimp on education fall behind in the drive for progress. The advancement of ICT has resulted in major and positive advancements in the educational system, allowing knowledge to be accessed from anywhere. Many people who are unable to attend traditional classes benefit from the e-learning system, which has been embraced by most modern civilizations. However, technology cannot be utilized to replace traditional face-to-face learning. The combination of traditional education and eLearning is extremely beneficial, and many industrialized civilizations are reaping the benefits. COVID-19's rapid global expansion has recently brought the old educational system to a halt. Lockdown and seclusion have kept billions of children out of school. To combat the spread of COVID-19, the majority of countries have declared school closures. Distance learning is the only way to keep the educational system moving in such a situation. The current eLearning infrastructure, on the other hand, was not prepared for such a quick change from traditional education to eLearning. However, the current eLearning infrastructure was not expecting this rapid paradigm shift from the traditional educational system towards eLearning.

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Chapter 6
Computational Intelligence Against Covid-19 for Diagnosis Using Image Processing Techniques in Healthcare Sector

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Abstract Coronavirus 2019 (COVID-19) medical images detection and classification are used in artificial intelligence (AI) techniques. Few months back, from the observation it is witnessed that there is a rapid increase in using AI techniques for diagnosing COVID-19 with chest computed tomography (CT) images. AI more accurately detects COVID-19; moreover efficiently differentiates this from other lung infection and pneumonia. AI is very useful and has been broadly accepted in medical applications as its accuracy and prediction rates are high. This paper is developed and aims to fight against corona through AI using computational intelligence in detecting and classifying COVID-19 using Densnet-121 architecture on chest CT images from a global diverse multi-institution dataset. Furthermore, data from clinics and images from medical applications improve the performance of the proposed approach and provide better response with practical applications. Classification performance was evaluated by confusion matrices followed by overall accuracy, precision, recall and specificity for precisely classifying COVID-19 against any condition.

Keywords Coronavirus · Artificial Intelligence (AI) · Classification · Detection · Multi-institution dataset

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_6

6.1 Artificial Intelligence Based Disease Detection

COVID-19 which is caused by SARS-CoV-2 [1] was initially identified in December 2019 and has become a global pandemic [2]. An escalating viral epidemic as COVID-19 applies more demand on the limited resources used in health care [3]. To reduce and avoid human pains from being plagued due to disease, a tool is required which can simplify the process of diagnosing, monitoring and providing treatment to the humans infected by COVID-19 [4]. Particularly, this requirement is necessary in resource-scarce settings like countries with low or normal economic conditions [5, 6]. Pandemic due to COVID-19 has infected around 3 million humans globally. Recognizing this disease at the earliest is necessary as treatment given earlier helps to recover soon and moreover ensure patient isolation and control the spread of this disease.

Another approach to detect COVID-19 is to use medical imaging tools which play a significant role in managing the infected or suspected patients. It is noteworthy that only through clinical suspicion COVID-19 can be detected precisely and not through X-rays or CT images since these may show similar patterns of other diseases [7]. However, findings from chest CT are normal with few patients at the beginning stage of COVID-19 and hence only chest CT has limited negative prediction to entirely get rid of infection [8], stressing the necessity to include clinical data in diagnosing COVID-19. Chest CT images are more specific and sensitive instead of chest radiography in diagnosing SARS-CoV-2. Few cases exists where findings with CT images exist before the inception of clinical symptomatology [9].

AI is the study and development of techniques which reproduce the intelligence of human. These techniques are promising in various fields like online advertising, computer vision, fraud detection, automatic driving, robotics and so on. Moreover, it is successful in medical field like diagnosing diseases, monitoring and providing treatment for patients, discovery of drugs, epidemiology and so on. AI has a great research hope to deal with the recent challenges faced by human [10]. AI acts as the key to support academic and clinical investigations of COVID-19 and upcoming crisis [11]. As an example, at the start of outbreak, China made a first move in providing a set of measures to prevent the spreading of the virus which involved several AI based approaches. By this, investigation on implementing these ideas was carried out like using facial recognition cameras for tracking the infected people, drones to sanitize places [12], robots for distributing food and medicines, etc. At present, RT-PCR (Reverse Transcription Polymerase Chain Reaction) test is adopted for detecting COVID-19. RT-PCR is involved in the detection of sputum of virus RNA or nasopharyngeal swab. This RT-PCR test is more time-consuming but on the other hand, the COVID-19 case is eventually increased day by day in countries like the USA, India, Brazil, and other countries. Also, the cost of PCR is more expensive as it costs around 6500 INR. PCR exhibits minimal detection rate and to achieve accurate results repeated tests are required. To prevent this pandemic, a fast and accurate method is required for COVID-19 diagnosis. To achieve faster results Chest X-rays and CT are adopted for detection of COVID-19 pandemic. Several researchers expressed that X-ray and CT exhibit abnormalities in the COVID-19 infected patients. Both techniques are effective for earlier COVID-19 detection than conventional RT-PCR tests. In the early stage, identification of COVID-19 is performed with an effective imaging technique that limits the disease spread. The medical physician is focused on designing an effective support tool integrated with artificial intelligence techniques for COVID-19 diagnosis. Artificial intelligence method involved in infected lung CT image segmentation.

There exists several applications where AI based techniques are applied to handle the impacts caused by COVID-19. The applications include processing clinical data and images related to COVID-19, pharmaceutical studies and epidemiology. Moreover, research based on AI techniques has been carried out. Mainly, the classification was based on the applications; however, when the application was same, then they were subdivided based on the AI techniques used. Few examples of AI techniques involved are Deep learning, Artificial Neural Networks, machine learning and evolutionary approaches. AI techniques have been widely used in diagnosing and providing treatment. Recently, this pandemic situation has posed a new challenge in the field of science. There occurs a necessity to develop intelligent systems to assist practitioners of health systems under pressure for diagnosing, monitoring, predicting the conditions of patients and offering treatment. The hybrid DL reduces both the error rate and the computational time compared with other classic deeper learning techniques, achieving a high precision level in classification.

This paper is developed with the motivation to fight against corona through AI using computational intelligence in detecting and classifying COVID-19 using Densnet-121 architecture on chest CT images. A DenseNet121 classification model is proposed in this paper for classifying the patients as infected or not. Experiments are carried out and comparisons with the familiar confusion matrix are performed to estimate effectiveness of proposed DenseNet121 classification model with chest CT scanned COVID-19 images. The remaining part of paper is arranged as: Sect. 6.2 describes related existing works, Sect. 6.3 elaborates about system proposed, Sect. 6.4 presents obtained results and finally conclude with Sect. 6.5.

6.2 STATE-OF-ART Methods

Numerous research work has been carried out in detecting COVID-19 and few related works are presented in this section.

Hu et al. [13] designed a faster and accurate AI model on ShuffleNet V2 [14], for training in transfer learning applications. CT dataset used for experiment contained 48 SARS images, 76 bacterial pneumonia images, 397 non-infected images, and 521 COVID-19 infected images. Translation, rotation, flip, adjustment in brightness, and flip with adjustments in brightness was applied on the images to increase number of training images. Respective values obtained for specificity, recall, and AUC were 91.58%, 90.52%, and 0.9689.

Gozes et al. [15] constructed a comprehensive system for detecting COVID-19 disease which involved lung segmentation, detection of COVID-19 in CT images, and with predefined threshold identifying cases as COVID-19. Different datasets were involved at training as well as testing stages, and pretrained network ResNet50 was involved in detecting COVID-19. Corresponding specificity, sensitivity, and AUC values obtained were 98%, 94%, and 0.9940.

Kassani et al. [16] utilized various pretrained networks like MobileNet [17], Xception [18], InceptionV3 [19], InceptionResNetV2 [20], and ResNet [21] forfeature extraction from images available in the public dataset. These features were then trained with six machine learning procedures which included decision tree, XGBoost, random forest, Light GBM, Bagging and AdaBoost. Among these, it was proved that Bagging classifier produced optimal accuracy on the features extracted using the above mentioned network.

Soares et al. [22] a new deep neural network (DNN) approach named Convolutional support estimator was employed to detect COVID-19. Han et al. [23] used AD3D-MIL model in DNN for processing CT scanned images which semantically generated 3D instances of these images. In [22], an explainable deep learning approach was developed to process CT images. A segmentation network based on U-Net DNN was designed in [24] which used attention mechanism to identify the features obtained which was helpful for classification. DNN based nCOVnet was developed in [25] for processing CT scanned images to detect COVID-19.

Xueyan Mei et al. [26] employed AI techniques to combine chest CT identifications with the history, clinical symptoms, and tests conducted at laboratory to quickly identify COVID-19. Around 905 patients were tested using real time as well as next-generation sequencing RT–PCR. When 279 patients were tested, AI system attained AUC of 0.92 and equal sensitivity with that of the senior thoracic radiologist. Moreover, this AI system provided better detection rate of 68% for COVID-19 by using RT–PCR with the normal CT scanned images where these were classified as negative by radiologists. With CT scanned images along with its relevant clinical history, this AI system more quickly identify patients with COVID-19.

In [27], a novel lightweight DNN based mobile application was designed which is three-player knowledge transfer and distillation architecture. This included a pretrained physical network which extracted features from CXR imaging involving numerous CT images. In few of the recent research, Deep Learning in smartphones is employed for processing X-Rays to diagnose COVID-19. A novel method introduced in [28] takes non-contrasted chest CT images as input and segmented lungs, lesions and lobes. Here deep learning approach and deep reinforcement learning were integrated to estimate the lung severity and involvement of lobe which measures the abnormalities and the existence of high opacities.

The major aim is to enhance the classification process of COVID-19 images. To deal with segmentation, in [29], consistency-based loss function was developed to promote output predictions to be reliable with spatial transformations involving CT images. In [30], hierarchical classification approach was introduced to handle imbalanced datasets. It was observed that texture features is also a major visual feature of CXR images.

The major challenge in diagnosing COVID-19 using CT images is todifferentiateCOVID-19 and pneumonia which express identical clinical attributes. To handle this, UVHL (Uncertainty Vertex weighted Hypergraph Learning) is developed in [31]. Here, several features were extracted and the relationship among various cases was formed using hypergraph structure in which every case in the hypergraph is represented as a node. In this, ambiguity of nodes was estimated and used as a weight. Finally, on the hypergraph, learning process is carried out for predicting new test cases. Hence, to handle the issues faced by the existing approaches, this paper introduces Densenet-121 based classification model to classify patients infected with COVID-19. In [32] a handy solution is presented to detect COVID-19 from thrust rays and to differentiate between those that are normal and affected by viral pneumonia with deep revolutionary neural networks (CNN). In this work the transfers are assessed in three pre-trained CNN models (EfficientNetB0, VGG16 and InceptionV3). The reason behind the choice of these specific models is their precision and efficiency balance with fewer relevant parameters for mobile applications. In [33] to detect forgery in COVID-19 medical data by using CNN in the error level analysis (ELA) by verifying the noise pattern in the data. The proposed improved ELA method is evaluated using a type of data splicing forgery and sigmoid and ReLU phenomenon schemes. The proposed method is verified by manipulating COVID-19 data using different types of forgeries and then applying proposed CNN model to data to detect data tampering. The results show that accuracy of proposed CNN model on the test COVID-19 data is approximately 92%. Five cutting edge technologies and their astounding applications have been presented in [34], which can be used to reduce and remove COVID-19 issues. Artificial (AI) technology, 3D printing (3DPT), BDA, HPC and telecommunication technology encompass TT. This work explores the usage of COVID-19 technology and aims at stimulating development of future research and developments for COVID-19 by means of AI, 3DPT, BDA, HPC, and TT. In [35], DNN was developed for automatic COVID-19 detection in x-ray images. Developed method was stated as Dark CovidNet with the implementation of the classification model. The developed classification model incorporated a real-time object detection system. The developed model incorporated a convolution layer count of 17 and provided an accuracy of 98.08% and multi-class value was achieved as 87.02%. In [36], a classification of the COVID-19 database was introduced through the transfer learning approach. To withstand the normalization of dataset and noise elimination, cost-sensitive attributes and smooth loss function were considered. The model was trained based on the publicly available CT chest dataset for the classification of COVID-19 patients. The developed method provided 93% accuracy, 94% specificity, and 91% sensitivity. In [37], for the classification of chest CT images in COVID-19, the CNN model was included. In this CNN model, a multi-objective differential evolution technique was included. Similarly, in [38] a CNN network with Xception pre-trained model was developed for classification. The analysis was based on the consideration of X-ray images obtained into 4 classes such as Pneumonia, COVID 19, Normal, and Pneumonia bacteria. Analysis of results expressed that classification accuracy achieved was 89.6%. In [38], feature extraction was performed for classification of COVID and Non-COVID for X-ray images.

In [39], a Resnet was developed for the extraction of features with a classification model for differentiating COVID and non-COVID images. The developed classification model utilized a smooth loss function. This model provided an accuracy value of 93.01%. The main Component analysis (TMPCA) is described in the [40] Multi-stage tree-structured analysis. The TMPCA approach leads to dimensional reductions at the sequence level without labelling training information, as opposed to traditional word-to-vector embedding. In addition, it can maintain the sequential input sequence structure. We show that TMPCA works computationally and can facilitate text-classification tasks based on sequence by retaining high mutual information mathematically between input and output. In the unattended UMNMT framework [41] the loss of consistency based on the image is unattended and aimed to simultaneously learn bidirectional multi-modal translation. Our inference model can be translated with the picture or without by alternating training between multi-modal and uni-modal.

6.3 System Model

The architecture of the DenseNet-121 classification model for classifying COVID-19 cases is depicted in Fig. 6.1. DenseNet has numerous convincing benefits: improves the vanishing-gradient problem, makes feature propagation stronger, encourages in reusing features and, decreases the number of parameters considerably. Proposed model is employed in extracting features using its own learned weights on kaggle dataset. As COVID-19 dataset is existing, pre-trained neural networks are involved in diagnosing coronavirus. The publicly available dataset incorporates different types of pathologies for pre-processing of jpg format. The CT image dataset varies images at different dimensions ranging from 152 to 1853. The analysis expressed that the average height of the image is 491 and the average width value of 124–383. On the whole, the average width value is measured as 1485. The dataset is classified with lesion segmentation to differentiate COVID and non-COVID patients. The analysis is based on the consideration of image lesions with consideration of various labels such as pleural effusion, ground glass, and consolidation. All image label lesions are presented for scanning CT lung images.

6.3.1 DenseNet-121

The architecture of DenseNet resembles that of the convolutional neural network and contains four Dense Blocks with different layers. Consider, DenseNet-121 model which has [6, 12, 16, 24] layers in four Dense Blocks but [6, 12, 32] layers occurs in DenseNet-169. DenseNet has a 7 × 7 Conv layer followed by 3 × 3

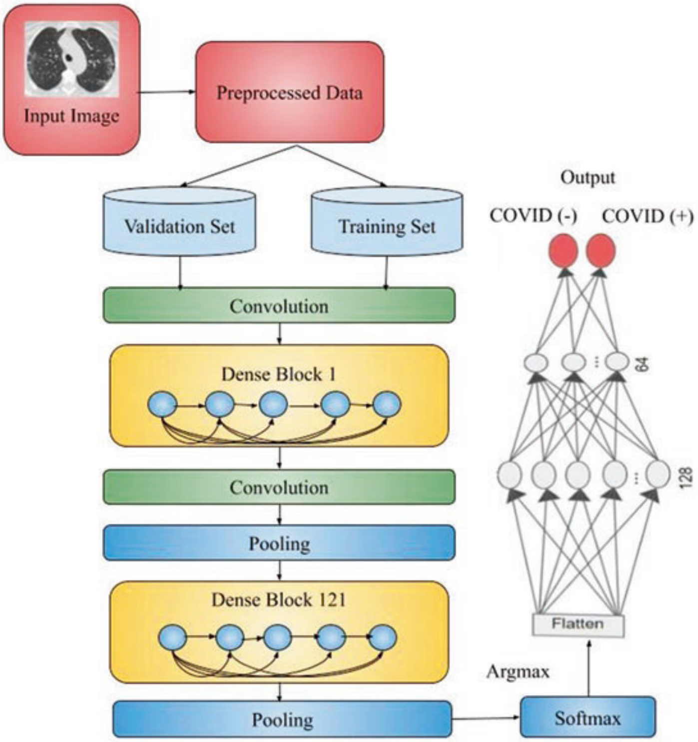

Fig. 6.1 DenseNet121 classification model

MaxPooling layer each with stride2. The classification layer follows the next dense block which accepts the feature maps of every network layer for the process of classification.

Moreover, convolutional operations within each architecture is the BottleNeck layers which implies that 1 × 1 conv decreases the total input channels and 3 × 3 conv layer performs convolutional operation on the inputs transformed with reduced number of channels instead on the actual input.

Every BottleNeck layer generates K feature maps and are combined with the existing feature maps. Thus, numbers of inputs are more specifically with the following network layers. This layer is used to reduce the computational necessities and makes the operation more efficient. 1 × 1 convolutional bottleneck layer can be used before every 3 × 3 conv layer thereby number of input feature-maps are reduced, and hence computational efficiency is improved.

In this approach, every layer is connected directly to all other layers in a feed-forward direction. Every network layer receives the concatenated feature map of preceding layers as inputs and where nonlinear functions like ReLU, batch normalization, and pooling or convolution is implemented. After this function, concatenated feature map of every layer is provided as input to the successive layers.

Concatenating is not successful with carrying size of feature maps; thus, pooling operation is necessary by modifying the size. To make this operation easier, architecture is split into several blocks, as DenseBlocks, and the transition layers between these blocks perform the operations like batch normalization, pooling and convolution. In general, every function producing k feature maps is a hyper parameter known as growth rate which defines number of feature maps contributed to network by every layer. Once contributed, these maps are accessible anywhere in the network.

As with that of the classical architecture, here one layer need not be replicated to another. Usually, in the network, every layer produces k feature maps which have several inputs. Hence, 1 × 1 conv layer is involved in bottleneck layer for reducing the input feature maps to 4 k. Compactness is also a one more benefit of DenseNet which has the capacity to minimize number of feature maps required at transition layers. If m feature maps are present in a Dense Block, then the number of feature maps change to θm, where $0 < \theta \leq 1$ is compression factor. Additional benefits of DenseNet architecture include enhances vanishing gradient issue, makes feature propagation stronger, and minimizes the parameters involved.

The concatenation of features is define mathematically as:

$$z^{l} = H_{l}\left(\left[z^{0}, z^{1}, \ldots, z^{l-1}\right]\right) \tag{6.1}$$

where, H_l is a non-linear composite transformation function contains batch normalization (BN), subsequently with ReLU function and a 3 × 3 conv layer. z^0, z^1, …, z^{l-1} denotes the concatenated feature map related to layers 0 to l-1 which makes implementation easier. For the purpose of down-sampling, Dense Blocks are created in architecture of network and are separated by transition layers which contain BN followed by 1 × 1 conv layer and at last an average 2 × 2 pooling layer.

DenseNet121 is also satisfactory with the lower growth rate due to its structure where the feature maps are assumed to be at global state in network. Thus, every subsequent layer access every feature maps of the preceding layers. Every layer adds the feature maps to the global state where the feature maps provided as input at 1^{th} layers $(FM)^1$ is given by

$$(FM)^{1} = k^{0} + k(l-1) \tag{6.2}$$

Here, in input layer, channels are given by k^0. For enhancing the efficiency of computation, 1 × 1 conv layer is used prior to each 3 × 3 convlayer which reduces the input feature maps that are usually high compared to the output feature maps k. 1 × 1 conv layer called bottleneck layer is used which produced 4 k feature maps.

The DenseNet121network to extract features having successive sigmoid activation function for binary classification which replaces softmax activation function is used in DenseNet121 structure. Sigmoid activation function converts that outputs that are non-normalized to binary outputs either as 1 or 0. Hence, helps finally in classifying COVID-19. Sigmoid function is described as:

$$y = \frac{1}{1 + e^{-(\Sigma w_i x_i)}} \tag{6.3}$$

where, y is the neuron output, w_i and x_i are weights and inputs correspondingly.

6.4 System Results

6.4.1 Dataset

CT scan kaggle dataset used for experiment is accessible at www.kaggle.com/plameneduardo/sarscov2-ctscan-dataset. This dataset totally contains 2492 CT scan images in which 1262 are positive COVID-19 (+) cases and the remaining 1230 are negative COVID-19 (−). Figure 6.2 shows a few examples of CT COVID-19 (+) images of patients present in the dataset used.

Proposed classification model obtained accurate results of 96%. The effects of false negative and false positive rate is given in Fig. 6.3 using confusion matrix from which it is clearly found that this proposed model produces less false negative and false positive rates.

Accuracy (Ac) is ratio of all correctly identified cases to total number of cases and is calculated as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \tag{6.4}$$

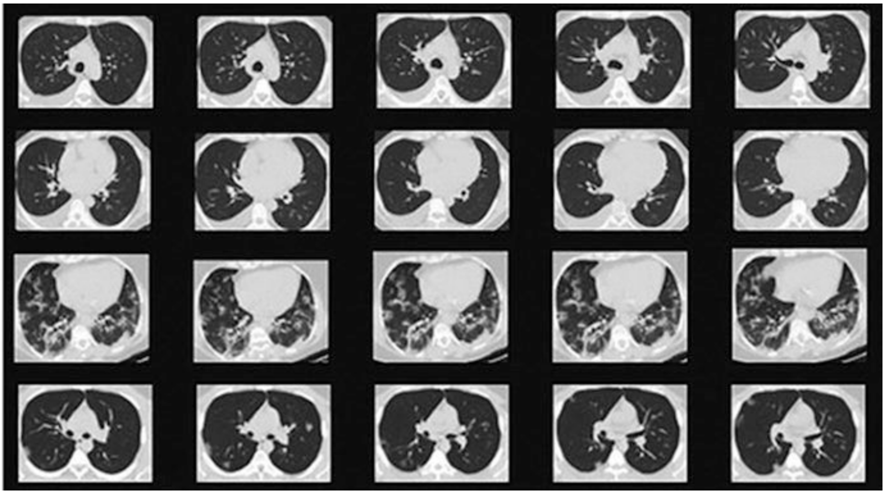

Fig. 6.2 CT scan sample images from dataset

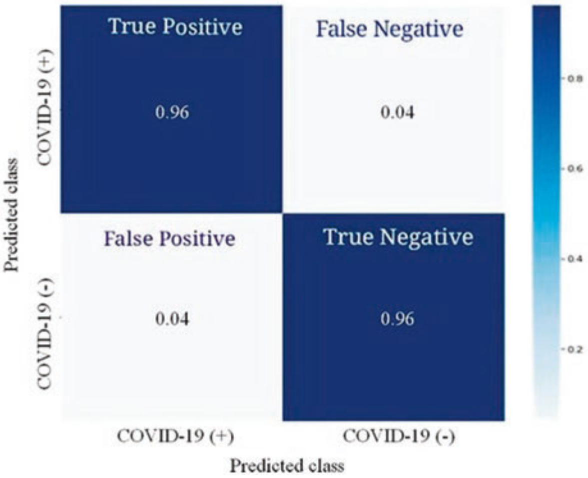

Fig. 6.3 Confusion Matrix of proposed classification approach representing rate of TP, TN, FP and FN produced from kaggle dataset

Precision is the measure which evaluates the exactness of the classifiers. Mathematically precision is given as

$$Precision = \frac{TP}{TP + FP} \tag{6.5}$$

When the precision value is low, it is said that classifier has produced large number of FP.

Recall termed as sensitivity is a parameter which defines the completeness of the classifier. It is estimated as

$$Recall = \frac{TP}{TP + FN} \tag{6.6}$$

When the recall value is low, it is said that the classifier has produced large number of FP.

Specificity (Sp) is actual negatives which are classified correctly; i.e., COVID-19 (−) cases are classified as individuals with no COVID-19. Sp is given as:

$$Specificity = \frac{TN}{TN + FP} \tag{6.7}$$

The below Fig. 6.4 shows performance of existing and proposed methods. X axis and Y axis shows parameters like precision, recall, specificity and values obtained respectively. Purple, Teal and Olive green color shows the ResNet, ImceptionResNetV2 and DenseNet-121 respectively. When compared to existing method, proposed method achieves better results (Table 6.1).

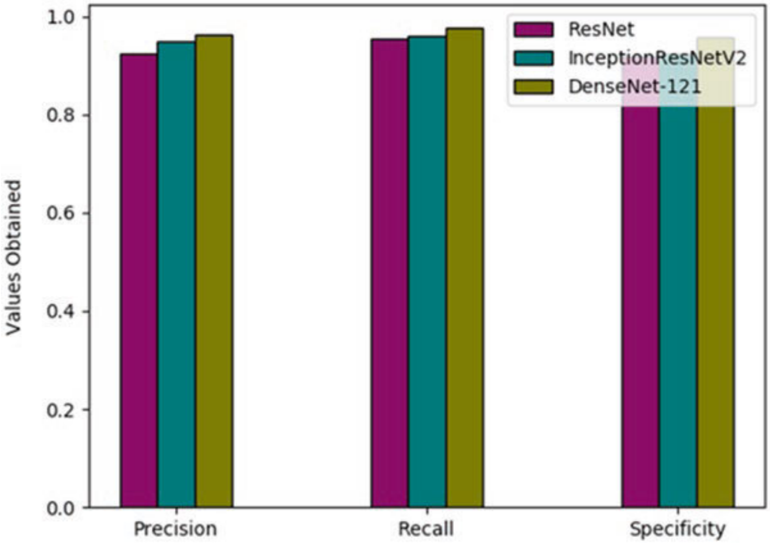

Fig. 6.4 Comparison of the existing and proposed method

Table 6.1 Performance of Existing and proposed method

Parameters	ResNet	InceptionResNetV2	DenseNet-121
Precision	0.923	0.949	0.962
Recall	0.953	0.961	0.976
Specificity	0.918	0.925	0.958
Accuracy	92.91%	93.74%	96.11%

The below Fig. 6.5 shows performance of accuracy for existing and proposed methods. X axis and Y axis shows methods like ResNet, ImceptionResNetV2, DenseNet-121 and accuracy values obtained in percentage respectively. Green, Red and Blue color shows the ResNet, InceptionResNetV2 and DenseNet-121 respectively. ResNet achieves 92.91%, InceptionResNetV2 achieves 93.74%, DenseNet-121 achieves 96.11%. When compared to existing method, this method achieves better results.

Receiver operating characteristic (ROC) curve is a graph plotted with two parameters namely true positives and false negatives depicting performance of classification. Below Fig. 6.6 represents ROC curve for existing and proposed methods. X axis and Y axis shows FPR and TPR respectively. Green, Red and Blue color shows the ResNet, InceptionResNetV2 and DenseNet-121 respectively. ResNet achieves 0.95, InceptionResNetV2 achieves 0.87, and DenseNet-121 achieves 0.97. When compared to existing method, proposed method achieves better results.

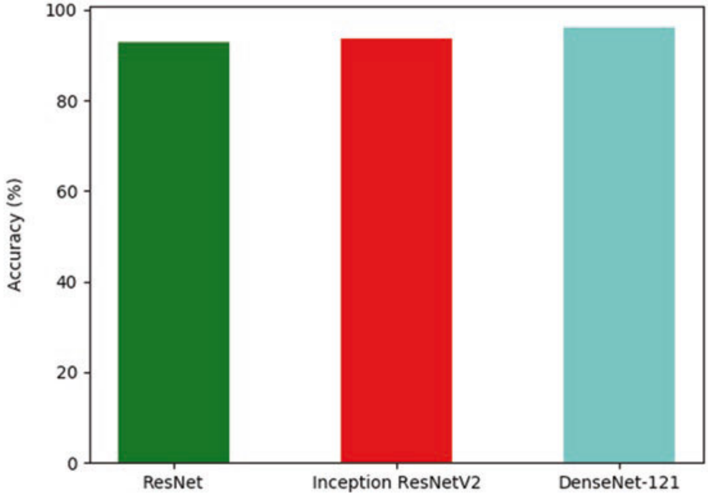

Fig. 6.5 Performance of accuracy for Existing and proposed method

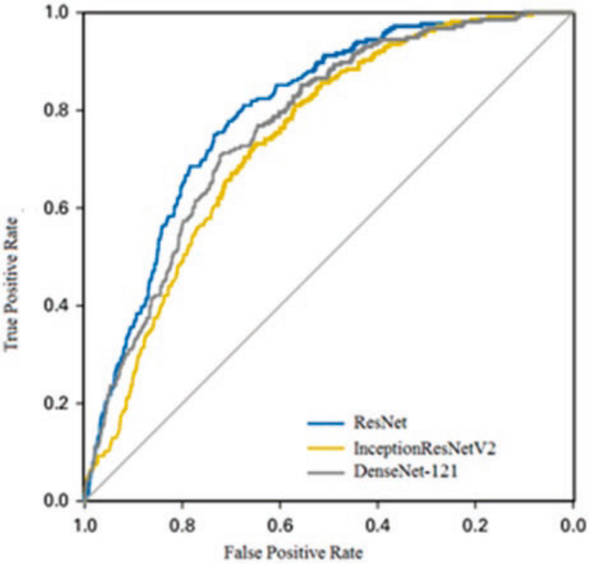

Fig. 6.6 ROC Curve of existing and proposed method

6.5 Conclusion

As the facility of CT scans is mostly available in almost all medical institutions, proposed model can enhance process of diagnosing COVID-19. This paper aims to check whether the individual has been infected or not. This paper evaluates an AI technique for the detection of COVID-19 and classification using Densnet-121 architecture on chest CT images is taken from the global diverse multi-institution dataset. Furthermore, clinical data and medical imaging improved the performance of the proposed model in practical applications. Classification performance was evaluated by confusion matrices followed by overall accuracy, precision, recall and specificity. The proposed model achieves 96% accurate classification results. Future work plans to focus on the growth of health services that lead to an increase in data generation, causing problems with design for data access and data structure. This is done by including game-theory process with multi-agent concept inside the Alexnet architecture to improve the overall accuracy.

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Chapter 7
Social Economic Impacts for Covid-19 Pandemics Using Machine Learning Based Optimization Algorithm

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Abstract As the number of COVID-19 patients grows exponentially, not all cases are likely dealt with by doctors and medical professionals. Researchers will add to the fight against COVID-19 by developing smarter strategies to achieve accelerated control of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), virus that causes disease. Proposed method suggests best ways to optimize protection and avoid COVID-19 spread. Big benefit of the hybrid algorithm is that COVID-19 is diagnosed and treated more rapidly. Pandemic diseases possibilities are handling with help of Computational Intelligence, using cases and applications from current COVID-19 pandemic. This work discusses data that can be analyzed based on optimization algorithm which provides betterCOVID-19 detection and diagnosis. This algorithm uses a machine learning model to decide how the hazard function changes concerning characteristics of potential methods to find parameters in optimization of machine learning model, which has in many cases been shown to be accurate for actual clinical datasets.

Keywords Computational intelligence · Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) · COVID-19 · Optimization algorithm · Clinical datasets

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_7

7.1 Social Impacts on COVID-19

Since December 2019, Wuhan has been expanding across the whole world with the new corona-virus (SARS-CoV-2). By 18 April worldwide more than 2 million confirmed cases and 150,000 deaths had been reported. (https://www.worldometers.info/coronavirus/). As cure or vaccination of a novel COVID-19 disease is not available, early detection must offer an incentive for suspected individuals to be isolated at once and to decrease risk that healthier population will get infected [1].

WHO has declared a coronavirus disease and it is currently expanding [2]. There are 3,581,884 confirmed cases, contributing to 248,558 deaths, were registered as of 4 May 2020 [3]. Biggest discrepancy between CoV-2 pandemic and associated viruses, such as SARS and MERS, is CoV-2's ability to expand easily through human interaction and leave about 20%, infected individuals, without symptoms [4].

Also, some studies have shown that CoV-2 disease is more severe for people with a poor immune system [5, 6]. This CoV-2 activity involves creation of a rigorous mathematical basis for controlling distribution and automation of complex decision-making tracking instruments.

It is necessary to develop, administer, evaluate and combine innovative strategies with cline trials and, in particular, the development of pharmaceutical evidence, genome and public health knowledge on an increasing network of people and the movements of the infected individuals.

By using these data, researchers determine how and where disease is likely to spread and alert certain areas of disease to fit arrangements needed by ML and AI. History of travel by infected individuals may be automatically monitored to examine epidemiological associations with disease transmission.

In other words, some influences on group transmission were studied. Effective and cost-effective technology to store and interpret such enormous data for further analysis needs to be built. Usage of cloud computing and AI solutions needs to be organized [7]. Alibaba has produced solutions for cloud and AI that support China, battle coronavirus, forecast outbreak peak, scale, and length and are reportedly carried out in real-world experiments in different regions of Chinese with 98% accuracy [8]. Currently, various institutes for public and personal care produce monumental amounts of data which are difficult to handle. For analysis and decoding the helpful information from these data, there is also a need for powerful machine-controlled data processing tools. This information is extremely helpful for health professionals who know why disease occurs and who can treat patients more efficiently and at higher cost. Data processing provides a new info on care that is successively beneficial as a medical call, such as medical appointments, insurance policy calls, treatment option, prognosis of health, etc., for creation of bodies.

Several primary-known research focus on various issues and data processing concerns in care. For each analysis and prediction of different diseases, data processing is also used. Some analytical study was designed to improve accessible data processing methods in the nursing sector in order to increase results and several studies have been developed into new treatment methods and frameworks.

Furthermore, it has been observed that a variety of data processing techniques, such as classification area units used by health services, increase their capacity to generate patient health calls. ML-based CT-Image Analytics Solution can be used to overcome various forms of pneumonia that can be useful in tracking COVID-19 patients [9]. In [10] Details are shown. Vaccine production is improved by use of multiple ML and AI methods, by studying gene sequences and molecular docking [11]. ML [12] is used to process vast quantities of data and smartly forecast disease transmission. It has proven potential to learn local dependencies between pixels implicitly. However, the pixel-specific loss function of these methods still limits the learning of multi-scale spatial limitations in an end-to-end training process, which lacks the capability to enhance. Compared to patching, labeling or class imbalance is a problem for CNNs trained on whole pictures. While patching methods can test a balanced amount of patches per class, pixels from various classes are frequently uneven in whole-image training methods. The spread of COVID-19 continues to seriously and significantly influence the global economy in the context of public health. Labor dislocation, collapse of companies and stock crashes are just some of the consequences of this global pandemic lockdown. The influence of COVID-19 will result in a global economic downturn in the year 2020, as well as a decrease in economic growth to 3% according to the International Monetary Fund (IMF). Rest of the chapter discussed in Sect. 7.2 is related works, system models in Sect. 7.3, results and discussion in Sect. 7.4 and conclusion in Sect. 7.5.

7.2 State of Art Methods

Tuli et al. (2020) enhanced statistical model applies to analyze and forecast epidemic's expansion [13]. Probable hazard of COVID-19 in countries around world has been forecast by using an improved ML model. This research has revealed that iterative weighting can be enhanced for creation of a predictive method for Generalized Inverse Weibull distribution. Framework was used on a cloud computing network to forecast growth behavior of disease more reliably and in real time. A more reliably data-driven methodology would be incredibly useful for government and people to proactively respond.

Dandekar et al. [14] global COVID-20 diagnostic model has been developed by introducing a neural network module to classical SIR epidemiological model. Trend breaks down the contribution to infection time series to examine as well as compare role of quarantine management policies in control of dissemination of the virus in heavily affected regions in Europe, North America, South America and Asia. Our findings for all continents are usually closely correlated between strengthening of quarantine controls learned from model and steps taken by respective governments of regions.

Abbasimehr and Paki [15] Three hybrid approaches are proposed to predict COVID-19 time series methods on integration of 3 deep learning models with Bayesian optimization algorithm, such as multi-head focus, LSTM and CNN. Both models are designed based on technique of multiple performance forecasting, which enables multiple time points to be expected. For each model, Bayesian optimization approach automatically chooses best hyper parameters and increases efficiency of forecasting. We also performed studies and tested suggested models against baseline model with publicly accessible disease data obtained from Johns Hopkins University's Coronavirus Resource Center.

Findings reveal that deep learning models are superior to benchmark models for short and long term predictions. In fact, for short-term predictions mean SMAPE of best deep learning model is 0.25 (10 days ahead). Best deep learning model even gets an average SMAPE of 2.59 for long-term forecasts?

Lu et al. [16] with data analysis, simulation, and optimization a hybrid prediction framework is proposed. To ensure precision and stability, multi-target optimizer is used as a prediction model, SVM. Data show, for example, that hybrid models proposed are superior to bottom-line models in both forecast accuracy and reliability, taking daily energy demand of US. Also, selection of input specifications is addressed, and findings indicate that method taking into account regular infections is most predictable and stable, and that it has a high potential in real-world applications.

Waheed et al. [17] A framework for producing synthetic CXR images is proposed by introducing a model called CovidGAN based on ACGAN (Auxiliary Classifier Generative Adversarial Network). Furthermore, we show that for COVID-19 detection, CNN efficiency can be improved with synthetic images produced by CovidGAN. Classification alone with CNN gave a precision of 85%. Accuracy increased to 95% by inserting synthetic images produced by CovidGAN. We hope that this approach will accelerate identification of COVID-19 and lead to stronger radiological systems.

Han et al. [18] document our initiative to make COVID-19 screening with low labels highly reliable and interpretable. We suggest AD3D-MIL, in which a 3D chest CT is classified as a bag of instances. After potential contamination areas, AD3D-MIL wills semanticipate generation of deep 3D instances. To gain insight into contribution of individual instances to a bag mark, AD 3D-MIL further extends a centered pooling approach to 3D instances. Finally, AD3D-MIL discovers Bernoulli's bag-level label distributions for easier learning. 460 examples of CT have been collected, 230 examples of CT from 79 COVID-19 patients, 100 examples of CT in 100 typical pneumonia patients and 130 examples of CT in 130 pneumonia-free patients. A variety of observational tests indicate that precision of our algorithm amounts to 97.9%, 99.0%, and 95.7%, respectively. These benefits make our algorithm an important support method for COVID-19 screening.

Ouyang et al. [19] offers a new 3D CNN to focus areas of lung infection while taking diagnostic decisions. We then establish a double-sample approach to minimize imbalance. Largest multi centre CT data forCOVID-19 from 8 hospitals was analyzed in our system (to our greatest knowledge). We receives 2186 CTs for five-fold cross-validation in training-validation stage from 1588 patients. We use a further separate large-scale research range of 2796 CT scans in 2057 patients during testing stage. This method classify COVID-19 image with an area of 0.944 AUC, 87.5% precision, 86.9% sensitivity and 90.1% specificity and 82.0% F1-score. This output enables a radiologist withCOVID-19 diagnosis from CAP to likely benefit from this algorithm, especially at early stage of COVID-19.

Roy et al. [20] new completely annotated LUS dataset photos collected from numerous Italian hospitals are given, with labels indicating degree of severity of disease in graphic, video and pixel phases (segmentation masks). In specific, we are introducing a novel deep network from Spatial transformer networks concurrently anticipating magnitude of disease associated with an input structure and supplying pathological objects for weakly supervised localization. Also, we implement a new approach based on unanimous for efficient video-level frame score aggregation. Tests carried through on proposed dataset show successful findings on all tasks under review, opening way for potential DL studies on LUS data for COVID-19 aided diagnosis.

Yousri et al. [21] alternative method which extracted information from X-ray images leverages a new method of selection of features to create corresponding features. An improved cuckoo search optimization (CS) algorithm (free order) and four heavy doll distributions are thus proposed in place of Lévy flight, which will improve efficiency of algorithm throughout phase of COVID-19 classification optimization. Three grades, called daily patients, COVID-19, and pneumonia, are included in a classification process. Suggested FO-CS variants were validated in first sequence of experiments with eighteen UCI data sets. Two data-sets for COVID-19 X-ray images were considered for second series of experiments. Compared to good optimization algorithms, proposed solution results were compared. Results test supremacy of proposed method to provide precise results for UCI and COVID-19 data sets.

Khan et al. [22] benefits of hyperparameter optimization for a Gaussian process regression contains number of reported cases and deaths for 21, March 2020 to 10, 2020, were studied. Polynomial Regression is often contrasted. Gaussian Loop Regression model demonstrates better efficiency.

Kavadi et al. [23] propose a framework for the global COVID-19 pandemic prediction of PDR-NML. For statistical analysis of best parameters in data collection, we have employed progressive partial derivatives linear regression method. Next paradigm for standardized forecasts was nonlinear. Results indicate that in Indian community, suggested ML approach has outperformed state-of-the-art approaches and can also be a handy instrument for other nations to make predictions.

Jayakumar et al. [24] The COVID-19-pandemic unearthed seven lessons, the courses include corporate elements, education, on-line presence, network communication, cyber security, healthcare and the significance of life. The reaction to the unknown outbreak is more closely examined by this investigation. If a possible pandemic occurs in the future, it aims to offer the right approach.

Khalil et al. [25] the good education system has been stated to develop good people. In the course of growth, the nations that compromised their education live far behind. The combination of traditional education and e-learning is quite successful and many industrialized civilizations benefit. In recent years, COVID-19's rapid growth has put a stop to the traditional system of education.

Brohi et al. [26] Five advanced technologies have been shown, with extraordinary applications, capable of mitigating and eliminating COVID-19 difficulties. The technologies included Artificial Intelligence, 3d Printing, Big Data Analytics, HPC, TT. This research studies the application of COVID 19 technologies to promote future research and to build COVID 19 solutions with AI, 3DT, BDA, HPC, and TT. This research is based on research projects throughout the world.

Ozturk et al. [27], For the automatic detection of COVID-19 in X-ray pictures, DNN has been developed. In order to implement the classification model, the developed approach was called Dark CovidNet. A real-time object detection system was included in the created categorization model. The designed model featured a 17-compact layer number and had a 98.08% accuracy and an 87.02% multiclass value.

Beers et al. [28] A PGGAN was trained to synthesize medical images of fundus images that suggest premature vascular ROP and multimodal MRI images of the glioma. Progressive development of GANs involves the training of the image generator to initially generate synthetic images in low resolution (8 × 8 pixels), which are then fed into a discriminator which differentiates these synthetic images from the real down-sampled images. Additional convolutionary layers are then used to produce images that double the resolution before the goal resolution is reached. We show in this work that the medical images can be realistic in two independent fields; fundus photographs that indicate vascular pathology linked to premature retinopathy and gliome magnet resonance imaging in multimodal form. We also show that finely known pathological elements, such as retinal arteries and tumour heterogeneity, can be retained or strengthened using segmentation maps.

Xue et al. [29] Suggest two GAN networks, a Segmentor and a Critical network, which explored the link between a binary brain tumour map and MRI brain images. The critic has a multi-scale loss role to maximise whilst the segmentor is trained by the critic using just gradients, in order to minimize multi-scale loss function. We have demonstrated that a SegAN framework for the segmentation problem is more effective and stable and results in superior performance than the most advanced U-net segmentation process.

Schlegl et al. [30] The GAN study used patches in the retinal region for data distribution for healthy tissue. In the retinal pictures, GAN was then evaluated for anomaly on both unseen and healthy imaging patches.

Gozes et al. [31] Construction of a comprehensive COVID-19 illness diagnosis system involving pulmonary segregation, COVID-19 detection in CT images and the predefined COVID-19 threshold In the training phases as well as the test phases several data sets were involved, with the pre-trained ResNet50 network detection involving COVID-19. Ninety Eight percent, 94%, and 0, 9940 were the corresponding specifications, sensitivities, and the AUC values.

Lin et al. [32] Combined CRF and CNNs for the better exploitation of spatial links among pixels Conditional Random Fields Combined Deep CNNs were also employed with promising results in the field of segmentation of medical pictures. Ronneberger et al. [33] included an FCN, U-net in electron microscopic stacks for segmentation of neural structures. In certain ways geographical context information

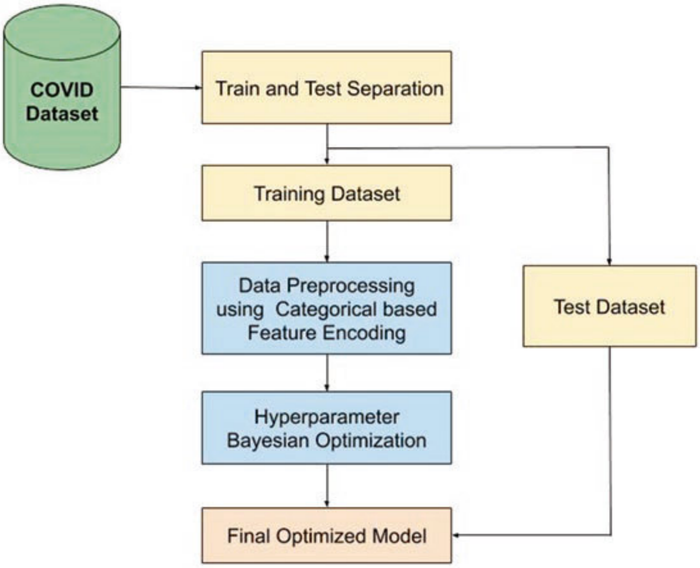

Fig. 7.1 Proposed Architecture

may be captured by using patches and multistage inputs. However, the computer costs for patch training are very costly and the location accuracy is in agreement.

7.3 System Model

Framework Model optimizes model for a precise forecast of COVID-19 cases, of increasing and decreasing numbers of cases in near future, and of date on which pandemic can be expected to end in different countries. Figure 7.1 represents proposed architecture.

7.3.1 Preprocessing Dataset

In terms of 80% and 20%, dataset is separated into train and test datasets. For model testing and optimization, we use train dataset. In categorical feature encoding stage, categorical dependent feature encoding technique can handle missing values, as seen in Fig. 7.1. Then dataset number variable can be translated into diagnostic target variable that has two categories: involvement and lack of cardiac disease.

7.3.2 Hyper-Parameter Bayesian Optimization (HBO)

After preprocessing of test and train dataset, binary classification using Bayesian optimization target variable is utilized. Bayesian Optimization is utilized to tune hyper parameters. Hyper-parameter optimization is to determine right hyper-parameters for a given method that provides best results when evaluated on a validation range. In form of equation, hyper-parameter optimization is given as:

$$x^{*} = \arg\min_{x \in X} f(x) \tag{7.1}$$

In this f(x), target score that is evaluated in validation score is to be minimized; x* is a set of hyper parameters that generate lowest score and any value in X field can be taken by x. Problem with optimizing hyper parameters is that testing objective role to find answer is incredibly expensive. We must train a model on training data, forecast validation data and, while trying various parameters, calculate the validation metrics. This process cannot be done manually, with a large number of hyper-parameters and models like assemblies or DNN which take days to practice.

For a great number of hyper-parameters, manual search is intractable. Even these strategies are inefficient because, when choosing next hyper-parameters to evaluate, they do not take previous assessments into account. They waste a large amount of time testing wrong set of hyper-parameters many times. On other hand, Bayesian optimization considers prior tests before determining next test hyper parameter set. It encourages itself to focus on those areas of search space that it believes would offer most promising validity scores by choosing its hyper-parameter combinations in an educated way. Usually, to get to optimal range of hyper-parameter values, this approach requires less iteration. And we can confidently assume that, after diligent reading, Bayesian optimization is extended to widely utilized machine learning methods [34].

As collection of hyper-parameters greatly influences efficiency of model, hyper-parameters can be very complex. Careful tuning of these hyper-parameters is, therefore, necessary. Grid quest (GS) is used in previous studies for hyper-parameter tuning of models [35] that have fewer hyper-parameters in their methods, but it will be difficult for our proposed model because our model requires a large number of hyper-parameters. Bayesian optimization is an efficient method of globally maximizing objective functions that are expensive to assess [36].

Bayesian hyper-parameter optimization strategy that was used to optimize proposed model is presented in this subsection. Majority of problems with machine optimization are black box problems where f(x) is a black box function. It is field that is most useful for Bayesian optimization techniques. Model used for this method is considered a surrogate model to simulate objective function. A popular model of surrogacy for Bayesian optimization is Gaussian Procedures (GPs) [37, 38]. A Gaussian process is used to model unknown goal feature space (GP). GPs offer an ability to set previous distributions over smooth, covariant and mean space.

A typical choice of covariance function is Matern kernel 2.5, which is utilized in proposed method. Task of procurement function is to help us to achieve best objective function. Acquisition functions are determined to conform to an intrinsic, strong acquisition feature meaning. It optimizes acquisition feature to get next measurement stage. Ensuring typical acquisition functions are expected, MPI and UCB. EI, most used acquisition feature, will be used in proposed model. Suppose that f is objective function and that xt is its sampling point:

$$x_t = \arg\max_x u\left(x \mid \mathcal{D}_{1:t-1}\right) \tag{7.2}$$

Where u is the feature of acquisition that in our case is Expected Improvement (EI) and $\mathcal{D}_{1:t-1} = \left\{\left(x_1, y_1\right), \ldots, \left(x_{1-1}, y_{1-1}\right)\right\}$, contain t-1 samples that were drawn from f so far.

For t = 1,2,3 … repeat:

- Find next sampling point by maximizing role of acquisition over GP. $x_t = \arg\max_x u\left(x \mid \mathcal{D}_{1:t-1}\right)$
- Obtain a potentially noisy sample by testing objective function f. $y_t = f(x_t) + \epsilon_t$
- Add new sample (x_t, y_t) to previous samples $\mathcal{D}_{1:t} = \mathcal{D}_{1:t-1}, \left(x_t, y_t\right)$ and update the GP.

7.4 Results and Discussion

For the COVID-19 forecast, the outcomes and discussion of the suggested approach using Bayesian optimization are used and we assess success with various performance metrics. Finally, there is an experiment to equate efficiency of proposed model with other applications of machine learning. Using measurement metrics such as sensitivity, precision, specificity, AUC of ROC maps and F1-score to assess effectiveness of proposed system. Precision is proportion of overall subjects accurately identified.

$$Accuracy = \frac{\sum TP + \sum TN}{\sum TP + \sum TN + \sum FP + \sum FN} \tag{7.3}$$

Number of patients with a positive condition is sensitivity.

$$Sensitivity = Recall = \frac{\sum TP}{\sum TP + \sum FN} \tag{7.4}$$

Specificity is percentage of individuals who have no negative illness. Recall is same as sensitivity.

$$Specificity = \frac{\sum TN}{\sum TN + \sum FP} \tag{7.5}$$

Precision is defined as subjects correctly classified subjects as positive from total subjects.

$$Precision = \frac{\sum TP}{\sum TP + \sum FP} \tag{7.6}$$

A harmonic means of accuracy and recall is F1-Score. These are

$$F1 - Score = \frac{2 \times Recall \times Precision}{Recall \times Precision} \tag{7.7}$$

where TP and FP represent correct and incorrect classification of COVID-19 subjects. Similarly, TN and FN denote percentage of subjects not possessing heart disease who are correctly and incorrectly listed, respectively. Plots of TPR and FPR plots at various gradient thresholds ROC (Receiver Operating Characteristic Curve).

$$TPR = \frac{\sum TP}{\sum TP + \sum FN} \tag{7.8}$$

$$FPR = \frac{\sum TN}{\sum TN + \sum FP} \tag{7.9}$$

7.4.1 Dataset

Various databases have been made freely accessible in this respect. More data must be recorded, produced and analyzed as COVID-19 spreads globally [39, 40]. Covid-19 is a set of data held by Our world in Data from COVID-19. Data regarding confirmed cases, deaths and tests are updated regularly. Dataset is available on https://ourworldindata.org/coronavirus-source-data

To define prediction effects, confusion matrix shown in Fig. 7.2 is used. Description of estimation outcomes of all dataset instances used for research is included.

Table 7.1 shows the proposed model performance with different performance metrics and its data on training and testing. The metrics used for evaluation are accuracy, Specificity, Sensitivity and F1-Score.

Figure 7.3 shows the proposed testing model results. X axis represents performance metrics and Y axis represents values obtained. Maroon color indicates the testing data. The proposed model achieves accuracy is 0.93, Specificity is 0.97, Sensitivity is 0.87 and F1-Score is 0.91 respectively.

Figure 7.4 shows the proposed training model results. X axis represents performance metrics and Y axis represents values obtained. Maroon color indicates the training data. The proposed model achieves accuracy is 0.87, Specificity is 0.91, Sensitivity is 0.83 and F1-Score is 0.85 respectively.

Fig. 7.2 Confusion matrix of proposed model

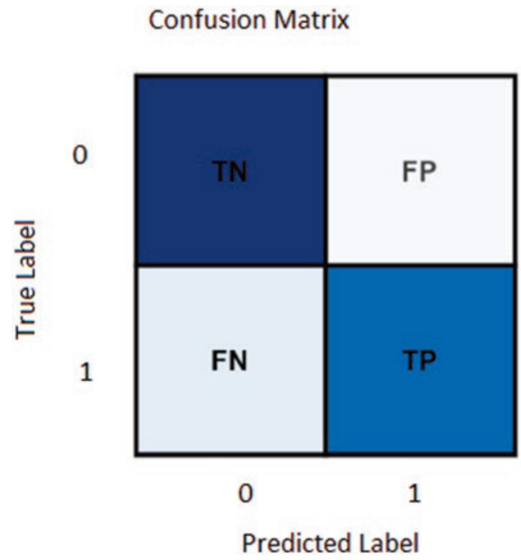

Table 7.1 Performance of Proposed model

Performance metrics	Data	
	Testing	Training
Accuracy	0.93	0.87
Specificity	0.97	0.91
Sensitivity	0.87	0.83
F1-Score	0.91	0.85

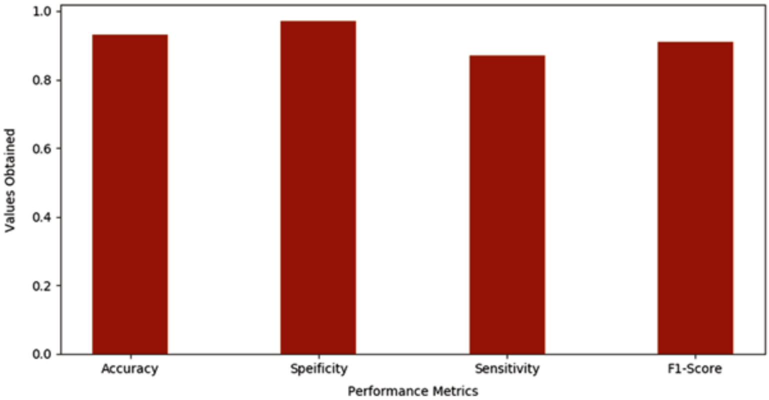

Fig. 7.3 Proposed testing model performance

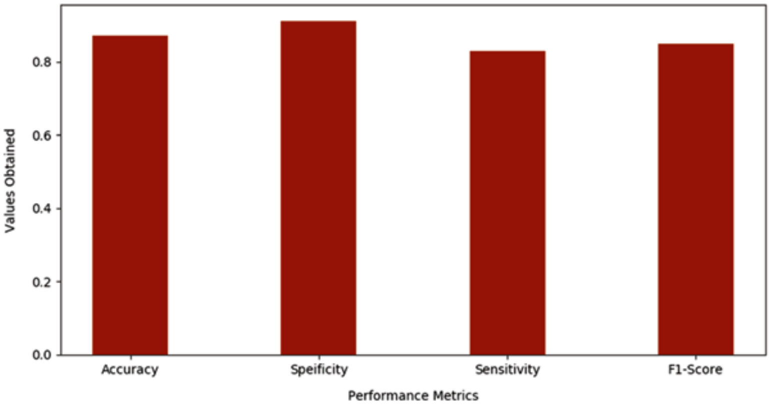

Fig. 7.4 Proposed training model performance

7.5 Conclusion

Proposed model is used to optimize model for reliable evaluation of COVID-19 cases, increase and decrease in cases in foreseeable future, and date when pandemic could be predicted to end in different countries. Based on optimization algorithm that offers improved COVID-19 identification and diagnosis, data can be analyzed. Bayesian optimization was used by proposed approach as a hyper-parameter optimization strategy that has proven to be a very successful method to get right hyper-parameters. Using four separate assessment parameters, namely precision, sensitivity, specificity, F1-score, proposed model was evaluated. Proposed diagnostic approach would improve consistency of decision-making during diagnosis of COVID 19 process on basis of experimental results. Future work concentrates on need for research in the areas of security and privacy issues related to technologies used for COVID-19 developments. Furthermore, technology should be utilized to assist and motivate frontline healthcare practitioners and officials in the fight against COVID-19.

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Chapter 8
Computational Intelligence Using Big Data for Fight Against Covid-19 Pandemic in Healthcare Environment

Ashok Kumar Munnangi, Ramesh Sekaran, Arun Prasath Raveendran, and Manikandan Ramachandran

Abstract In world, COVID-19 disease spread over 214 countries and areas which efficiently affects every aspect of our daily lives. In various areas, motivated by recent applications and advances of big data and computational intelligence (CI), this research aims at increasing their significance in COVID-19 response like prevention of severe effects and outbreaks. To improve diagnosis efforts, assess risk factors from blood tests and deliver medical supplies, CI is used during COVID-19. To forecast future COVID-19 cases, CI is used. To check goodness as high accuracy prediction method, the proposed method is checked with real-world data which focus on CI and big data, method which are used in current pandemic. In upcoming days, to enact necessary protection plans, it is very difficult to detect as well as diagnose. For computational methods with help of big data, this research provides prediction and detection of COVID-19. For predicting and detecting cases of COVID-19, performances of proposed models are used as criteria. To improve detection accuracy of COVID-19 cases, proposed method increases combination of big data analytics and CI models with nature-inspired techniques.

Keywords Computational intelligence · COVID-19 · Pandemic · Big data · Diagnosis

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_8

8.1 Computational Intelligence in COVID-19

Medical industry is pursuing new approaches to track and manage dissemination of COVID-19 pandemic [1] in context of this global health crisis. Extreme acute respiratory syndrome coronavirus 2, a beta-coronavirus [2], triggers COVID-19. On 31 December 2019 in Wuhan, Hubei Province of China, first contaminated case of COVID-19 was identified and was swift to spread to almost every country, 215 countries and areas worldwide. There is no evidence of reductions in number of contaminated and dead cases and management of situation.

There are confirmed cases 1,853,265 and dead cases 118,854, with Europe accounted for about 46.2% and 66.7% of cumulative cases, as recorded by European Center for Diseases Prevention and Control [3] (accurate as of April 14 2020). More specifically, as Corona Board 1 study indicates, there are already very high numbers of cases, of +83, 039 and + 6, 295 infected and dead, with a fatality rate of 6.34%.

As in other industries, in field of modern health amount of data generated daily also grows exponentially [4]. In period, many diseases, epidemics, and even pandemics occurred worldwide, according to studies by World Health Organisation (WHO). Figure 8.1 shows most recent ones.

Modern healthcare systems move from volume-based systems to value-based systems that put a growing demand on health data for the optimisation of resources, enhanced care quality, patient happiness, and outcomes of health. The usefulness of health data for value-based health systems management changes from the use of health data to the reporting of facts to the generation of operational knowledge that can be used to design novel treatments, anticipate therapeutical results and deliver healthy lifespan. Advanced methods for health data analysis that enable (a) a) patient/citizen involvement into the medical process, (b) omnipresent domestic

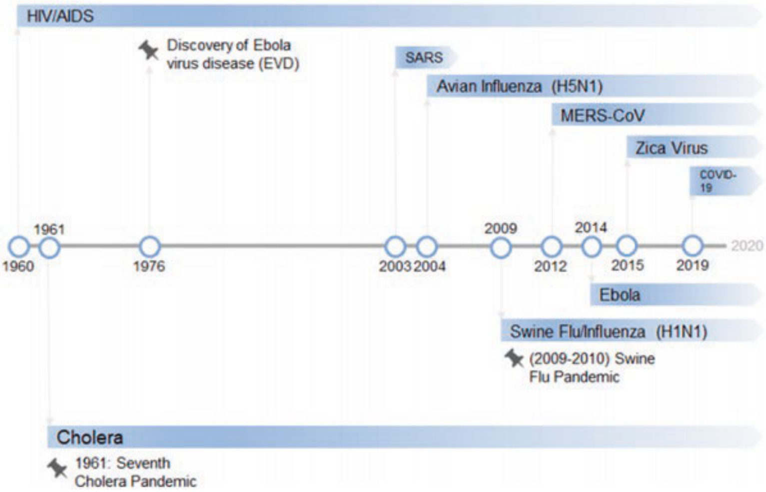


Fig. 8.1 Outbreaks, epidemics and pandemics timeline

healthcare services, extending beyond traditional institutions, (c) improved capturing and integrating heterogeneous healthcare data sources and (d) personalising health data. Health analysis currently comprises sophisticated ways for capturing, integrating and analysing heterogeneous, structured data from clinical and personal health sources in real time to give health care knowledge that is predictive, tailored and patient-centred. A series of intelligent analytical data methods for the data sciences for data management and AI methods for data analytics have been developed by the confluence of Big Data and Artificial Intelligence. Most notably, intelligent methods of health data analysis have the ability to learn, autonomously summarise and understand non-linear connections and causal links inherent in the data. Smart health data analysis (such as: (a) accuracy medicine, (b) forecasting trends and results of disease, (c) healthcare diagnostics for life, (d), support for point of care diagnostics and therapeutic decision making, e) monitoring of ethnographic and (f) optimised use of the healthcare system, are now being used. Machine learning (ML) approaches provide models and associations in data to explore interactions and simulate based on unseen events. ML methods include models. ML methods consist of supervised learning (labeled data learning), unmonitored learning (detection of hidden patterns in data and/or extraction features) and reinforcement education [5]. As ML methods like this can also be classified into techniques for regression, cluster approaches, methods for estimating density and approaches for dimensional reduction. Computational Intelligence (CI) is a subset of ML methods intended to simulate the processing of human knowledge and reasoning processes for the processing of diverse and unknown data sources by algorithms. CI-technologies form a collection of analytical methods and techniques inspired by nature that is created to solve complex real-world information issues that cannot operate as a result of mathematical and conventional modeling: high complexity, unsureness and stochastic nature of systems. The Core CI method trio is produced to solve this growing class of real-world issues, including FL, EA, ANN.

By integrating future healthcare analytics, Big Data changes the health care industry. Doctors can make fast decisions by using Big Data Analytics, on basis of outcome. To provide quality data, big data analytics plays a vital role in handling information that is produced from different resources. Big data plays an important role in healthcare. Big Data has features such as volume, range, velocity and veracity. Big Data not only determines scale but also determines lessons from unstructured, dynamic, heterogeneous, noisy, voluminous data and longitudinal, as information rises dramatically day-by-day [6]. It attempts to compile medical evidence over years into medical libraries, and to digitize the patient histories of payers and providers.

Big data analytics' key problems in the field of health care include the processing, preservation, search, distribution and review of healthcare data. It is also a daunting job to arrange and merge the data after separating them from various layers. In this phase, the medication focused on the reduction of risk must be taken care of in the reduction of mistakes in clinical judgment support and evidence. In compliance with security and safety methods, quality information should be reviewed on – step. Moreover, patients may benefit from lower rates of health care. Real-time

BigData research is the main contribution of the healthcare sector to make predictive decisions. The Big Data chain in public health also needs to be developed because of the need to strengthen successful strategies provided by health sector. Since patients are the final patients in the healthcare sector, they can therefore benefit from money and make informed decisions to protect themselves. These problems should be met as soon as possible by the health sector because they are never standardized [7]. The typical deficiency noted in many exercises of health analysis is (a) the choice of the wrong/suboptimal method of analysis, because of lack of understanding of the relationship between a problem type and the proper analytical options and the method's working; (b) improper data management because data provenance is not understood; and (c) inadequate implementation of a data analysis method.

Rest of this chapter presented Sect. 8.2 is related works, Sect. 8.3 discusses system model, Sect. 8.4 details results and discussion and conclusion in Sect. 8.5.

8.2 State of Art Methods

Ying et al. [8] Use two-dimensional slices, including open cv lung areas. Every 3D chest CT image extracts 15 slices of the entire lungs and each 2D slice inputs Deep Pneumonia, the proposed profound learner-oriented CT diagnostic system (DLD). A pre-trained ResNet-50 will be used to extracted the top K information from each image and applied the Feature Pyramid Network (FPN). The value of each detail is paired with an attentiveness module. Images of Chest CT were taken in 88 COVID-19 cases, in 101 bacterial pneumonia patients and 86 stable patients. Model produces results with an accuracy of 86.0% and 94% accuracy for pneumonia diagnosis.

Zhang et al. [9] ResNet model for X-ray images is available to detect COVID-19. This model contains 2 tasks: one for COVID-19 detection and other for anomaly recognition. The role of abnormalities identification provides an anomaly in the classification score to optimize COVID-19 score. From those two datasets are included X-ray images of 70 patients with COVID-19 and 1008 non-COVID-19 patients with pneumonia. 96.0%, 70.7%, along with an AUC of 0.952 respectively, are sensitivity and specificity.

2D CNN model is indicated to be classified between COVID-19 and standard viral pneumonia in manually delineated area patches in [10]. Chest CT images are being seen in 99 patients (i.e. 44 COVID-19 and 55 common viral pneumonia). Test data sets represents 73.1% accuracy, 67.0% precision and 74.0% sensitivity.

Xu et al. [11] Often utilize candidate infection areas segmented by V-Net model, and region patches, along with the craft features of comparatively distant infection from edges, are sent to ResNet-18 network. Included were CT pictures of 219 patients with COVID-19, 224 patients with Influenza-A, and 175 stable persons. The model's average accuracy is 86.7%.

Shi et al. [12] Using random forest that has shifted. Image is divided into left/right lung, five lung lobes and 18 pulmonary segments during the pre-processing stage, with the aid of a 3D VB-Net [13]. Chest CT images of 2685 patients are included in the results. Results reveal that 90.7% of sensitivity, 83.3% of specificity, and 87.9% of accuracy. Furthermore, results of the test are grouped according to infection sizes which indicate a low sensitivity to patients with small infections.

Five of the most relevant problems in the answer to covid-19 are raised in [14]. In [15], an AI algorithm that utilizes CT images, clinical signs, history of exposure as well as laboratory tests to diagnose covid-19 cases is proposed. Data from 905 patients were obtained from the authors, 419 of whom are laboratory-confirmed positive cases.

In [16], five machine learning algorithms are utilized for processing data of patients and prediction of the mortality risk of patients, namely logistical regression, elastic net, minor partial regression, random forests and versatile bagged discriminant analyses. In [17, 18], the development of a model forecasting the mortality of patients is achieved with different lean-machine methods consists of KNN, SVM and random forest. ML method is utilized for forecasting death and vital incidents in New York in a related attempt [19].

In [20] an algorithm to help make clinical judgment during the pandemic is introduced. In [21] various ML models, including SVM, Decision Tree, KNN, GNB, etc., estimate the age groups in the disease model.

In [22] is used for recognizing patients who may experience extreme coV-19 using a multivariate logistic regression paired with a feature-selection method. In [23] provides a basis for the latest functionality of the Graph Neural Network, which is then used for the classification of nodes using a self-supervised and unattended learning mix. The device is utilized to predict patients' infection and severity. Multivariate logistic regression as well as deep learning method was utilized to determine risk of the developing malignant infection of a patient with mild symptoms [24].

In [25], a data set is used to create a model that forecasts the weak pronostics in covid-19 patients of 13,690 patients in Brazil. Data from a cohort of 1590 patients from 575 health centers were used in [26] to train deep learning method that determines covid-19 patients contracting serious disease based on clinical features. In [27] a feasible approach to identify COVID-19 from chest X-rays differentiates between normal and viral pneumonia affected by DCNN is presented. Three CNN models (EfcientNet B0, VGG16 and Inception V3) pre-entrained in this research were evaluated by means of transmission. The reason for choosing these specified models is their accuracy and efficiency balance with fewer mobile applicable parameters. The dataset utilised for the study is open to the public and compiled from many sources. This study uses profound learning and performance measurement (accuracy, recall, specifcity, precision, and F1 scores). Five modern technologies and their striking applications were disclosed in [28], which may be utilised in mitigating and eliminating COVID-19 difficulties. AI, 3DPT, BDA, HPC and TT. This research examines the application of COVID-19 technologies to promote future research as well as to develop COVID-19 solutions employing AI, 3DPT, BDA, HPC and TT. The research focuses on COVID-19 solutions. In [29] method using a cluster-based routing technique is proposed. In the proposed method, a cluster head (CH) acts as a gateway between the cluster members and the external network, which helps to reduce the network's overhead. In clustering, the cluster's lifetime is a vital parameter for network efficiency. Thus, to optimize the CH's selection process, three evolutionary algorithms are employed, namely, the ant colony optimization (ACO), MOPSO, and CLPSO. Performance of the proposed method is verified by extensive experiments by varying values of different parameters, including the transmission range, node number, node mobility, and grid size. A comprehensive comparative analysis of the three algorithms is conducted by extensive experiments. The results show that, compared with the other methods, the proposed ACO-based method can form clusters more efficiently and increase network lifetime, thus achieving remarkable network and energy efficiency. The proposed ACO-based technique can also be used in other types of ad-hoc networks as well. In [30] it recommended to use a design model to boost the rate of failure detection as the test case selection and prioritying framework. First, we choose test cases for components commonly accessed with observation patterns and second, prioritise test cases for the adoption of certain tactics. An experiment and a comparison with other methodologies validated the proposed framework (previous faults based and random priority). Experimental findings therefore suggest that adjustments have successfully been verified in the proposed framework. The suggested methodology subsequently boosts the rate of failure detection (i.e. more than 90%) over past defects and random priorities (i.e., more than 80% respectively). In order to follow the COVID-19 outbreak and improve health and strategies, the high precision proposed by the AI technique [31, 32] is of great importance. The engagement of huge technology is essential along with the following uses, as scientists, scientists or doctors can be successfully helped in expediting COVID-19 research and development. In [40] the authors showed that they can get 0.901 accuracy, with a positive predictive value of 0.840 and a negative predictive value of 0.982, after training with 499 CT volumes and testing on 131 CT volumes. This study provides a quick way of identifying the patient with COVID-19, which can offer tremendous assistance in timely quarantine and medical treatment. The research in [33] introduces an abnormality quantification procedure based on DL and DL in COVID-19. The entry of uncontrasting chest CT pictures into the suggested learning model while the result is gravity scores such as POO, LSS, POHO and LHOS. In the proposed learning model, the results are good, as Pearson's correlation between ground reality and projected output is 0,97 in POO, 0,98 in POHO, 0,96 in LSS and 0,97 in LHOS, when the data set is trained and tests are 568 CT images and 100 samples.

8.3 System Model

The proposed system model is shown in Fig. 8.2. This system is used to diagnose the COVID-19 pandemics. The COVID dataset is used for data collection process then data is moved from the computational intelligence and big data analytics

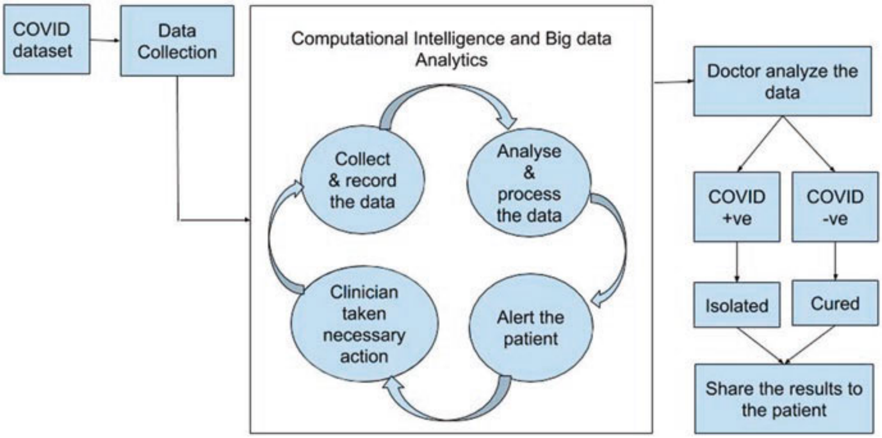


Fig. 8.2 Proposed system model

process. In this section, the data are collected and record that can be analyzed and processed the data, then alert the patient based on analyzing the data finally clinician takes necessary action to the patient. The data can be analyzed by the doctor whether the patients have COVID positive or Negative, if the patient result is positive then the patient is isolated, if the patient result is negative then the patient is cured and finally the results are shared with the patient. Early treatment and forecasting are important as one of the most effective ways for combating the COVID-19 epidemic. The reverse transcription polymerase (RT-PCR) detection technique is currently a standard tool for classifying respiratory viruses. Some work was done to enhance this approach and other alternatives in response to the COVID-19 virus. However, these approaches are frequently time-consuming and costly, have a poor true positive rate, and require particular ingredients. Furthermore, because of restrictions on budgets and technology many countries suffer from a lack of test kits. The usual approach is not therefore adequate for rapid detection and monitoring requirements during the pandemic COVID-19.

8.3.1 COVID Dataset

Illness caused by SARS-CoV-2 virus is COVID-19. A global COVID-19 pandemic was reported in 2020. Reaction to COVID-19 pandemic, COVID-19 has been established by White House and a consortium of leading science groups. CORD-19 is a resource of more than 200,000 scientific articles, including over 100,000 full-text, COVID-19 and SARS-CoV-2. To develop more insights into the current battle against this infectious disease, the globalized scientific community will be provided with this publicly accessible dataset to incorporate the latest advancing natural language and AI technologies. The exponential acceleration of new coronavirus literature is making it impossible for health science communities to keep up with these methods. These approaches are increasingly urgent.

8.3.2 Data Collection

During a pandemic, manner in which data is gathered and quality of the data collected face challenges. Data requirements did not uniform as data are gathered by government employees exposed to illness conditions, creating physical and emotional risks. The details were also not updated promptly. Against context of rapid spread of COVID-19 virus, to determine condition of outbreak and its risks, and to prevent confusion among the population, urgent data updates were necessary.

Owing to a lack of understanding of the danger of the disease at an early stage, the lack of sophisticated data processing means, the huge number of subjects participating in data collection and disclosure and eventual "fragmentation" of large data platforms, however, much of the data has not been revised immediately or optimally. Manual data processing, of course, can result in delays, dissimulation, imprecision and monitoring.

8.3.3 Computational Intelligence and Big Data Analytics

CI is a collection of computational methodologies and methods inspired by nature to solve complex real-world problems that can be useless for mathematical or conventional modeling for a few reasons: the processes may be too complicated for mathematical logic, may involve some uncertainties during the process, or may simply be stochastic. It is crucial to keep people healthy at present and to monitor the situation promptly. But it is still necessary and necessary to analyse how personal data are secure and private. The Zoom video conferencing application scandals its security and privacy issues 4 are a display of this dilemma. During this pandemic, authorities can ask their citizens to supply the personal data necessary to control the issue, to build up to date laws and to take prompt measures, such as the location of GPs and CT tests, diagnostic reporting, travel paths and everyday activities. Data is a necessary to ensure that any AI and Big data platforms are successful; nevertheless, usually, if not officially asked, people will not volunteer their data. There is a compromise: privacy/safety and performance.

8.3.4 Big Data for COVID-19 Fighting

Capacity of big data to tackle infectious diseases such as COVID-19 is proven [34, 35]. Big data may offer some successful options to better counter the epidemic of COVID-19. Big data allows one to consider COVID-19 in terms of outbreak monitoring, the structure of the virus, epidemic treatment and development of vaccines, by CI analyses [36].

For example, large data connected to smart IC tools may produce extensive model simulations with coronavirus data sources for outbreak estimations. This enables health officials to monitor coronavirus transmission and to design better steps to prevent coronavirus transmission [37]. Big-data models also support future COVID-19 forecasting through the way that they can aggregate vast volumes of data for early detection. Also, large-scale COVID-19 experiments will help to establish extensive, highly accurate treatment options from a range of real-world sources, contains infected patients [38, 39]. It will also allow healthcare providers to consider the progression of the virus and a better response to multiple diagnoses and treatments.

Also, AI (and explicit AI [40]) aims at logic and reasoning to construct human intelligence that imitates a learning machine, classifies, and predicts potential outcomes, such as classifications of COVID-19 symptoms. A variety of realistic cases will clarify and address the possible use of each technology in the war against COVID-19. s: A larger dataset provides the basis for the COVID-19 epidemic for AI and big data platforms. Therefore, [1] incentives are needed to invite more people and entities to contribute their own data. For the following reasons, incentives are necessary: 2) the quality of data should be ensured to increase the accuracy and performance in the learning models, and the data should be provided in vast quantities by the persons/entities which the government is unable to request to give their data.

8.4 Results and Discussion

The findings and discussions of this method to assess the polarity of feelings in the sorted texts in the three groups 1 (positive), 0 (neutral) and − 1 (negative).

Figure 8.3 shows the entire dataset sentiment polarity. X and Y-axis show the neutral, positive, negative and values obtained respectively. The neural achieves 58,124, positively achieve 26,375, negative achieves 18,472 in 10^4 respectively.

In comparison, Figs. 8.4 and 8.5 display the approach used to measure probability density for generating data on the relationship between public opinion frequency and time. X and Y axis is time and values obtained respectively. Maroon, Green, Orange is Negative, Positive, Neutral respectively.

In addition, AI has become an interesting technology to facilitate the production of vaccines and drugs. AI employs smart analytical instruments for

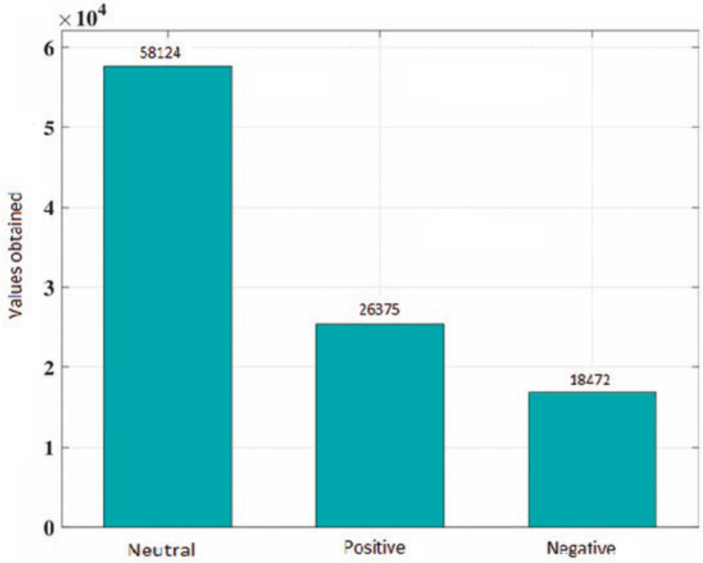
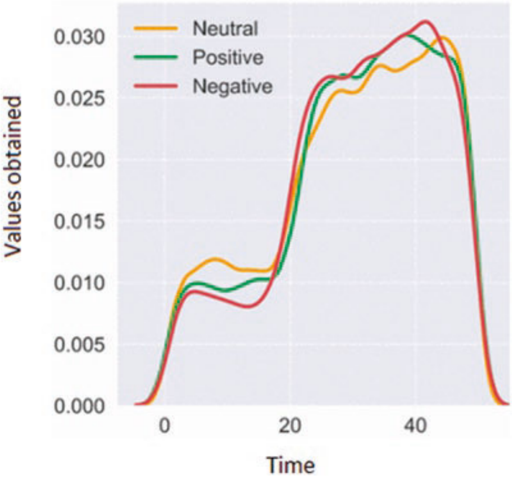


Fig. 8.3 Entire dataset sentiment polarity

Fig. 8.4 Probability density estimation on public opinion



forecasting the effective and safe vaccine/medication against COVID-19 which would be helpful in economic and scientific terms through data sets provided by health organisations, governments, clinical laboratories and patients. AI uses them. Big data, however, have been demonstrated to be able to deal with the COVID-19 epidemic. Big data could offer promising ways to help combat the pandemic of COVID-19. Big data helps us to comprehend COVID-19 in terms of

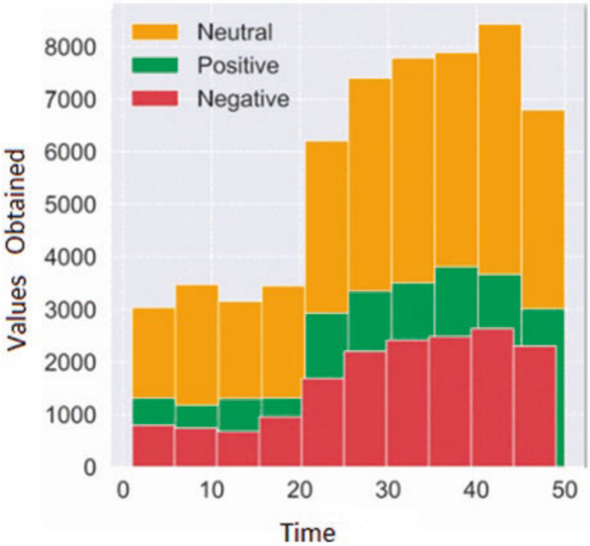


Fig. 8.5 Probability density estimation on time

its virus and illness structure in combination with AI analytics. Big data Big data can aid providers from early diagnosis and disease analysis to treatment result prediction in many medical operations.

8.5 Conclusion

Big data could deliver many promising solutions to help tackle pandemic in COVID-19. Big data allow us to understand Virus structure and disease production in terms of COVID-19, by integrating it with CI analytics. Big data can assist healthcare providers from early diagnosis, condition analysis and estimation of patient outcomes and reliability of data processing for improved COVID-19 diagnosis and treatment in different medical operations. To deliver newly powerful applications to tackle COVID-19, CI and Big Data should be combined with other digital technologies. For future research, further case studies and expert publications on the use of Big Data Analytics and AI in medical setup must be required. This might happen if stakeholders and practitioners in the healthcare system employ these technologies in the real world to further discover the potential of big data analysis and artificial intelligence to improve health quality. Systematic and structured method used in the framework includes both conceptual and technological elements and hence leads research in this area. During the planning of their research activity, others might use the classification scheme and framework.

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Chapter 9
Prediction of Corona Virus Disease Outcome and Future Forecast the Trend of COVID-19 in India: Observational Study

Amit Kumar Mishra, Ramakant Bhardwaj, and K. Sruthila Gopalakrishnan

Abstract This work is motivated by the disease caused by the novel corona virus Covid-19, rapid spread in India. An encyclopaedic search from India and worldwide social networking sites was performed between 1 March 2020 and 20 Jun 2020. Nowadays social network platform plays a vital role to track spreading behaviour of many diseases earlier then government agencies. Here we introduced the approach to predict and future forecast the disease outcome spread through corona virus in society to give earlier warning to save from life threats. We compiled daily data of Covid-19 incidence from all state regions in India. Five states (Maharashtra, Delhi, Gujarat, Rajasthan and Madhya-Pradesh) with higher incidence and other states considered for time series analysis to construct a predictive model based on daily incidence training data. In this study we have applied the predictive model building approaches like k-nearest neighbour technique, Random-Forest technique and stochastic gradient boosting technique in COVID-19 dataset and the simulated outcome compared with the observed outcome to validate model and measure the performance of model by accuracy (ACC) and Kappa measures. Further forecast the future trends in number of cases of corona virus deceased patients using the Holt Winters Method. Time series analysis is effective tool for predict the outcome of corona virus disease.

Keywords Corona virus trend · COVID-19 · Machine learning · Predictive modelling · K-nearest neighbour technique · Random-Forest technique and stochastic gradient boosting technique · Holt Winters Method · Mathematical modelling

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_9

9.1 Introduction

The World Health Organization (WHO)-China office, informed the case of pneumonia detected in Wuhan city of China province on 31 December 2019 [1]. This novel virus further known as corona virus, COVID-19 (formally known as 2019-nCoV) [3]. This virus circulates in entire globe which affect all age groups and spared through physical contact of persons, resulting a serious health issue worldwide. From 11 January 2020 to till date i.e. 20 May 2020, total death worldwide due to COVID-19 noted 32,3156 and 4.86 million total confirmed cases [1]. First case of COVID-19 reported in India on 30 January 2020 and Ministry of Health and Family Welfare provided the data, total 11, 2196 corona cases and 3435 deaths in country [4, 2].

In this study, we use epidemiological data collected during COVID-19 outbreak in India in between 1 March 2020 and 20 May 2020 [5]. Here a model is developed to predict death or recovery from the unlabelled cases of COVID-19.

9.2 Data and Methods

9.2.1 Data Sources

Different sources were used to collect data for the Covid-19 trend identification. An application data is collected from internet [5] which has been developed to report live situation on corona virus pandemics in India. Validity and accuracy of reported data of this application is maintained by live updating of data based on state news bulletin, Official sites of Chief Ministers office /Health ministry, Press conferences, ANI reports and social networking platforms like Twitter, facebook etc. That data contains demographic details about the corona virus decease patients and deep analysis of Total cases, daily update of cases, cases by states, growth trends etc. Another source of data taken from social platform [3] used to show statistics of current trend in COVID-19 worldwide. This statistics and research was referenced to use data of World Health Organization and National Center for Health Statistics etc. This data contains worldwide statistics of total confirmed deaths, deaths trend on daily basis, cases growth rate with global comparison, testing pattern like testing pattern per thousand people, daily tests, test per case, confirmed case etc. Data used for this study validated by compare it with reports of Ministry of Health and Family Welfare [4]. They scheduled update the data periodically on situation of outbreaks of COVID-19 in India.

9.2.1.1 Data

In this study, we have considered the data of pandemic of COVID-19 from 1 March 2020 to 20 May 2020. Till date total 112,196 confirmed cases out of which 63,339 active cases, 45,422 recovered case and 3435 deaths reported. Age density of Death and Recover cases shown in Fig. 9.1.

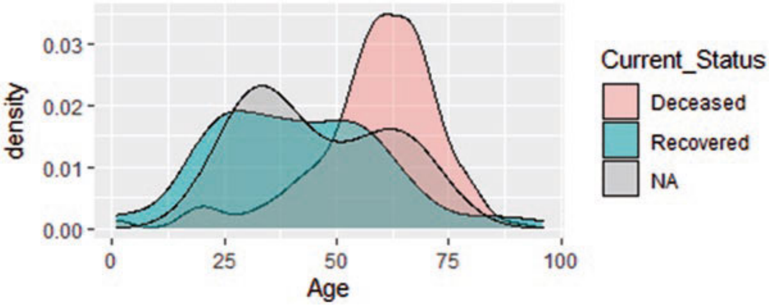

Fig. 9.1 Age density graph of death and recover cases

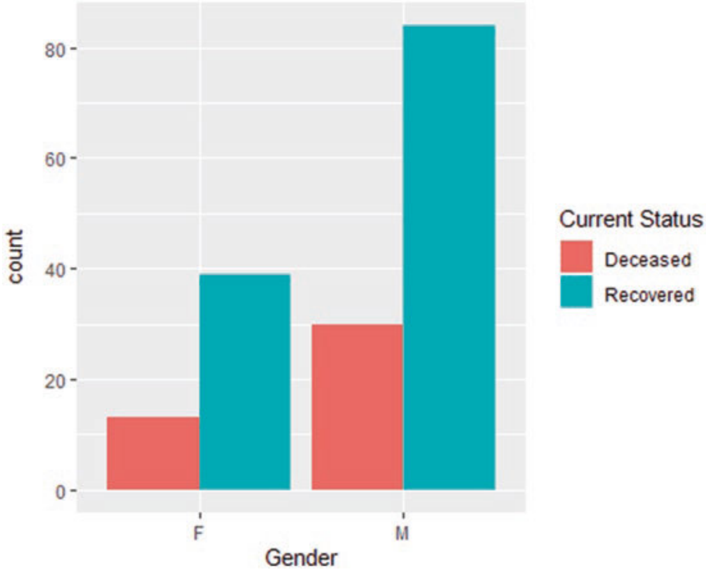

Fig. 9.2 Recovery and death ratio for male and female cases

Figure 9.2 show the recover case of Female patient and Male patients (based on data available till now and it is not sufficient and complete to provide accurate statistics).

Figure 9.3 shows the weekly time line data of recovered, deceased and hospitalized cases till 30 April 2020.

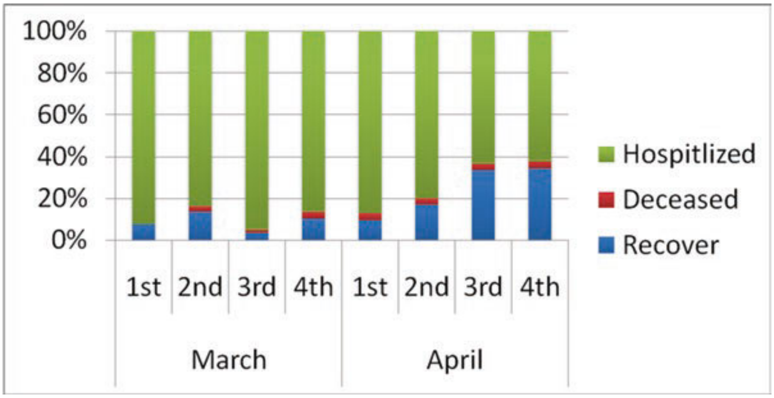

Fig. 9.3 Time line data of COVID-19 cases till 30 April 2020

9.2.2 Methods

Machine learning gives many ways to discover pattern and predict COVID-19 outcome from dataset of corona virus. In this study we used few machine learning techniques, such as Random Forest [6, 7], Stochastic gradient boosting [8, 9] and k-nearest neighbour [10], which have played an essential contribution to the field of data science.

This paper introduced a method of machine learning for predict the outbreak of corona virus outcome using web data. This framework of our introduced method is illustrated in Fig. 9.4.

9.2.2.1 Statistical Steps

In first step, we extract the features of our data to get important trend through machine learning model. This step is necessary to reduce the size of number of input features and to get important features out of that. Further checked the missing data values in data and imputed it with multivariate imputation by chained equation [11]. Most of the data mining algorithm cannot deal with missing data, so they exclude the data completely from model. If dataset is large and missing value is less then it is better to exclude them but if data set is small then better is to impute the missing values.

Consequently in step two, Fig. 9.5 shows the machine learning models will be used with different model parameters offered to train the model using training data.

In forth step, detection will get perform with proper feature subset and efficient model chooses through their accuracy and kappa value. The appropriate trained model used to predict the outcome of corona virus decease.

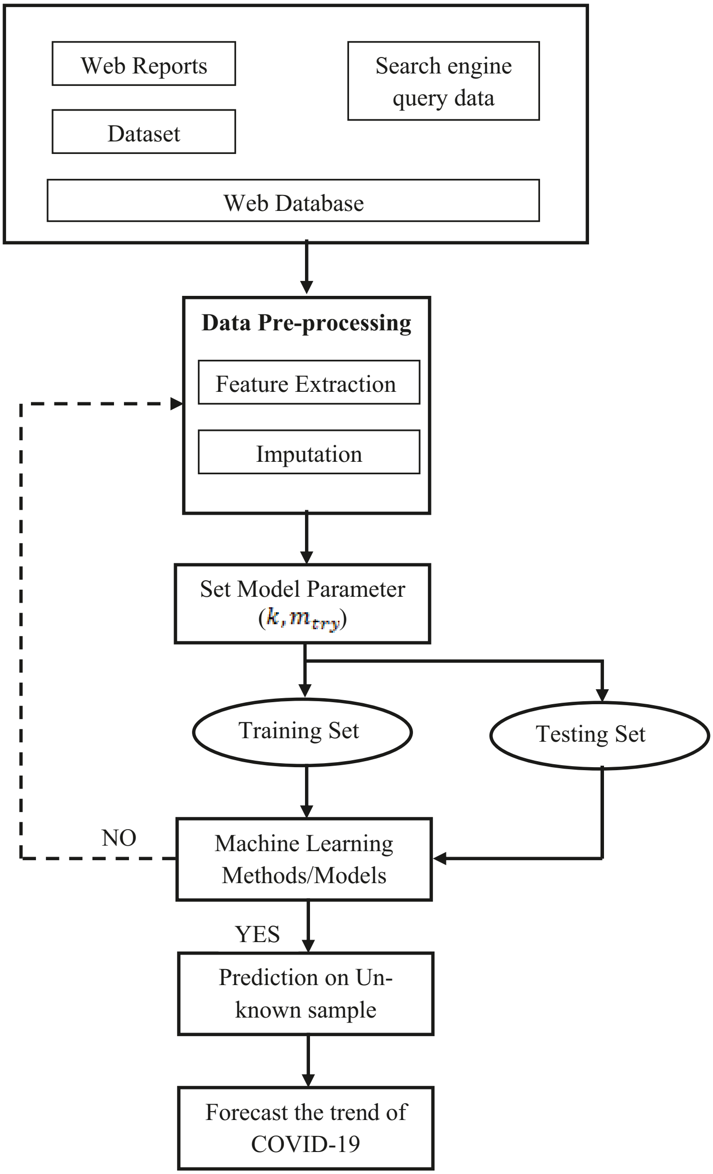

Fig. 9.4 Block diagram of proposed model

Additionally, the performance of prediction has been evaluated by the measures like Accuracy (ACC) [12], which is a measurement of closeness to specific value and another measure is Cohen kappa coefficient [13], which is a statistics to measure the inter-rater reliability for qualitative items:

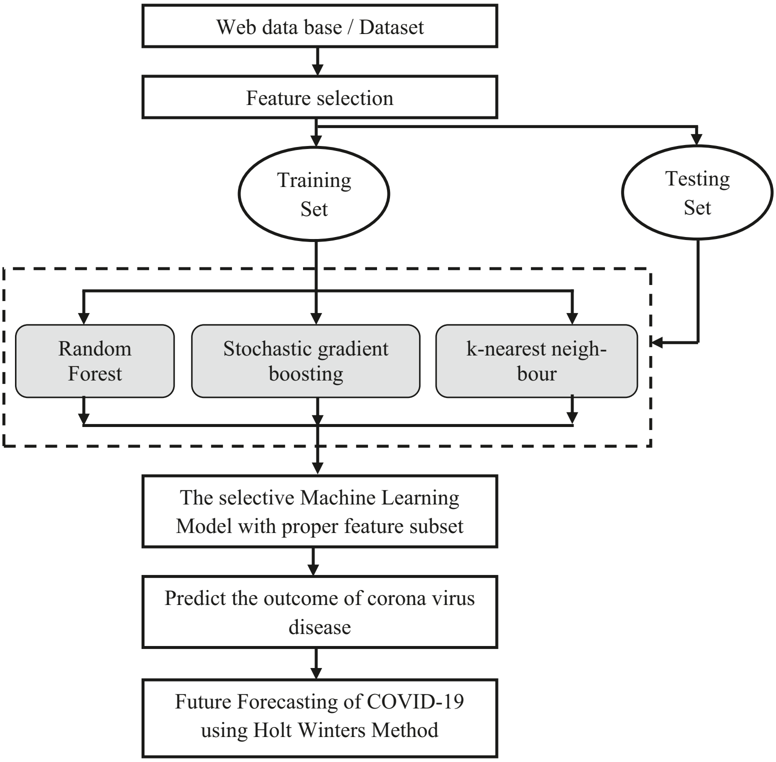

Fig. 9.5 Machine learning model

$$ACC = \frac{TP + TN}{P + N} = \frac{TP + TN}{TP + TN + FP + FN}$$

where:

TP = True positive; FP = False positive; TN = True negative; FN = False negative

Kappa statistics is to measure the agreement value K between two raters. Each raters classify N numbers of items into C classes of item categories. Here maximum value of K represents the complete agreement between raters.

$$K = \frac{p_o - p_e}{1 - p_e} = 1 - \frac{1 - p_o}{1 - p_e}$$

Where,

p_o is observed agreement between raters.
p_e is hypothetical probability of chance agreement.

$$p_e = \frac{1}{N^2} \sum n_{k1} n_{k2}$$

Where, k is categories, N represent to observations and n_{ki} 0.Finally in fifth step, Future forecasting have been done by using Holt Winters Method [14], which is a triple exponential smoothing method. It is an appropriate technique only when trend and seasonality present in the time series dataset. It decomposes the data into three components: Level, Trend and Seasonality, which can be calculated as follows:

$$L_t = \alpha\left(\frac{D_t}{S_{t-s}}\right) + (1-\alpha)(L_{t-1} + T_{t-1})$$

$$T_t = \beta(L_t - L_{t-1}) + (1-\beta)T_{t-1}$$

$$S_t = \gamma\left(\frac{D_t}{L_t}\right) + (1-\gamma)S_{t-s}$$

Where,
L_t is level of series of period t.
$L_{t-1}$is smoothed value for period t-1.
D_t is actual value at period t.
T_t is trend at period t.
S_t is seasonality estimate at period t.
α is smoothing constant for Level $(0 \le \alpha \le 1)$
β is smoothing constant for Trend ($0 \le \beta \le 1$)
γ is smoothing constant for Trend ($0 \le \gamma \le 1$)
s is time period that select in seasonal cycle.

Next, forecast has been done by using following equation:

$$F_{t+m} = (L_t + mT_t) * S_{t+m-s}$$

Where,

m is number of period ahead to be forecast i.e 1 for this case.
F_{t+m} is Winter's forecast for m period ahead into future.

"Goodness of fit", which shows the accuracy of the forecast has been evaluated by four standard measures: Mean Absolute Deviation (MAD) [15], Mean Square Error (MSE) [16], Root Mean Square Error (RMSE) [17] and Mean Absolute Percentage Error (MAPE) [18].

$$MAD = \frac{\sum_{t=1}^{n} |D_t - F_t|}{n}$$

$$MSE = \frac{\sum_{t=1}^{n} (D_t - F_t)^2}{n}$$

$$RMSE = \sqrt{\frac{\sum_{t=1}^{n}\left(D_t - F_t\right)^2}{n}}$$

$$MAPE = \frac{\sum_{t=1}^{n}\frac{\left|D_t - F_t\right|}{D_t}}{n} \times 100\%$$

Where,

D_t is actual value at period t.
F_t is Winter's forecast value for actual value.

9.3 Results

9.3.1 Overall Incidences

A time interval data were collected and verified with MoHFW. Figure 9.6 shows the average incidence from 30 January 2020 to 20 May 2020 in each region of India where corona virus deceased case were more than 1000.

In above histogram, we can see that most of the most of the regions in India fluctuate around the national average corona virus deceased incidence level. Among all the regions in the India, Maharashtra, Gujarat, Delhi, Rajasthan, Tamil Nadu and Uttar Pradesh regions have highest incidence, which is more than average of national average incidence. However, the incidences of corona virus decease in India, such as the Punjab, Haryana and Bihar regions, is low, less than one fourth of the national average.

Figure 9.7 show the nationwide trend of virus deceased cases from the beginning of COVID-19 incidences in India till 30 April 2020. The virus impact starts from mid march and mostly peaks in April month after second week.

9.3.2 Model Training

9.3.2.1 Random Forest, Stochastic Gradient Boosting and K-Nearest Neighbour

Here the training results evaluated using Random forest, stochastic gradient boosting and k-nearest neighbour technique respectively. Total 226 samples used to predict categorical outcome class (Deceased or recovered) based on 30 predictors. Here bootstrap sampling done using 226 samples with repeating 25 times each. Each table (Tables 9.1, 9.2 and 9.3) have different tuning parameters for different learning algorithms used here for training purpose. Random forest use single tuning

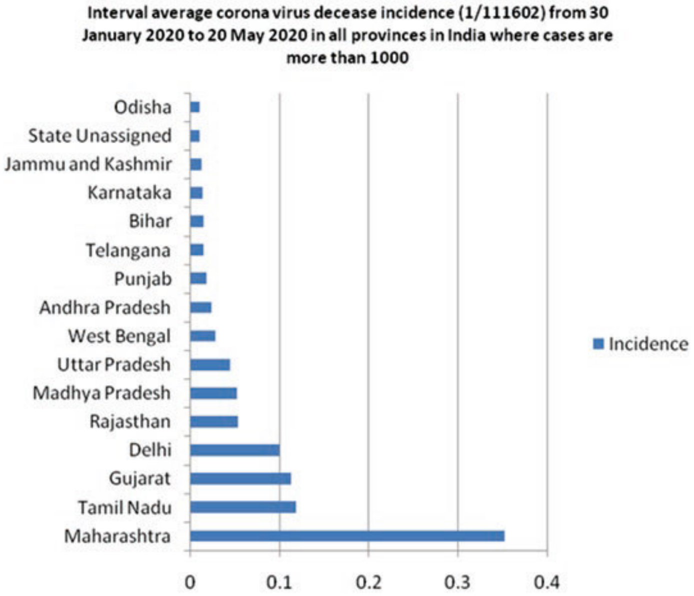

Fig. 9.6 Time interval average corona virus decease incidence (1/23,041) from 30 January 2020 to 20 May 2020 in all provinces in India where cases are more than 1000

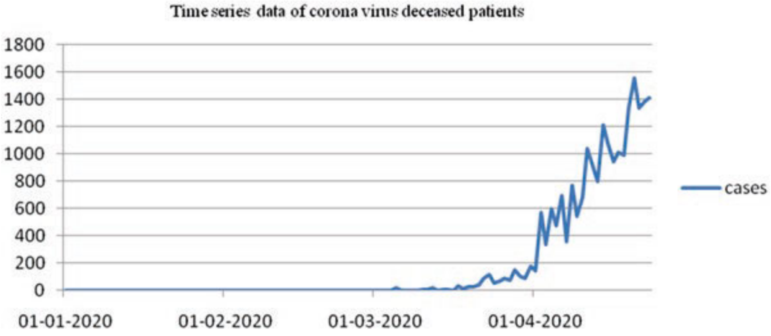

Fig. 9.7 Time series analysis of COVID 19 deceased patients

parameter m_{try} i.e. number of predictors which is used to split the classification. Stochastic gradient boosting uses two tuning parameters interaction depth and n trees along with constant shrinkage. K-nearest neighbour technique uses kmax parameter which means to maximum number of classes for classification of closed labelled neighbours.

The final value used for the model was mtry = 2.

The final values used for the model were n.trees = 150, interaction.depth = 3, shrinkage = 0.1.

Table 9.1 Tuning parameters of random forest technique

m_{try}	Accuracy	Kappa
2	0.92	0.80
3	0.91	0.78

Table 9.2 Tuning parameters of Stochastic gradient boosting

interaction.depth	n.trees	Accuracy	Kappa
1	50	0.8624	0.674
1	100	0.9064	0.782
1	150	0.9191	0.811
2	50	0.9142	0.799
2	100	0.9162	0.804
2	150	0.9178	0.808
3	50	0.9145	0.801
3	100	0.9163	0.805
3	150	0.9223	0.819

Table 9.3 Tuning parameters of k-nearest neighbour

kmax	Accuracy	Kappa
5	0.885	0.731
7	0.885	0.731
9	0.886	0.734

The final values used for the model were kmax = 9, distance = 2 and kernel = optimal.

9.3.2.2 Comparison of Model Training Algorithms

Table 9.4 shows the performance characteristics of all three types of training models. It seems that Random Forest model is best model as per performance among all.

Figure 9.8 visualize the boxplot diagram of comparison of performance characteristics.

9.3.3 Prediction

Table 9.5 shows the prediction of testing data, where actual outcome of patients are known and for the testing purpose we have changed it to unknown outcome and tried to predict it using trained model of all three learning algorithm. It has been

Table 9.4 Performance characteristics of training models

	Accuracy			Kappa		
	rf	gbm	knn	rf	gbm	knn
Min	0.86	0.87	0.84	068	0.73	0.63
1st Qu.	0.90	0.90	087	0.772	0.777	0.705
Median	0.92	0.91	0.88	0.82	0.80	0.73
Mean	0.92	0.91	0.88	0.82	0.80	0.73
3rd Qu.	0.94	0.92	0.90	0.86	0.84	0.76
Max	0.95	0.94	0.92	0.90	0.87	0.83
NA's	0	0	0	0	0	0

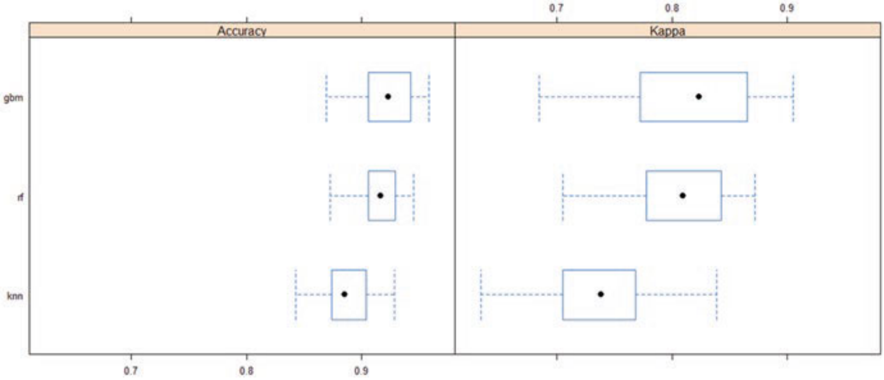

Fig. 9.8 Performance comparison of all three models used for training data

identified that Random forest and stochastic gradient boosting techniques predicated outcome with higher accuracy i.e. 90% in compare to k-nearest neighbour trained model.

Table 9.6 shows the predictive results of all three predictive models. Here we have 10 patients' details, which show current fitness condition of all patients along with their previous and current status of outcome.

Probability of predictions predicted by Random forest, stochastic gradient boosting and k-nearest neighbour techniques are shown in Table 9.7.

Table 9.5 Testing of outcome prediction of COVID-19 diseased patients

			Outcome prediction of COVID-19 diseased patients					
Case_ID	Actual status	Current Status (Testing)	Random Forest	Accuracy in %	Stochastic gradient boosting	Accuracy in %	k-nearest neighbour	Accuracy in %
36	Recovered	Unknown	Recovered	90%	Recovered	90%	Recovered	80%
57	Recovered	Unknown	Recovered		Recovered		Deceased	
135	Recovered	Unknown	Deceased		Deceased		Recovered	
430	Deceased	Unknown	Deceased		Deceased		Deceased	
558	Recovered	Unknown	Recovered		Recovered		Deceased	
855	Deceased	Unknown	Deceased		Deceased		Deceased	
860	Deceased	Unknown	Deceased		Deceased		Deceased	
863	Deceased	Unknown	Deceased		Deceased		Deceased	
1015	Recovered	Unknown	Recovered		Recovered		Recovered	
1293	Deceased	Unknown	Deceased		Deceased		Deceased	

Table 9.6 Outcome prediction of COVID-19 diseased patients

Case_ ID	Previous Status	Current status	Outcome prediction of COVID-19 deceased patients					
			Random Forest	Accuracy in %	Stochastic gradient boosting	Accuracy in %	k-nearest neighbour	Accuracy in %
4	Hospitalized	Deceased	Deceased	**70%**	Deceased	**70%**	Deceased	**70%**
136	Hospitalized	Recovered	Deceased		Deceased		Deceased	
165	Hospitalized	Deceased	Deceased		Deceased		Deceased	
285	Hospitalized	Recovered	Deceased		Deceased		Deceased	
1056	Hospitalized	Recovered	Recovered		Recovered		Recovered	
1289	Hospitalized	Deceased	Deceased		Deceased		Deceased	
1572	Hospitalized	Recovered	Deceased		Deceased		Deceased	
1879	Hospitalized	Deceased	Deceased		Deceased		Deceased	
3021	Hospitalized	Deceased	Deceased		Deceased		Deceased	
4534	Hospitalized	Deceased	Deceased		Deceased		Deceased	

Table 9.7 Probability of Outcome prediction of COVID-19 diseased patients

	Probability of Outcome prediction of COVID-19 diseased patients					
	Random Forest		Stochastic gradient boosting		k-nearest neighbour	
Case_ID	Deceased	Recovered	Deceased	Recovered	Deceased	Recovered
4	0.944	0.056	0.963	0.036	1	0
136	1.0	0.0	0.970	0.029	1	0
165	0.998	0.002	0.986	0.013	1	0
285	0.958	0.042	0.963	0.036	1	0
1056	0.016	0.984	0.116	0.883	0	1
1289	0.982	0.018	0.984	0.015	1	0
1572	0.960	0.040	0.965	0.034	1	0
1879	0.974	0.026	0.971	0.028	1	0
3021	0.998	0.002	0.984	0.015	1	0
4534	0.996	0.004	0.928	0.071	1	0

9.4 Forecasting Using Holt Winters Method

Initialisation

$$S_i = D_i\left[\left(\frac{1}{s}\right)\left(D_1 + D_2 + D_3 + \ldots + D_s\right)\right]$$

$$L_i = \frac{D_i}{S_1}$$

$$T_i = \frac{D_i}{S_1} - \frac{D_{i-1}}{S_s}$$

From the incidence trend in India, the corona virus incidence mostly starts increasing in March from 17th March 2020 onwards. Here we took India COVID-19 incidence data from 1 April 2020 to till 20 May 2020 for modelling and forecasting (Fig. 9.9).

Table 9.8 shows the smoothing parameters chooses for this forecast,

To validate the predictive capability of model used, we use the constructed model Holt Winters to predict the corona virus incidence from 1 April 2020 to till 20 May 2020 and then compared the actual deceased patients' numbers for that day with predicted values. The model fitted the data reasonably well (Fig. 9.10) with 15.17 MAPE. It shows that the Holt Winters Forecast model was Good [19] for forecasting COVID-19 deceased incidence in India.

We also construct a Holt Winters Future Forecast model (Fig. 9.11) for predicting next 11 days values for total cases of corona virus deceased patients from 21 May 2020 to 31 May 2020 (Table 9.9).

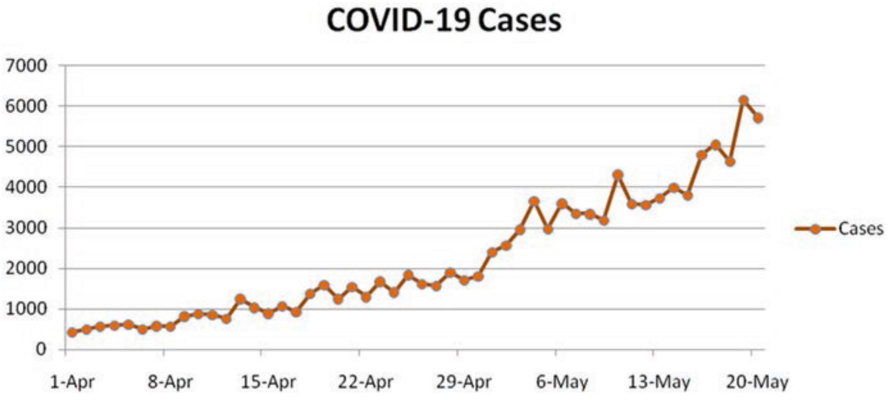

Fig. 9.9 Score of number of corona virus deceased patients increase pattern

Table 9.8 Smoothing parameters initial value

Parameters	
Alpha(α)	0.42
Beta(β)	0.42
Gama(γ)	0.99

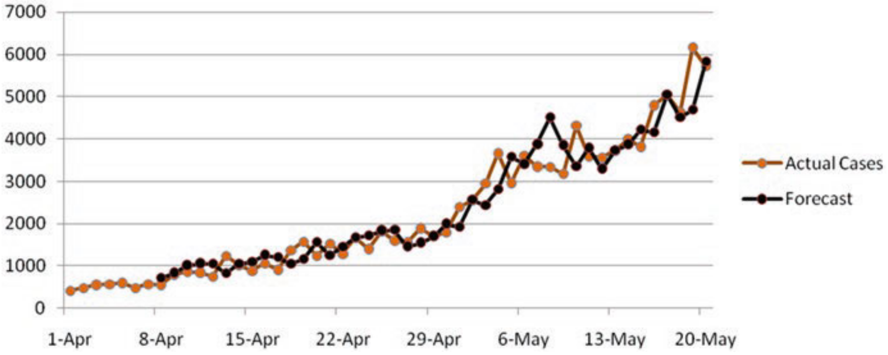

Fig. 9.10 Holt winters forecast model for COVID-19

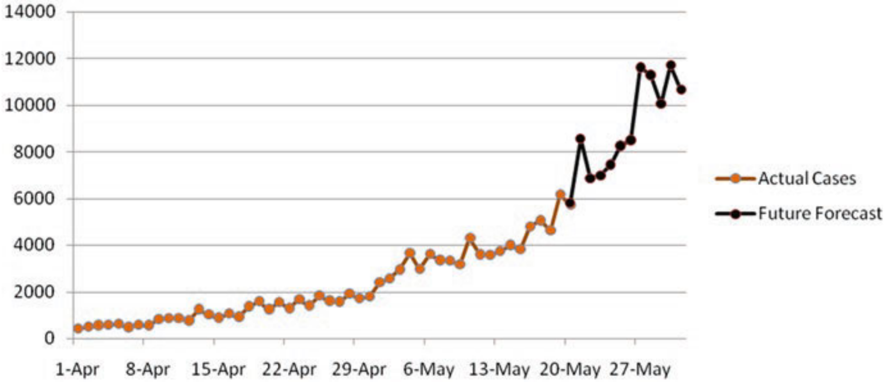

Fig. 9.11 Holt winters future forecast model for COVID-19

Table 9.9 Data table of future forecast of COVID-19

Sno	Date	Cases	Level	Trend	Seasonal	Forecast	Error	|Error|	Error^2	|%Error|
1	17-May	5049	5138.73	241.0228	0.98109	5048.511	−0.488568	0.48856	0.23869	0.009676
2	18-May	4628	5551.26	313.0570	0.83334	4511.104	−116.89527	116.895	13664.5	2.525826
3	19-May	6154	6623.54	631.932	0.92783	4688.935	−1465.0649	1465.06	2146415.	23.80671
4	20-May	5716	7068.89	553.565	0.80891	5819.891	103.89101	103.89	10793.3	1.817547
						Future forecast				
5	21-May					8552.1708				
6	22-May					6855.8701				
7	23-May					6979.9162				
8	24-May					7446.3633				
9	25-May					8255.0056				
10	26-May					8495.2111				
11	27-May					11596.051				
12	28-May					11280.093				
13	29-May					10042.598				
14	30-May					11694.996				
15	31-May					10643.848				

Table 9.10 Error measured by standard measures

Error measures	
MAD	325.7057
MSE	205281.2
RMSE	453.0797
MPSE	15.17755

9.5 Discussion

Corona virus decease put its impact directly or indirectly to all of us now days. The corona virus mutates according to environment easily as well as very quickly, which results a COVID-19 pandemic this year. This leads to social, economical and medical burden in country. We cannot repel the virus but we can minimize the impact of decease. In this behavioural study, we have introduced the statistical and forecasting model based on statistics for predicting number of cases of corona virus deceased patients. It will help to get the idea of research for COVID-19 prevention in future and also can guide for public health.

The Machine learning model used to train the data (Table 9.1, 9.2, 9.3 and 9.4) and the accuracy of the training model calculated (Fig. 9.8). Finally the outcome of COVID-19 decease tested (Table 9.5) and predicted (Table 9.6) with its probability of prediction (Table 9.7).

The Holt Winters method applied in different forecasting areas [20–21]. The national corona virus decease shows less seasonality and increasing fluctuation (Fig. 9.7). In this study, we select India as an example to construct a predictive model with corona virus decease incidence from 1 March 2020 to 20 May 2020 (Fig. 9.9). Then, we forecast the number of cases of COVID-19 and compared with actual number of cases (Fig. 9.10) and at last future forecast the total number of cases (Fig. 9.11) of corona virus deceased patients in India for next 9 days (Table 9.9) with reasonable accuracy (Table 9.10).

The accuracy of forecasting can increase by tuning the parameter α, β and γ more accurately. The Holt Winters method can forecast for short term with more accuracy. For this study, we have data with less time period, so the prediction and forecasting will deviate moderately.

Acknowledgments The author appreciates the covid19india.org: A volunteer-driven crowd sourced effort to track the corona virus in India, Our World in Data: a scientific online publication that focuses on large global problems such as poverty, disease, hunger, climate change, war, existential risks, and inequality and last but not the least, Ministry of Health and Family Welfare (MoHFW), Govt. of India for helping and supporting to get the COVID-19 incidence data for research and study.

Conflict of Interest The authors declare that they have no conflict of interest.

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Chapter 10
Treatment of Novel Coronavirus (2019-nCoV) Using Hinokitiol (β-thujaplicin) Copper Chelate

R. Anandan, Noor Zaman Jhanjhi, and B. S. Deepak

Abstract Human Coronavirus (HCoV) or Novel Coronavirus (2019-nCoV) is probably a brand new version of coronavirus that belongs to Betacoronaviruses kind Human Coronaviruses, similar to the Severe Acute Respiratory Syndrome (SARS) coronavirus and Middle-East Respiratory Syndrome (MERS) coronavirus. China recorded the number one case of this virus in December 2019 at Wuhan, the capital town of Hubei province. By 27 March 2020, 10:00 CET, nearly 23,335 humans died out of 509,164 showed instances recorded throughout the world. By the give up of January 2020, China showed that the Novel Coronavirus (2019-nCoV) transmitted from one human to another. This studies pursuits to research a completely specific medicament called "Hinokitiol Copper Chelate" towards the large quantity 2019-nCoV Spike Glycoprotein with a unmarried receptor binding domain. This take a look at gives a super version for Hinokitiol Copper Chelate to be examined in silico towards 2019-nCoV Main Protease.

Keywords Hinokitiol Copper Chelate · COVID-19 · 2019-nCoV · Human coronavirus

10.1 Introduction

Hubei province and its sprawling capital city Wuhan, China recorded the first case of coronavirus disease 2019 (COVID-19) on December 31, 2019 at the WHO country office in China. On January 30, 2020, WHO declared the Wuhan outbreak (COVID-19) a public health emergency of international concern and issued a

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_10

surveillance draft in January 2020, stating that any traveler who has visited Wuhan city or the Hubei province in China, 2 weeks before the onset of the first case reported to the WHO country office, China, was suspected to be COVID-19 positive [14]. In addition, the organization has distributed an interim guide to all laboratories worldwide performing tests for the new outbreak and a control guide to prevent infection from specimens [14]. Viral pneumonia is associated with an unknown animal sold in Huanan fish market for epidemic emergency [8, 14]. As of March 27, 2020, 10:00 a.m. CET, 509,164 cases have been confirmed positive for the 2019-nCoV outbreak, resulting in 23,335 patient deaths worldwide [WHO source]. On January 20, 2020, the National Health Commission of the People's Republic of China ruled that the Wuhan outbreak, also known as the COVID-19 outbreak, was human-to-human transmissible [14]. According to the data, six strains of coronavirus (CoV) have been recorded, excluding the new 2019-nCoV [14]. COVID-19 belongs to human coronavirus-like betacoronaviruses (HCoV) such as MERS, OC43, HKU1 and SARS while 229E and NL63 are members of the alphacoronaviruses. According to the World Health Organization, the SARS and MERS coronaviruses were the most destructive strains of CoV until the outbreak in Wuhan (COVID-19), killing around 800 people each. According to the WHO, MERS has a mortality rate of 36% while SARS has 10% [14].

10.1.1 Evolution of Virus

Viruses are microscopic infectious entities that reproduce by infecting the cells of other creatures. DNA or RNA, capsid (a protein coat), genomic material that covers the genome, and sometimes an envelope that encapsulates the capsid make up their overall structure. Diversity of creatures they infect, their lifecycle system, and the influence they take on their masses, despite their limited number of components. It is estimated that mammals are infected with approximately 320,000 distinct viral species [1]. The sum of viral species is expected to be around 3.6 million (if this number is extrapolated to include all vertebrate species), showing an incredible breadth of diversity. They are the most common biological object on earth, research estimates around 1030 viruses in the ocean alone [49]. The distinct properties that define viruses explain this surprising diversity. It should be noted that they are constantly changing. The main factors I commend for the rapid evolution of the virus are the short generation time, large population size, and high mutation rates. These entities evolve on a time scale that we can observe and record, allowing us to better understand how evolutionary methods affect microbial populations. This rapid development has serious implications for communicable diseases such as influenza. Each year, viruses evolve considerably, requiring the development and distribution of a new vaccine against many epidemics. These entities are able to evolve robustly to expand their host range and infect new animals; when viruses change range and include humans, it will have serious public health effects. Despite these drawbacks, the rapid evolution of viruses allows scientists to use their DNA/RNA as a template to study and understand their evolutionary methods. The rate in which viruses evolve is one of the most important aspects of evolution. Unfortunately, the dynamic forces that control the rate of molecular evolution of viruses are complicated. The frequency of molecular evolution in other organisms essentially follows the neutral theory, which postulates that the degree of neutral mutations (the rate of mutation), is the only property that affects the frequency of evolution [29]. The theory's success in calculating evolutionary frequencies [3, 30, 36] is not always true for viruses, with molecular clock dynamics being both supported [18, 31] and denied [27]. Our ability to determine the exact association between the rate of viral evolution and the neutral theory is complicated by the complexity and diversity of viral life cycles. The rate at which virials mutate is remarkable because they span a wide range of values, making it a crucial element in defining the rate of evolution. Replacement frequencies of up to 108 for each nucleotide site for each cell infection (s/n/c) are observed in DNA viruses, while replacement rates of up to 103 (s/n/c) are observed in RNA-like DNA viruses [12, 44]. For slow-mutating viruses (RNA and double-stranded DNA viruses), previous research has established that the relationship between mutation rate and evolutionary rate is linear [45]. For more rapidly evolving viruses, however, this linear link is broken (retroviruses and single-stranded RNA) [45]. Moreover, since virus life cycles are so diverse and incorporate factors within the host, especially the reproductive relationship within the host increases the explanatory power [37]. We may increase our ability to capture the components that affect current viral mutation rates as more data on empirically determined parameter values become available. Figure 10.1 shows a graph comparing the rate of virus evolution to the rate of mutation.

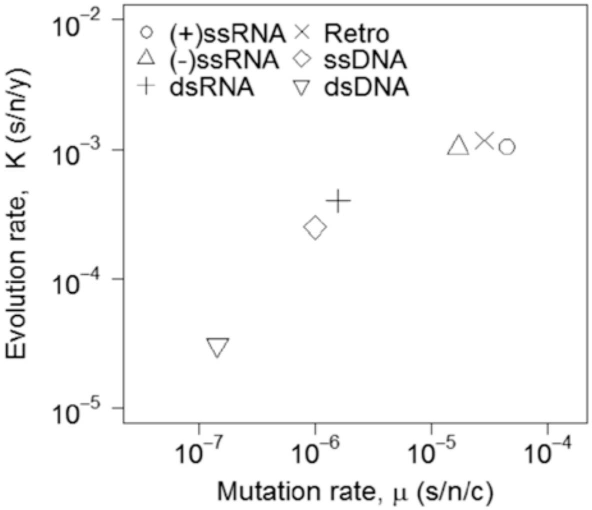

Fig. 10.1 Virus mutation rate against evolution rate

For each Baltimore class, the mutation rates () versus the mean evolutionary rates on the logarithmic scale (K) (data from [44, 45] respectively). dsRNA, double-stranded RNA; Retro, retrovirus; ssDNA, single-stranded DNA; dsDNA, double-stranded DNA; (+) ssRNA, positive-sense single-stranded RNA; () ssRNA, negative-sense single-stranded RNA; The ability to infect a new host range or species is a crucial aspect of virus evolution. The infection of a new host, both by geographical proximity and by adaptation, indicates a new niche to be discovered for a virus, with consequent adaptive radiation [7, 38, 40]. Many viruses that infect humans have their origin in zoonotic transmission [10, 50]. The rapid evolutionary rate of zoonotic viruses that have acquired the potential to infect humans is partly responsible for their dominance; approximately one new emerging viral disease appears each year [25]. RNA viruses are the category of viral species capable of successfully infecting humans [25, 26]. This success is directly associated with their robust evolution rates, which are the result of faster evolution rates. These faster rates of evolution improve the ability of viruses to spread to previously uninfected species. Unfortunately, the particular selection forces leading to the expansion of the host interval are unclear and most mutation techniques allowing viruses to expand their interval are still unknown.

10.1.2 Host Range Expansion

The process of identifying the viruses that can increase their range of hosts and the host species targeted by viruses may be a complicated analysis based on multiple variables. Simply said, for a disease to properly increase its host range, there are three essential processes. Exposure is the first step. Host jumps are frequently triggered by environmental conditions that alter the population or proximity of either species, hence raising the risk of contact [23]. The pathogen and host must be compatible on a variety of levels (for example, transmission route, infectious dosage, and/or cell receptor). The most important hurdle for viruses in this step is to use the cell receptor of the new host species to attach with the viral spike protein. Following which, compatibility between these two components, may not be adequate for some viruses. For example, a few viruses need specialized host cell components such as proteases to promote viral entry [17, 48, 51]. Viruses like avian influenza suffer critical barriers in infected the host cell receptors, like difference in the temperature of avian airway and the temperature of human [47]. The pathogen must be efficiently transferred between individuals of the new host species in the third step [58, 59]. Most zoonotic infections cannot be transferred efficiently between people [57], making humans least vulnerable to these situations. Zoonotic viruses are capable of starting catastrophic outbreaks when are compatible with receptors in human cells and are capable of transmitting efficiently between humans. The main reason for the failure of H5N1 pandemic is that, though H5N1 avian influenza is capable of infecting humans through an avian species, it is its inability to transfer consistently between humans [22]. When all of the following conditions are met, a virus can successfully emerge into a new host species. Viruses can either become generalists by retaining the potential to infect the ancestor species after emergence or can become specialists by adapting to the environment of the new host. For example, the specialist HIV, which started in a monkey [15, 42], has evolved to the point where it can no longer infect nonhuman primate animals. The rabies virus, on the other hand, is a generalist, capable of affecting a variety of mammalian species with ease [41]. While the rabies virus is not typically transferred between humans, this is most likely due to behavioural dynamics rather than the virus's basic inability to spread. Previous research has looked into what factors may influence the choice of a specialist or generalist viral population [2], as well as the benefits and drawbacks of both infection techniques.

10.1.3 Coronavirus

Coronaviruses, a diverse family of viruses that have expanded their host range multiple times throughout their evolutionary history. These viruses are particularly large genomes (2832 kb) enveloped by positive-sense single-stranded RNA viruses and can contaminate high levels of mammalian and avian hosts. The genomes comprise a 3′ poly A tail and 5′ cap separated by the organization of the genome into non-structural protein genes and accessory and structural genes. The most important structural proteins include M (matrix), S (tip), N (nucleocapsid) and E (envelope). While helper genes vary between coronaviruses and may contain some strain-specific structural glycoproteins, the order of structural proteins is extremely conserved as S, E, M, and N, surrounding the viral element, forming a crown-shaped structure. Coronaviruses use a broad spectrum of cellular proteins as receptors [19, 20, 39] with a critical spike protein cleavage to mediate host virus membrane fusion and resulting cell entry. The natural reservoir species of many coronaviruses are rodents, bats and birds [33, 55, 56], with host range expansion having been dominant with more than 20 species currently affected by coronaviruses. So far, 6 HCoV (human coronavirus) have been detected. Development of these six HCoVs, four are connected with trivial respirational syndrome: HCoVNL63, HCoV229E, HCoVHKU1, and HCoVOC43. Two of these (HCoVNL63 and HCoV229E) are supposed to have instigated from bats. Though the standup hypothesis for HCoVOC43 was that it probably began from a bovine pool species [46, 48], new analysis propose that the initial host of this family, and perhaps HCoVHKU1 as well, might be a murine entity [56]. Apart from HCoVs that source slight indicators, 2 strains have been developed to source severe sickness, including severe acute respiratory syndrome coronavirus and Middle East respiratory syndrome coronavirus. Both the viruses combined have led to over One thousand and one hundred deaths, with Middle East respiratory syndrome coronavirus still socializing in the human inhabitants, producing sensitive concern due to the absence of therapeutics or vaccines. The risk to community wellbeing produced by the occurrence of these extremely pathogenic strains into

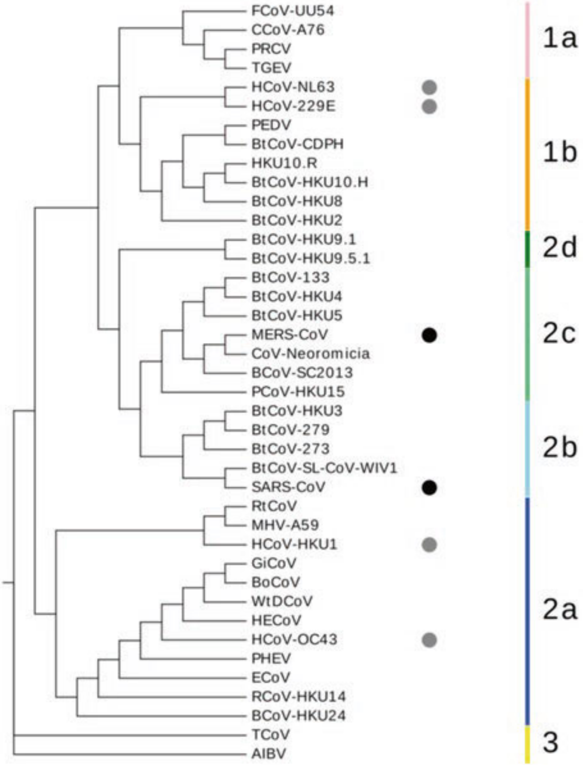

Fig. 10.2 Phylogenetic tree of whole-genome length coronavirus sequences

humans attracts consideration to the significance of understanding the evolutionary mechanisms and biochemical of coronavirus host range expansion. While, Few coronaviruses seem to be generalists, capable of contaminating numerous orders of mammals. For example, Betacoronavirus 1 has been detected in humans, dogs, and numerous ungulate species [15, 20, 21]. Other coronaviruses have been identified in only a single mammalian order, such as the numerous SARS like coronaviruses that have been detected only in bats [12, 27]. Bats exist as the largest reservoir for coronaviruses, potentially due to their diversity. The phylogenetic tree of full-genome length coronavirus sequences is shown in Fig. 10.2.

Phylogenetic tree of a subset of coronaviruses representing groups 1, 2 and 3 (the alpha, beta and gamma coronaviruses; colors indicate each selected group/clade). The recently revealed deltacoronavirus clade is not shown. The sequences were matched using MAFFT [28]. The phylogenetic tree was raised using supreme likelihood with the PhyML package [38, 39] and visualized using EvolView [35]. Black-specific viruses that seemed to cause severe illness; gray indicates viruses that cause mild illness; Circles indicate human coronavirus strains. Note that coronaviruses of the same clade infect many species. Refer to Appendix A for NCBI accession numbers and corresponding journal abbreviation keys. Physiology, immunology, and the ability to navigate large topographical regions through seasonal migrations [4, 15] For this reason, metagenomic studies have focused on investigating the prevalence and diversity of coronaviruses in bats. Studies have revealed different stages of CoV diversity in bats in North America [20] and China [45, 59], as well as the identification of distinct strains in bats worldwide [22]. Additionally, traces of new coronaviruses have been identified internationally, with recent findings coming from Mexico [1], Brazil [20] and South Africa [48]. The ongoing hard work to sample bat populations around the world will help us meticulously map their phylogenetic interpersonal relationships and adequately assess the prevalence and diversity of coronaviruses. The biggest public health concern comes from coronaviruses that take hold in fatal occupants and cause serious infections. The first of these, SARSCoV, emerged from batons in the deadly population in 2003 and infected people with a mortality rate of 9.6 before being controlled by public health measures [5, 7]. Despite heightened coronavirus awareness during this outbreak, reconstructing the evolutionary pathway that led to the expansion of the host range of SARSCoV has been surprisingly tricky. Severe acute respiratory syndrome coronavirus is strictly associated with club coronaviruses, with approximately 92 nucleotide sequences identical to its closest relative detected [33]. To date, no contagion equal to severe acute respiratory syndrome coronavirus has ever been isolated from batons, raising doubts whether the contagion is actually derived from this type of force. Data supporting an origin of the batons include a test for the coronavirus receptor for severe acute respiratory syndrome, angiotensin-converting enzyme 2 (ACE2). Coronavirus, a similar coronavirus fraternized in the club population before manifesting in humans [10]. Data refuting the original club thesis include the fact that, primarily, no club CoVs remained to employ ACE2 or ACE2 orthologs [33]. In fact, it took more than a decade before investigators could identify a SARS-like coronavirus capable of carrying the deadly Chinese horseshoe civet and the ACE2 club for cell entry [44]. The discovery of this contagion (club SLCoVWIV1) provides strong evidence that severe acute respiratory syndrome coronavirus is initiated by club force. Currently, the best supported thesis is that an intermediate host species, in particular the civet, played an important role in the attenuation of the host zone expansion event, either by evaluating a specific picky pressure or by bringing the contagion close to the man [39, 52]. However, the identification of the SLCoVWIV1 club suggests that a transitional host may not have been necessary for the emergence of SARSCoV in humans. Further exploration is needed to govern the exact mutation and cross-pathway of severe acute respiratory syndrome coronavirus to help reveal how deadly new pathogens develop. Positive selection on coronavirus host cell receptors is shown in Fig. 10.3.

(A) Human ACE2 (blue) linked to the receptor-binding domain of severe acute respiratory syndrome coronavirus (red) (PDB 2AJF), with homologous deposits under positive selection in marked bats [9]. (B) Human DPP4 (green) Middle East Related respiratory syndrome Coronavirus RBD (purple) (PDB 4L72), with homologous residues under positive selection in marked bats [7]. Structures displayed using PyMOL. In 2012, the Middle East respiratory syndrome coronavirus

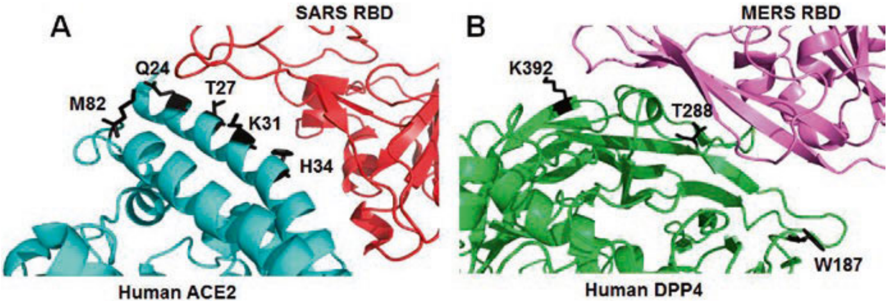

Fig. 10.3 Positive selection on coronavirus host cell receptors

emerged in humans residing in Saudi Arabia. As of November 2016, there remained 1813 confirmed cases with a mortality rate of 36% (WHO 2016). The Middle East respiratory syndrome coronavirus is phylogenetically grouped in the betacoronavirus C clade with the bat coronaviruses BtCoVHKU5 and BtCoVHKU4 [16, 19, 43]. Unlike SARSCoV, MERSCoV uses dipeptidyl peptidase 4 (DPP4) as an entry receptor [48]. To date, only MERSCoV and BtCoVHKU4 have been found to use DPP4 [13, 54]; the presence of a closely related bat coronavirus using the same host cell receptor as MERSCoV provides strong support for the emergence of MERSCoV from a bat lineage. The adaptation of MERSCoV to humans is specifically supported by the fact that MERSCoV uses human DPP4 (hDPP4) more efficiently than bat DPP4 (bDPP4), but BtCoVHKU4 uses both with equal efficiency [54]. So far, host cell receptors for BtCoVHKU5 and other closely related group 2c coronaviruses have not been identified. The similarity between MERSCoV and group 2c bat coronavirus strongly suggests that the Middle East respiratory syndrome coronavirus originated in bats. Moreover, as in the SARSCoV story, bDPP4 was found to be under strong positive selection, which could be due to circulation of DPP4 using coronaviruses in bats [5, 7]. It is unclear whether this signal comes from the ancestor of MERSCoV or from other coronaviruses that use DPP4, such as BtCoVHKU4. As with SARSCoV, the ancestral virus has been elusive without detection of a full sequence of Middle East respiratory syndrome coronavirus in a bat population to date. The best example was a coronavirus isolate from a bat population in which a 190 nucleotide fragment of the RNA-dependent RNA polymerase (RdRp) gene was 100% identical to respiratory syndrome coronavirus. Middle East [37]. The Middle East respiratory syndrome coronavirus has been detected in geographic regions far removed from its emergency origin in Saudi Arabia. RdRp gene sequences with 96.5% and 99.6% amino acid identities of Middle East respiratory syndrome coronavirus have been detected in bat populations in Mexico [1] and South Africa. South [23], respectively. These results underscore the importance of new metagenomic analyzes of bat viromes across broad geographic locations. Looking at the phylogenetic tree of coronaviruses, the lineages that have emerged in humans fascinate several clades. This suggests that there is no single zoonotic coronavirus lineage capable of expanding its host range in humans. On

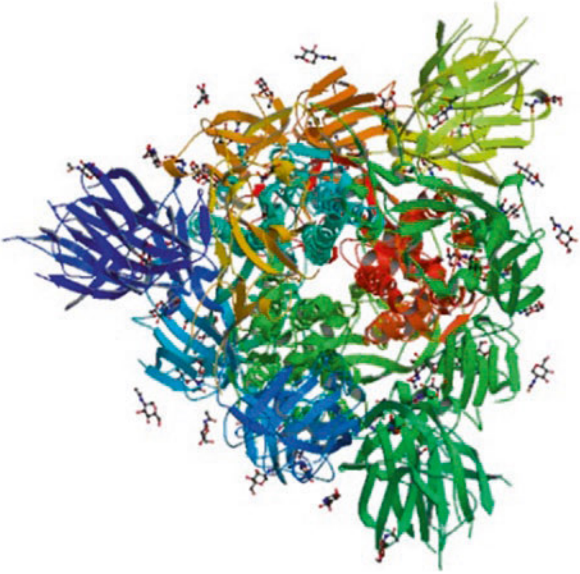

Fig. 10.4 Structure of 2019-nCoV spike glycoprotein with single receptor-binding domain before fusion (Prefusion). (Obtained from Protein Data Bank – PDB ID: 6VSB)

the contrary, many lines have been adapted for harvesting in the mortal population. Moreover, these lines use different host cell receptors to enter the cell. SARSCoV and HCoVNL63 use ACE2 [22, 32], MERSCoV uses DPP4 [48] and HCoV229E uses a protein called aminopeptidase N (APN). The receptor molecules of HCoVHKU1 and HCoVOC43 have not yet been identified, however the presence of acid sialic or acetylate acts as a receptor determinant [29, 34]. The diversity of receptors employed, combined with the large number of species that coronaviruses have evolved to infect, raises the question of whether nimbus infections have a greater capacity for host range expansion than other RNA infections. There may be unique characteristics of coronaviruses that impede their ability to develop into new species, providing an intriguing case study in host range treatment. Coronaviruses are generally very long (30,000 bp) single-stranded RNA viruses. These viruses are composed of two main groups of proteins: Structural Proteins: M Matrix, S Spike, E Envelope, N Nucleocapsid. Non Structural Proteins: RdRp, and nsp12 Protein. One most vital protein in the structure of the coronaviruses or any other RNA virus is the RNA Spike Protein. Hence this protein is targeted in a few RNA type viruses like Coronavirus (CoVs). The active site of Spike represents two successive aspartate residues in the receptor site of spike glycoprotein of RNA viruses that are highly conserved as they are surface accessible, outside the nucleotide channel. Structure of 2019-nCoV spike glycoprotein with a single receptor binding domain before fusion (Perfusion) is shown in Fig. 10.4.

10.2 Copper(II) Hinokitiol

The series of chemicals (αthujaplicin, Hinokitiol, γthujaplicin) isolated from Thuja plicata (western red cedar), Thuja accidentalis (Easter whitecdear) and obtuse Chamaecyprasis (Hinoki cypress) are called Thujaplicins (shown in Fig. 10.5). Thujaplicins were discovered in the 1930s and are called isopropyl cycloheptatrienolones. Tujaplicins are known for their antibacterial, antifungal and anticancer activities. In addition, the β-diketone part of Thujaplicins allows them to form chelates in the presence of many metal ions such as zinc, copper or ferric ions etc. The IUPAC names for thujaplicins are 2-hydroxy-3-propan-2-ylcyclohepta-2, 4, 6-trien-1-one [9]. The 2D structure of αthujaplicin (PubChem CID: 80297), hinokitiol (PubChem CID: 3611), γthujaplicin (PubChem CID: 12649) inspected in PyMol is shown in Fig 10.5.

There has been both medicinal and biological interest for compounds which had both hydroxyl and ketone functional groups adjacent to one another and along with anti-fungal or anti-bacterial properties. Two compounds with these properties are 6-isopropyltropolone (II), commonly known as Hinokitiol (hinokitiol) and 2-hydroxy-2, 4, 6-cycloheptatrien-1-one (tropolone I) [9].

On the other hand, Copper is known since decades as a cofactor of enzymes (cupro-enzymes) and proteins involved in fundamental cell mechanisms. Moreover, it exhibits considerable biochemical action either as a constituent of various exogenously administered compounds or directly as an essential trace metal. It has been scientifically proven that Copper has potent virucidal properties and that, it plays an astute role in the effective functions of immune system cells called neutrophils, lymphocytes (T and B type) and macrophages such that they are indeed involved in nonspecific immune functions such as the phagocytosis (eating) and chemical killing of infectious viruses or bacteria's, and specific immune functions like, the production of antibodies and lymphocytes [51]. Therefore the chelate of Hinokitiol and Copper (copper;6-propan-2-ylcyclohepta-2,4,6-triene-1,2-diolate) [37] with concentration below 20 μM (to inhibit cytotoxic action of Thujaplicin-copper chelates on Madin–Darby canine kidney- MDCK cells) should inhibit the Novel Coronavirus (nCoV-2019) [9] in three stages:

A. Viral Prevention
B. Replication
C. Release and Budding

In 1998, an experiment was conducted to test if Thujaplicin Copper chelates inhibited the replication of flu causing viruses (Human Influenza Viruses), where Thujaplicin substances and six of its metal chelates (Copper, Ferrous, Feric, Manganese, Zinc and Magnesium – thujaplicin chelate) were tested against Influenza viruses AtAichi/2/68/(H3N2), A/Shingapol/1/57(H2N2), (A/PR/8/34/(H1N1), and B/Lee/40). It was identified that Thujaplicin chelate of Copper showed the most effective inhibition of *influenza viruses* than Thujaplicin chelate of any other metal. Upon analyzing the impact of time dependent addition of copper

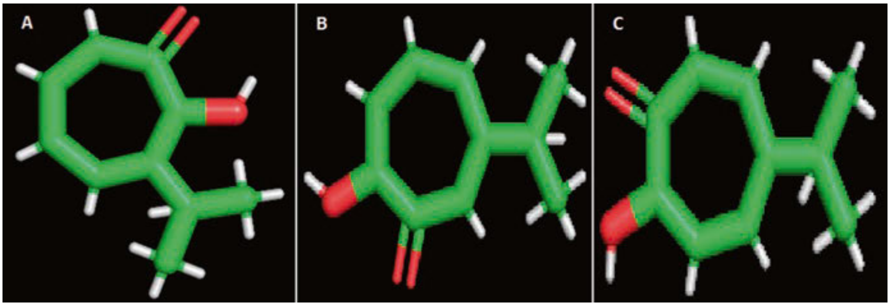

Fig. 10.5 (**a**) The 2D Structure of α-thujaplicin (PubChem CID: 80297) inspected in PyMoL, (**b**) The 2D Structure of Hinokitiol (PubChem CID: 3611) inspected in PyMoL, (**c**) The 2D Structure of γ-thujaplicin (PubChem CID: 12649) inspected in PyMoL

chelate on viruses, it was identified that treatment with Trans-Bis(3-Isopropyl-7-oxocyclohepta-1,3,5-trienolato)copper(II) (Hinokitiol chelate of copper) on or before 2 h post infection efficiently blocked the fusion of virus on apoptosis. Further, on comparing the results of experiments it was concluded that Hinokitiol-copper chelate was much more efficient than other chelates of copper [9].

Thus, Hinokitiol-copper chelate should also prevent the fusion of Novel Coronavirus (nCoV-2019) into the receptor cites of human cells if the patient is treated with Hinokitiol-copper chelate before appropriate hours post infection. Because, the inhibition of influenza virus described in the above experiment was primarily due to the antiviral property of the Copper than Hinokitiol because, if the inhibition of influenza virus was the action of Hinokitiol on the virus, the other Hinokitiol metal chelates should also have shown the same results while they did not. Hence it can be assumed that the antiviral activity shown in the experiment discussed above was primarily due to the Copper ion in Hinokitiol-copper chelate and that the action of Hinokitiol was to control the cytotoxicity of Copper ions on MDCK cells. On the other hand, it has been proved that the Cupric ions were able to inactive almost all the enveloped or non-enveloped, single-stranded or double-stranded DNA or RNA viruses with an efficiency between that of gultaraldehyde and liquid disinfections [28] which was also due to the presence of Copper ions, besides the fact that, reason behind the antiviral property of Copper is still unknown except an assumption that antiviral property of Copper is an outcome of its corrosiveness. Thus the same Hinokitiol-copper chelate should also be able to inhibit the replication and Novel Coronavirus. During another experiment published in 2015, to test if the Human Coronavirus 229E remained infectious on Common Touch Surface Materials, it was identified that copper and copper alloy surfaces caused rapid inactivation and irreversible decomposition of structure of viral RNA. The research article also reported to have observed a massive structural damage to the coronavirus exposed to copper and copper alloys [46]. Hence Hinokitiol-copper chelate should chemically be capable of preventing from Novel Coronavirus 2019 and should inhibit Replication and Release or Budding of COVID-19.

10.3 Molecular Docking

There has been both medicinal and biological interest for compounds which had both hydroxyl and ketone functional groups adjacent to one another and along with anti-fungal or anti-bacterial properties. Two compounds with these properties are 6-isopropyltropolone (II), commonly known as Hinokitiol (hinokitiol) and 2-hydroxy-2, 4, 6-cycloheptatrien-1-one (tropolone I) [9, 11].

On the other hand, Copper is known since decades as a cofactor of enzymes (cupro-enzymes) and proteins involved in fundamental cell mechanisms. Moreover, it exhibits considerable biochemical action either as a constituent of various exogenously administered compounds or directly as an essential trace metal. It has been scientifically proven that Copper has potent virucidal properties and that, it plays an astute role in the effective functions of immune system cells called neutrophils, lymphocytes (T and B type) and macrophages such that they are indeed involved in nonspecific immune functions such as the phagocytosis (eating) and chemical killing of infectious viruses or bacteria's, and specific immune functions like, the production of antibodies and lymphocytes [51]. Therefore the chelate of Hinokitiol and Copper (copper;6-propan-2-ylcyclohepta-2,4,6-triene-1,2-diolate) [37, 53] with concentration below 20 μM (to inhibit cytotoxic action of Thujaplicin-copper chelates on Madin–Darby canine kidney- MDCK cells) should inhibit the Novel Coronavirus (nCoV-2019) [6, 9] in three stages:

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10.4 Result

Results of prepared Ligand (Hinokitiol-copper chelate) and Receptor Macromolecule (Profusion structure of COVID-19 spike glycoprotein) obtained from AutoDockTools 1.5.6 (ADT) was inspected using PyMol. The 3D structure of prepared ligand and receptor macro-molecule is shown in Figs. 10.6 and 10.7.

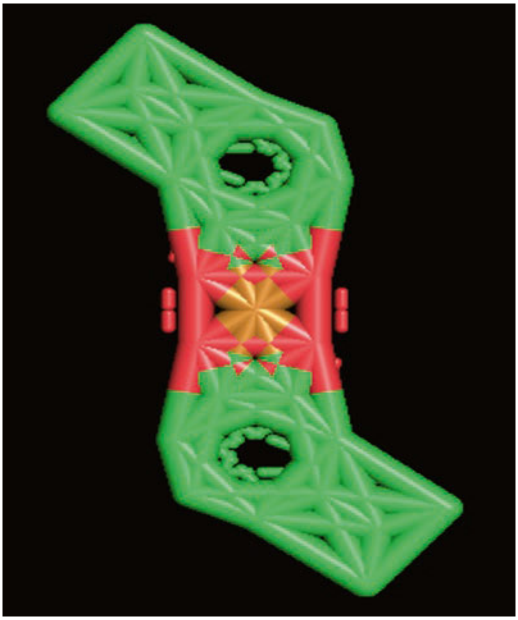

Fig. 10.6 3D Structure of prepared ligand inspected using PyMoL

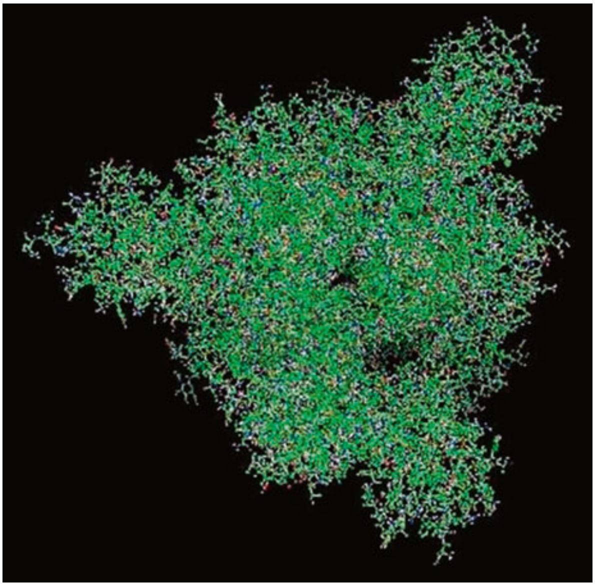

Fig. 10.7 3D Structure of prepared Receptor Macromolecule inspected using PyMoL

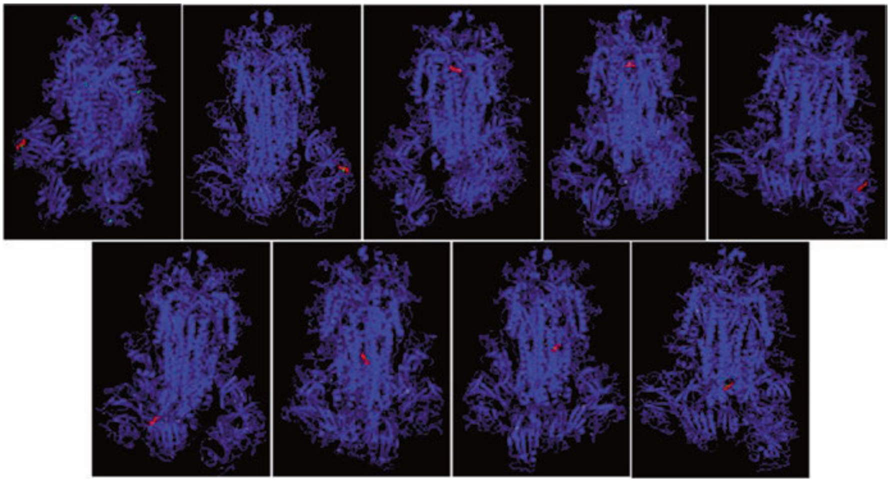

Fig. 10.8 Nine different poses of COVID-19 spike glycoprotein (in Blue ribbon) docked to the antiviral drug "Hinokitiol-copper chelate" (in Red licorice sticks) with polar contacts/interactions (in green color dotted lines) inspected in PyMoL

Results of Ligand (Hinokitiol-copper chelate) and Receptor Macromolecule (COVID-19 spike glycoprotein) obtained after docking using AutoDock Vina Software implemented in PyRx software was inspected using PyMoL. The binding of Ligand to the Receptor was observed in nine different poses at unique binding affinities, RMSD/ub values and RMSD/lb values. Nine different poses of COVID-19 spike glycoprotein (in Blue ribbon) docked to the novel antiviral drug

Table 10.1 Results of Ligand (Hinokitiol-copper chelate) and Receptor (COVID-19 spike glycoprotein) obtained after docking using AutoDock Vina Software implemented in PyRx software

Ligand pose	Binding affinity	RMSD/ub	RMSD/lb
POSE 1	−11.7	0	0
POSE 2	−11.4	6.189	0.521
POSE 3	−11.3	88.866	0.79
POSE 4	−11.3	89.386	87.163
POSE 5	−10.5	11	8.044
POSE 6	−10.5	71.316	68.518
POSE 7	−10.5	69.545	65.853
POSE 8	−10.5	67.935	65.351
POSE 9	−10.4	53.709	51.225

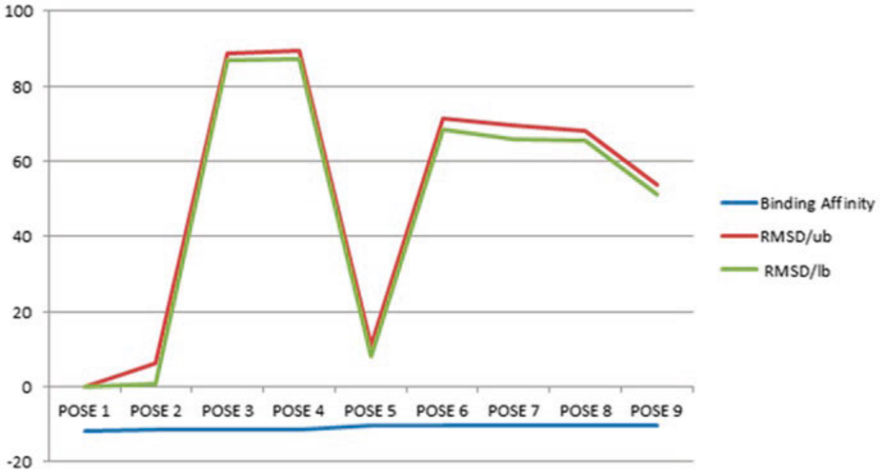

Fig. 10.9 Plot between Binding Affinity, RMSD/un, RMSD/lb and different poses of ligand (Hinokitiol-copper chelate) in the Receptor (COVID-19 spike glycoprotein)

“Hinokitiol-copper chelate” (in Red licorice sticks) with polar contacts/interactions (in green color dotted lines) are shown in Fig. 10.8. Further, the binding affinities, RMSD/ub values and RMSD/lb values are tabulated for each pose in Table 10.1, and are depicted as graph in Fig. 10.9.

10.5 Conclusion

The newly emerged novel coronavirus (nCoV-2019) has spread across the world and has registered close to 509,164 confirmed cases and 23,335 deaths by 27th March 2020, 10:00 CET [Source by WHO]. Increase in confirmed cases and deaths result in an increase in demand for an antiviral drug. Since it takes a long time to create a new antiviral drug for such a complex virus and for it to pass through *In vito, In vivo* and *In sito* tests to qualify to pre-clinical tests followed by clinical tests, there have been lot researches undertaken to test already available antiviral drugs on COVID-19 spike glycoprotein such that the drug can destroy the receptor site and inhibit fusion of the virus with to the human cell. The present study is one such work aimed to test Hinokitiol-copper chelate as a possible inhibitor to decrease the infection as quickly as possible. Thus, with reference to the above results, Hinokitiol-copper chelate can be suggested for pre-clinical tests against the COVID-19 (nCoV-2019).

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Chapter 11
Effects of Economic Liberalization on Poverty and Inequality in India – A Case Study of Pre-COVID-19 Period

Rohit Narayan and Satyendra Narayan

Abstract The purpose of this research is to study the effects of neoclassical trade liberalization policies enacted in India in 1991 to determine the effect on levels of poverty and income inequality. This research predicts that poverty and economic inequality will be reduced due to implementation of economic liberalization policies. The research uses empirical data from the National Sample Survey Organization (NSSO), in India and develops a regression model to determine the effects of economic liberalization on income inequality and absolute poverty. The results of the regression model suggest that income inequality and poverty decreased during the year liberalization policies were enacted, but is not statistically proven with enough confidence that liberalization is strongly correlated with a reduction in inequality and poverty. There is a weak statistical correlation that suggests inequality increased in the Indian urban sector, and decreased in the rural sector due to liberalization. In conjunction with a literature review where more robust data and econometric models are applied, the empirical analysis by complimented with the fact that in general income inequality decreased due to economic liberalization policies alone, holding all exogenous factors that affect income inequality constant. The literature review also confirms that poverty levels decreased with economic liberalization, holding all other exogenous factors that affect poverty constant. The implication of this research is that liberalization polices have been successful for overall development in India, and suggests that implementation of liberalization policies may be desirable in nations under similar circumstances as India in the era before its liberalization.

Keywords Economic Liberalization · Trade · Economics · Pre-COVID Economics

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_11

11.1 Introduction

The modern economy of India is one of the largest in the world, ranking 9th in the world by nominal GDP, and 4th by GDP using purchasing power parity (PPP) [13]. The country has grown rapidly at a pace of roughly 4–9% in the last several decades, and in the process has brought millions out of poverty [23]. India's fast paced growth makes is a key economic player in the world stage, and has potential to raise the living standard of its population of roughly 1.17 billion in size [13].

Socialist democratic policies such as extensive regulation, protectionism, public ownership, and trade restrictions were central policies during the years 1947–1991, and resulted in slow growth [18]. Since 1991, economic liberalization has opened up markets in India and lead to accelerated economic growth, resulting in India becoming one of the fastest growing modern economies. Two important questions are raised from a developmental economics perspective:

1. What does rapid growth do to alleviate poverty for the poorest individuals?
2. How are the benefits of growth distributed among individuals of an economy?

According to [20], economic development is a gradual process by which the per capita income of a country increases over time given that the number of people below the poverty line does not increase, and that the distribution of income does not become more unequal. Growth that is distributed unequally needs to be evaluated not simply on the basis of overall change but on the grounds of equality. According to [20], there are significant negative effects of increasing income inequality in a country, including economic inefficiency, decreasing social stability, and rise of rent-seeking behaviour.

This research is intended to study the growth of India due to growth liberalization and its effect on absolute poverty and the income inequality. The general consensus among economists is that economic liberalization, and free trade is a unambiguous net gain for society [10], and that economic liberalization has helped the world's poorest escape from poverty. Based on this consensus, this research predicts that increased growth in India due to neoclassical economic liberalization policies should lead to a reduction in absolute poverty levels and a reduction in income inequality.

This research is divided into several sections, it will first discuss the theory behind economic liberalization, the definition of economic liberalization and the benefits and drawbacks that it entails. Second, a brief economic history of India is discussed, outlining the key economic policies before liberalization and after liberalization. Third, using empirical data from various sources the link between economic liberalization, poverty and inequality will be analyzed. We will use key indicators that are hallmarks of liberalization, such as the Trade Openness Index (TOI). Some examples of poverty and inequality indicators will be Gini coefficient, and Headcount Index of people below the poverty line. Fourth, a literature review will be conducted to survey the results from similar research on this topic. Fifth, the cause and effects of inequality will be analyzed.

11.2 Overview of Economic Liberalization

A brief overview of economic liberalization has been presented in the following three sections based the relevancy of subject matter.

11.2.1 Introduction to Economic (Trade) Liberalization

Economic liberalization broadly refers to the minimization of government intervention in an economy, and greater influence of the private sector in an economy. The argument for liberalization is that it leads to greater efficiency, thus liberalization refers to the "removal of controls", to encourage economic development [6]. Liberalization may refer to the privatization of government institutions, decreased regulation in labour and factor markets, lowering the rate of corporate taxes and capital gains taxes, and fewer barriers to trade. In the case of developing countries such as India, liberalization primarily refers to decreased regulation and tariffs which result in greater foreign direct investment (FDI), which tends to vastly increase trade. In this research the terms 'Economic Liberalization' and 'Trade Liberalization' are used interchangeably, as they are linked concepts, and trade openness is arguably the biggest component of economic liberalization.

The rapid growth of the world economy in the past few decades has been driven in part by an even faster rise in international trade [12]. According to [12], the integration of world economy via trade has been a powerful means for countries to promote economic growth, development, and poverty reduction. This integration has raised living standards across the world especially in countries in Asia, where integration has led to a substantial rise in incomes [12].

It is true that economic liberalization is not universally and unambiguously linked to economic growth [21], as there are many exogenous factors that responsible for economic growth. However, it is fair to say that economic liberalization is a component that promotes growth by leading to lower prices, better information, and newer technologies [21]. Economic liberalization must also accompanied by its complementaries such as education, infrastructure spending, and macroeconomic financial policies [21] to have a positive effect on growth.

11.2.2 Benefits and Drawbacks of Economic (Trade) Liberalization

According to [21] most economic literature concludes that trade liberalization leads to an increased welfare derived from an improved allocation of domestic resources. Import restrictions tend to create an anti-export bias by raising the price of imports relative to exportable goods. Trade liberalization removes this bias and creates an incentive for exportable goods, instead of the creation of import substitutes [21]. This results in growth as the new allocation of resources is now in line with a country's comparative advantage [17]. Trade liberalization offers markets to compete internationally and thus have a potentially positive effect on the Gross National Income (GNI) of a country. It also allows an inflow of technologies into a developing country, which increase the productivity of developing country's firms. This can potentially increase exports and thus stimulate income growth in a developing country.

According to [5] there are substantial risks in trade liberalization including:

1. Brain Drain: With open markets there are fewer barriers to do business across borders, highly skilled persons in developing countries might be lured to developed countries for higher wages, benefits, and living standards.
2. Financial Sector Instability: Instability in larger financial markets can have a detrimental impact on smaller markets. For example, the housing bubble burst devalued mortgage assets held by foreign banks, bankrupting the financial system in countries such as Iceland.
3. Risk of Environmental Degradation: Pollution controls in developing countries are generally lower than developed nations, thus cheaper production in developing nations will results in greater environmental damage.

However, [5] goes on to say that the risks of economic liberalization are outweighed by the benefits and that what is needed is careful regulation.

11.2.3 Trade Liberalization and Poverty Reduction

According to [21], there are several ways which trade liberalization helps alleviate poverty in developing countries. In general, trade liberalization reduces the prices of imported goods and keeps prices of import substitutes low, thus increasing real incomes. Depending on the flexibility of wages and labour, the shift of resources between industries that occur in trade liberalization has potential to increase wages and employment. For example, if wages are flexible and labour is fully employed, then price changes caused by trade liberalization can impact wages.

11.3 Economic History of India

An attempt is made herein to describe economic history of India piecewise – since country's independence until 1991 and since 1991–2020.

11.3.1 Pre-liberalization Policies (Independence – 1991)

India gained independence in 1947 as a British colony, and chose to a state-lead industrialization strategy which involved central economic planning, high protectionism, and regulation of economic activity [3]. The key driver behind this strategy was years of colonial rule by the British, which was viewed as an exploitative period in Indian history, and thus economic policies focused on self reliance. Indian economic policy emphasized savings and capital accumulation for achieving economic growth, consistent with the Harrod-Domar model, thus India followed an economic policy of "state-controlled capitalism" [7]. Furthermore, according to [7]. India's economic policies were based on a socialist ideology, and private enterprise needed permission from the state. This created accompanying "red-tape" which is commonly referred to as License Raj, where licenses and regulations interfered with private enterprise. The impact of these policies resulted in a very slow rate of growth compared to today, and per-capita income growth averaged 1.3% [9]. Also, licenses were required for many key industries such as steel, electricity, and communications; people who acquired licenses developed monopolies [4]. Industries which were open to private investment without licenses were limited.

The first attempt at liberalization was in the 1980s, under the government of Rajiv Ghandi. However since there was still a "dominance of the socialist mindset", reform was very gradual and implemented slowly [7]. One of the key reforms was reduction of the Monopolies Restrictive Trade Practices (MRTP) act. This was originally put in place to prevent private monopolies and concentration of economic power [7]. Unfortunately, the regulations and controls associated with this act led to increased bureaucracy and inhibited growth of private industry [7]. Under a heavy socialist mindset, real economic reform did not take place until 1991, in response to a balance of payments crisis that India faced.

Until 1991, the Indian currency (rupee) was pegged to a basket of various international currencies, which lead a currency over-valuation. In combination with a current account deficit, and a decline in investor confidence, the rupee experienced a sharp exchange rate depreciation [11]. As a result, the government was very close to defaulting, and could barely afford 3 weeks worth of imports. This resulted in extreme political and economic uncertainty, leading to the downgrade in India's credit rating. Non-resident Indian investors started withdrawing money they had invested in India resulting in capital flight [7]. This crisis pushed India towards a policy change that embraced economic liberalization.

11.3.2 Post-liberalization Policies (1991 – Present)

Perhaps the biggest reform in India's economic liberalization was the reduction License Raj, which reduced the bureaucracy and red-tape that plagued India in the past. Public sector monopolies were ended, especially in areas which were not important strategically, or important in terms of security. Foreign Direct Investment (FDI) was considerably easier by replacing existing bureaucratic agencies with the Foreign Investment Implementation Authority (FIIA), to provide "one one-stop service to foreign investors by helping them obtain the necessary approvals and acting as a single point interface to the government" [14]. There was also a huge effort to attract FDI, which was thought to accelerate industrialization, structural change in the modern sector, and inflow of skilled labour and knowledge [7]. A new policy was implemented to automatically approve FDI in 34 key priority industries [7], allowing quick foreign investment without government intervention. A new government department, called the Foreign Investment Promotion Board (FIPB) was established to promote FDI in India [7].

The pegged exchange rate before 1991 was a restriction on imports and exports [14], the rupee was allowed to fluctuate leading to the creation of Indian foreign exchange markets. Before liberalization, tariffs were extremely high: the highest tariff rate was 355% and was reduced to 41% by 1995/1996 [14]. The average tariff rate dropped from 113% to 17% by 1993/1994 [14]. It is important to note that India still has a high rate of tariffs compared to rest of the world, suggesting further liberalization can still occur [14].

Additionally, India was motivated by the economic success of China's special economic zones, and other economic zones around the world. The government introduced special economic zones (SEZ), and thus far 12 SEZs have been created in India [14]. The primary motivation of this policy was to create a strong export sector which was vital for continued growth. A new five–year foreign trade policy was implemented in 2004–2009 lifting all quantitative restrictions on exports, and announced additional incentives for SEZs that are aimed at boosting exports [14].

11.4 Analyzing Poverty and Inequality in Post-liberalization Era: Trends in Data

Using MATLAB, attempts are made herein to analyze the poverty and inequality in India during the post-liberalization period. Techniques of data analysis and results are presented in the sections below.

11.4.1 Mathematical Techniques for Analysis

The primary mathematical technique used in the research is regression analysis in MATLAB. This is a technique for analyzing the relationship of 2 different variables, to determine how the value of a dependent variables changes with the value of an independent variable. Regression analysis estimates the conditional expectation of the dependent variable given the independent variable, that is, the average value of the dependent variable when the independent variables are held fixed.

Regression models involve the following variables:

1. Unknown parameters β
2. Independent variable X
3. Dependent variable Y

A regression model relates Y to a function of X and β

$$\mathrm{Y} \approx \mathrm{f}\left(\mathrm{X},\beta\right)$$

There main type of regression used in this research is polynomial regression, as an example the model may be of the form:

$$y_i = a_0 + a_1 x_i + a_2 x_i^2 + \cdots + a_m x_i^m + \varepsilon_i \left(i = 1,2,\ldots,n\right)$$

Then the model can he written as a system of linear equations:

$$\begin{bmatrix} y_1 \\ y_2 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} 1 & x_1 & x_1^2 & \ldots & x_1^m \\ 1 & x_2 & x_2^2 & \ldots & x_2^m \\ \vdots & \vdots & \vdots & & \vdots \\ 1 & x_n & x_n^2 & \ldots & x_n^m \end{bmatrix} \begin{bmatrix} a_0 \\ a_1 \\ a_2 \\ \vdots \\ a_m \end{bmatrix} + \begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \\ \vdots \\ \varepsilon_n \end{bmatrix}$$

Which when using pure matrix notation is written as

$$\vec{y} = \mathbf{X}\vec{a} + \varepsilon.$$

The vector of estimated polynomial regression coefficients (using ordinary least squares estimation) is

$$\hat{\vec{a}} = \left(\mathbf{X}^T \mathbf{X}\right)^{-1} \mathbf{X}^T \vec{y}.$$

For some datasets linear regression, is used. A full explanation is outside the scope of this article. The calculations are all done using MATLAB software commonly used in academia.

11.4.2 Indicators of Poverty, Inequality and Trade Liberalization

This section discusses the raw data used in the analysis and how the raw data represents poverty, inequality and economic liberalization. Comparisons using the raw data and statistical inferences about the papers hypothesis are formed using the data.

11.4.2.1 Gini Coefficient

One of the key indicators of economic inequality is the Gini coefficient, developed by statistician Corrado Gini. It measures the inequality of wealth distribution, and is a dimensionless number between 0 and 1. The closer the Gini coefficient is to 1, the greater the inequality in an economy. Graphically, it can be represented as the ratio of the area between the diagonal and the Lorenz curve divided by the total area of the half-square in which the curve lies.

Mathematically this can be written as the following if the Lorenz curve is represented by Y = L(X):

$$G = 1 - 2\int_0^1 L(x)\,dX$$

11.4.2.2 Coefficient of Variation

The coefficient of variation is a normalized measure of the dispersion of a probability distribution, in this case, it is the standard deviation of income divided by the mean of income. A higher coefficient of variation means incomes are more dispersed, and there is greater inequality. The formula for coefficient of variation is:

$$cv = \frac{\sigma}{\mu}$$

where σ is the standard deviation of the incomes in a country, and μ is the mean income in a country.

11.4.2.3 Indicators of Economic Liberalization

There are a few indicators that encompass economic liberalization including tariffs applied in trade, and the Trade Openness Index (TOI), which can be calculated as:

$$\text{Trade Openess Index}(\text{TOI}) = (\text{Volume of Exports} - \text{Volume of Imports}) / \text{GDP}$$

11.4.2.4 Indicators of Poverty

We use two main indicators of poverty for which data is readily available:

1. Headcount of persons below poverty line (% of population)
2. Human Development Index (HDI)

The HDI is a composite measure of development which signifies the level of development of a country measured on a scale from 0 to 1. This measure was created by the United Nations Development Programme (UNDP), and a higher HDI suggests greater development in a economy, which can be viewed as less poverty in a economy. Thus, HDI is a like an “inverse proxy” to poverty.

11.4.3 Data Sources

The Gini coefficient data, and coefficient of variation (CV) data come from the National Sample Survey Organization (NSSO), which is part of the Government of India. The NSSO collected Gini and CV data for many states and territories, treating urban and rural sectors of the Indian economy as separate entities. The data used in this research was extracted from a doctoral thesis by [1]; however, the original source of the data is the NSSO. Obtaining data directly from the NSSO requires payment to the organization in India, and a prolonged waiting time for delivery. Comparable statistics are not available from World Bank, IMF, or UNDP sources.

The HDI data is compiled from the UNDP, for the years before and after economic liberalization in India. Data used to compute the Trade Openness Index (TOI) and tariff data are taken from the World Bank.

This research will graphically analyze the Gini coefficient and coefficient of variation (CV) against time to determine whether or not income inequality increased or decreased during the era of liberalization. It also will graphically analyze HDI as a function of time to determine whether or not development increased or decreased during the era of liberalization. Further a regression analysis will show how inequality and poverty changed with changes in economic liberalization, using metrics such as Trade Openness Index (TOI) and tariffs rates as indicators of economic liberalization. Since all indicators are a function of time, time is an independent variable, and no longer considered in the regression analysis. The regression analysis is sufficient to determine any correlation between economic liberalization and inequality/poverty. Note that all observed samples used in regression analysis are from the same time periods.

The results of the regression are also included to provide a measure of statistical accuracy of the regression. In particular coefficient of determination R2 is the proportion of variability in a data set that is accounted for by the statistical model. A higher value of R2 is desirable, but not often possible due to many exogenous factors not accounted for in a particular model.

11.4.4 Graphical Results

The entire raw data used here is analyzed and graphed appropriately. The following sections provide a detailed description and interpretation of the graphs and parameters used in the mathematical analysis.

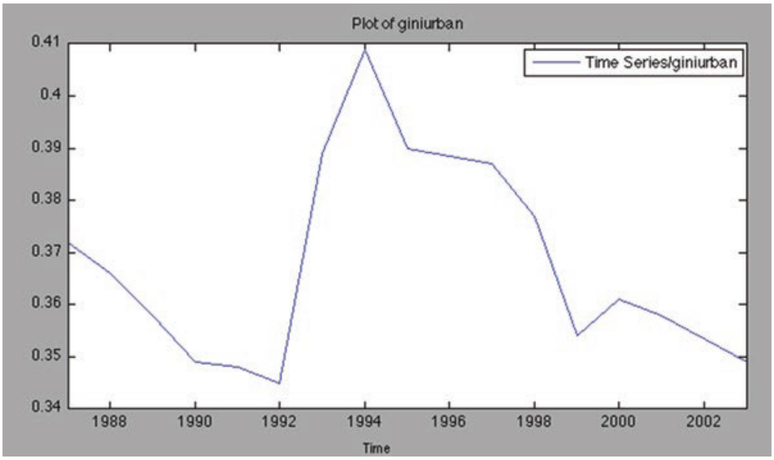


Fig. 11.1 Gini Coefficient – Urban Sector

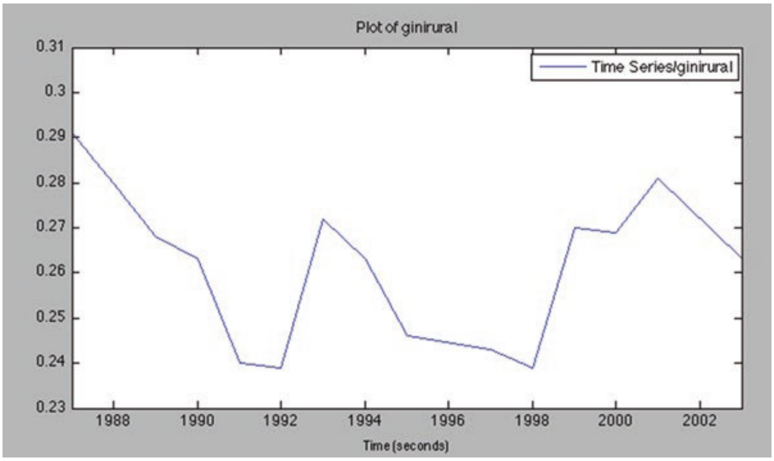


Fig. 11.2 Gini Coefficient – Rural Sector

The Gini coefficient for urban and rural sectors for all of India is plotted below (Figs. 11.1 and 11.2).

The Coefficient of Variation (CV) for urban and rural sectors for all of India are below (Figs. 11.3 and 11.4).

From the analysis we can see that during the year of liberalization, inequality did decrease, however it increased in the following years. In general, we can safely confirm there is no certain long-term trend in inequality, especially in the rural sector. The inequality during the liberalization year of 1991 is lowest in all observed years (1987–2003). Generally rural inequality is less than urban inequality.

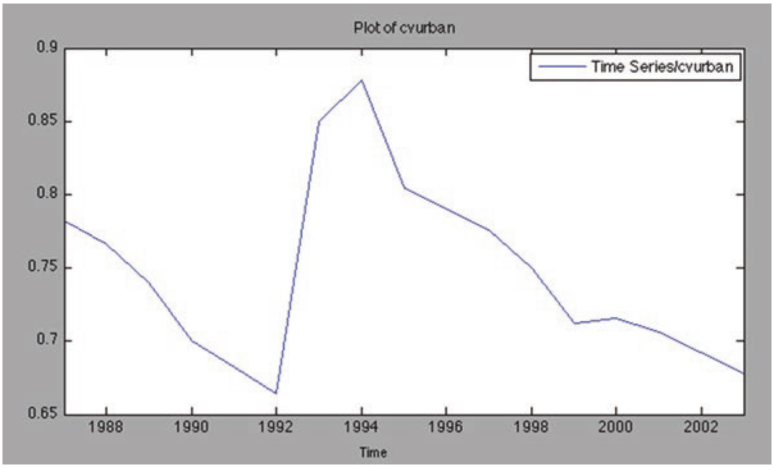


Fig. 11.3 Coefficient of Variation – Urban Sector

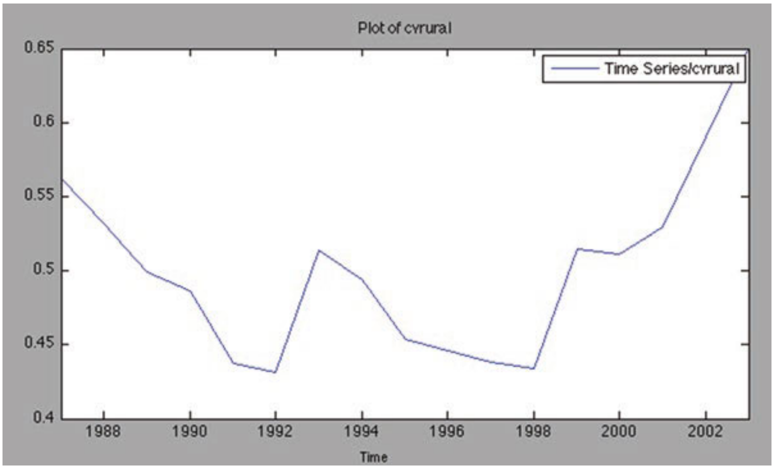


Fig. 11.4 Coefficient of Variation – Rural Sector

The Human Development Index (HDI) over the years before and after liberalization is shown in the Fig. 11.5 below.

HDI has increased almost linearly from 1980 to 2010, even in the liberalization year of 1991. The HDI can be interpreted as a blunt measure of absolute poverty, as it is in index designed to aggregate the well-being of an economy using 3 key metrics: life expectancy, education, and income, which are all inversely correlated with levels of poverty. From the graph, it is clear the growth in the HDI was present during the liberalization year of 1991, but whether or not liberalization was a

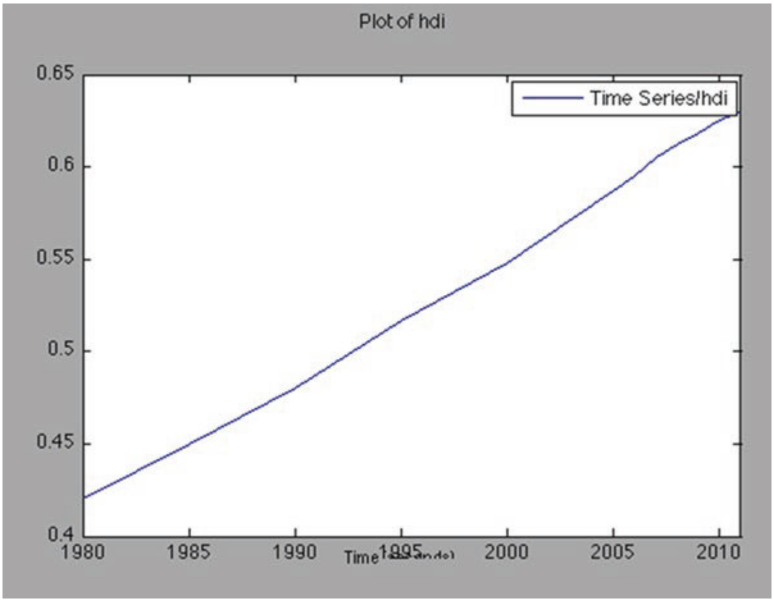


Fig. 11.5 HDI during time of liberalization

contributing factor in the growth of HDI is unclear. The rate of increase of HDI has remained roughly constant, even during the liberalization year. Thus, factors outside this model may also be responsible for the constant growth in HDI, such as greater effectiveness of public and private institutions, technology growth, empowerment of women, social changes etc.

11.4.4.1 Gini Coefficient in Urban Sector vs TOI

The regression results for Gini Coefficient in the Urban Sector vs Trade Openness Index (TOI) are shown in the Fig. 11.6 below.

The regression results indicate that there is weak statistical relation between trade openness and inequality. As the TOI increased, we see the inequality increase slightly. However, with a low R2 the correlation is very weak, suggesting many exogenous factors affect inequality other than trade openness.

11.4.4.2 Gini Coefficient in Rural Sector vs TOI

The regression results for Gini Coefficient in the Rural Sector vs Trade Openness Index (TOI) is shown in the Fig. 11.7 below.

The regression results indicate that there is weak statistical relation between trade openness and inequality. As the TOI increased, we see the inequality decrease

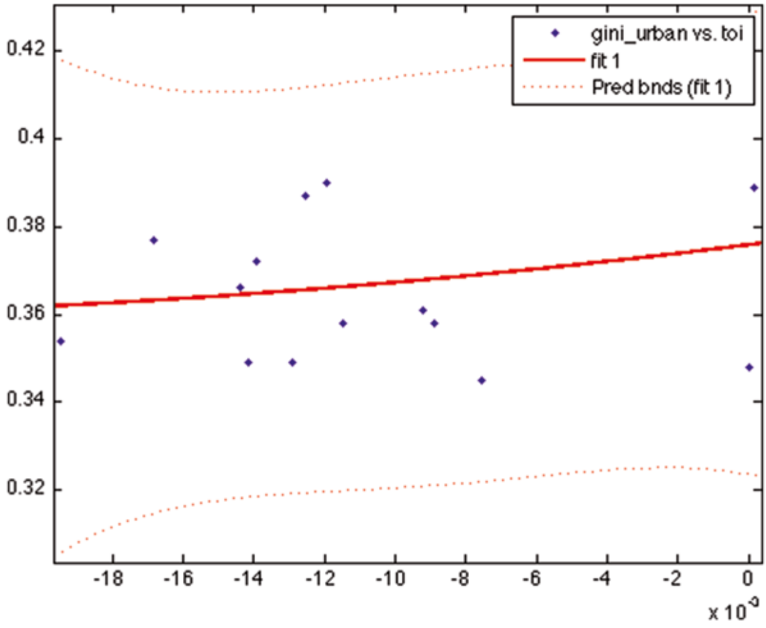
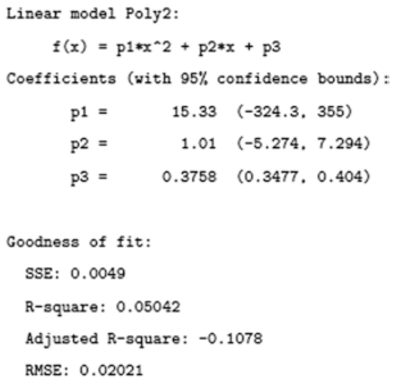


Fig. 11.6 Regression analysis: Gini Coefficient in Urban Sector vs TOI



```
Linear model Poly2:
     f(x) = p1*x^2 + p2*x + p3
Coefficients (with 95% confidence bounds):
       p1 =       15.33  (-324.3, 355)
       p2 =        1.01  (-5.274, 7.294)
       p3 =      0.3758  (0.3477, 0.404)

Goodness of fit:
  SSE: 0.0049
  R-square: 0.05042
  Adjusted R-square: -0.1078
  RMSE: 0.02021
```

slightly. This is in contrast with the urban sector where inequality increased slightly. Again, the R2 value is too low to strongly correlate trade openness and inequality, thus exogenous factors must be at play.

11.4.4.3 Poverty Headcount Index vs TOI

The regression results for Poverty Headcount Index vs Trade Openness Index is shown in the Fig. 11.8 below.

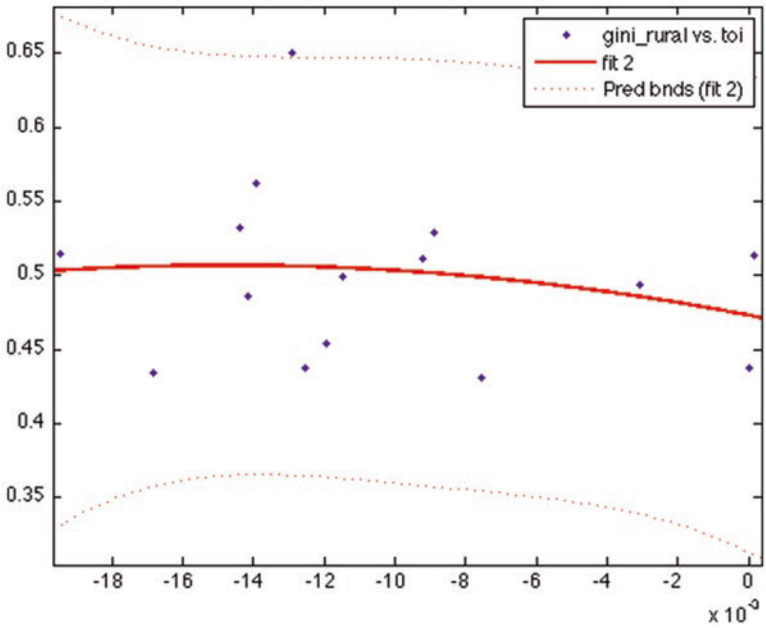
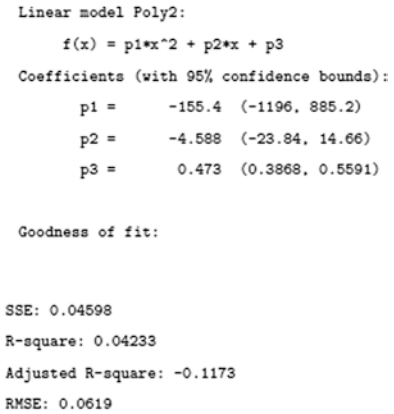


Fig. 11.7 Regression analysis: Gini Coefficient in Rural Sector vs TOI



```
   Linear model Poly2:
        f(x) = p1*x^2 + p2*x + p3
   Coefficients (with 95% confidence bounds):
          p1 =      -155.4  (-1196, 885.2)
          p2 =      -4.588  (-23.84, 14.66)
          p3 =       0.473  (0.3868, 0.5591)


   Goodness of fit:



 SSE: 0.04598
 R-square: 0.04233
 Adjusted R-square: -0.1173
 RMSE: 0.0619
```

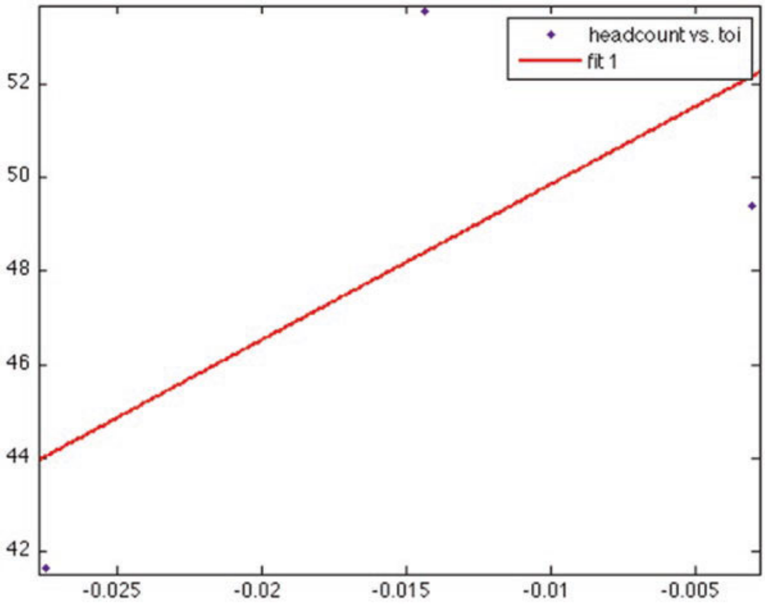
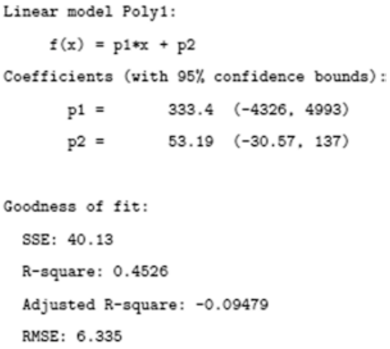


Fig. 11.8 Regression analysis: Poverty Headcount Index vs TOI



```
Linear model Poly1:
     f(x) = p1*x + p2
Coefficients (with 95% confidence bounds):
       p1 =       333.4  (-4326, 4993)
       p2 =       53.19  (-30.57, 137)

Goodness of fit:
  SSE: 40.13
  R-square: 0.4526
  Adjusted R-square: -0.09479
  RMSE: 6.335
```

The results of the regression suggest a strong correlation between Poverty Headcount Index (Percentage of population under $1.25 a day) and trade openness. However, our observed sample is quite small, and only consists of 3 points, thus no empirical correlation is established for these two variables despite the strong fit of the regression model. More data is desired to make further conclusions.

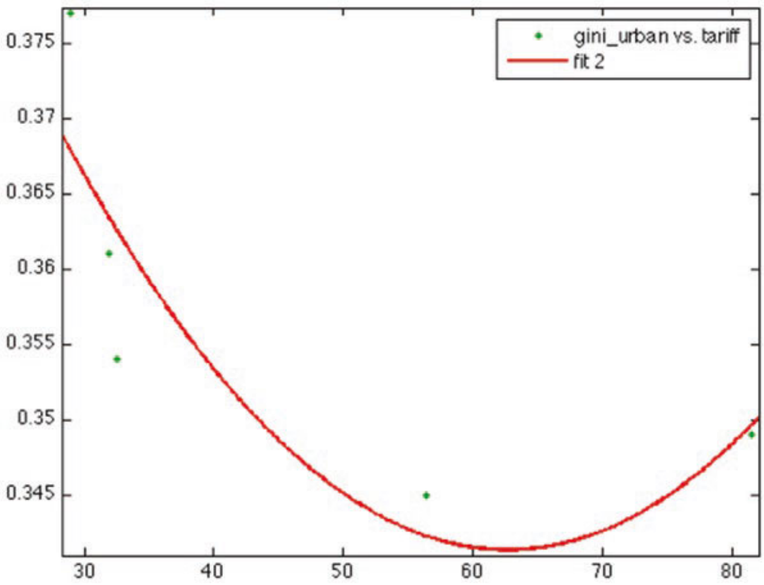
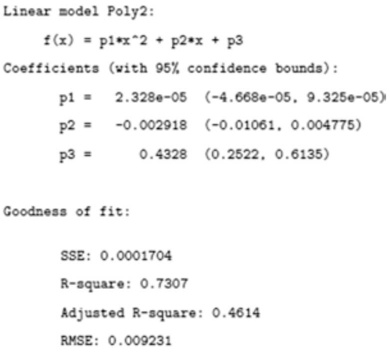


Fig. 11.9 Regression analysis: Gini Coefficient in Urban Sector vs Mean Tariff Rate



```
Linear model Poly2:
     f(x) = p1*x^2 + p2*x + p3
Coefficients (with 95% confidence bounds):
       p1 =   2.328e-05  (-4.668e-05, 9.325e-05)
       p2 =   -0.002918  (-0.01061, 0.004775)
       p3 =      0.4328  (0.2522, 0.6135)

Goodness of fit:

       SSE: 0.0001704
       R-square: 0.7307
       Adjusted R-square: 0.4614
       RMSE: 0.009231
```

11.4.4.4 Gini Coefficient in Urban Sector vs Mean Tariff Rate

The regression results for Gini Coefficient in Urban Sector vs Mean Tariff Rate are shown in the Fig. 11.9 above.

The regression results establish a fairly strong relationship between these two variables. As tariffs are reduced inequality increases in the urban sector.

11.4.4.5 Gini Coefficient in Rural Sector vs Mean Tariff Rate

The regression results for Gini Coefficient in Rural Sector vs Mean Tariff Rate are shown in the Fig. 11.10 below.

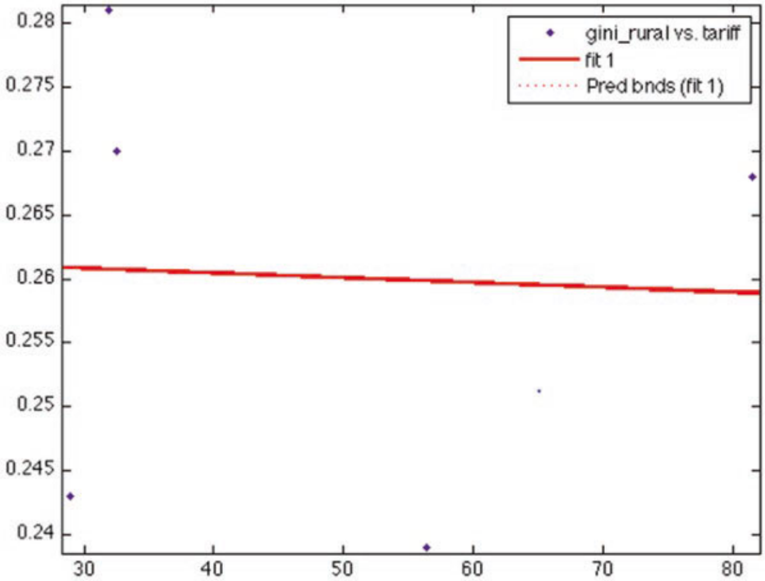
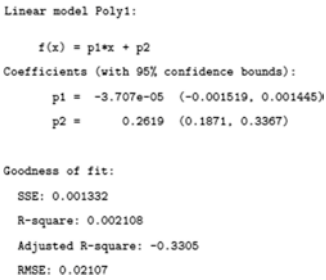


Fig. 11.10 Regression analysis: Gini Coefficient in Rural Sector vs Mean Tariff Rate



```
Linear model Poly1:

     f(x) = p1*x + p2
Coefficients (with 95% confidence bounds):
       p1 =  -3.707e-05  (-0.001519, 0.001445)
       p2 =      0.2619  (0.1871, 0.3367)


Goodness of fit:
  SSE: 0.001332
  R-square: 0.002108
  Adjusted R-square: -0.3305
  RMSE: 0.02107
```

The regression results show a weak relationship between these two variables. As tariffs are reduced there is almost constant inequality in the rural sector. The R2 value is quite low thus a definite conclusion cannot be drawn, this regression model is also limited by the low number of observations in the data sample.

11.4.5 Discussion of Results

From our time series graphs, we can see that inequality did decrease during the liberalization year, but increased shortly afterwards. In addition, the HDI did increase during the liberalization year. It is inconclusive if liberalization is the cause of these observations, but it may be a factor at play. From the regression analysis there is a weak trend that economic liberalization has increased inequality in the urban sector. It is observed that increasing the trade openness and decreasing tariffs results in a inequality increase in the urban sector. The trend in the rural sector is harder to understand, as there may be different exogenous factors at play. The regression suggests that inequality may decrease with increased trade openness. The effect of poverty headcount index vs trade openness was unexpected, it was observed that headcount of people living under \$1.25 a day increased with trade openness. This may be a statistical fluke as the observed sample data was extremely small, or other exogenous factors may be at play.

In general, the regression analysis suffered from a lack of observable data, and high variability. For most cases, the R2 values were unacceptable high to draw any definite conclusions, thus the regression analysis simply displays possible trends between liberalization and inequality, and liberalization and poverty. For a more definite proof, a literature review will be conducted in the following section, that outlines other papers that examine the topic of liberalization, inequality and poverty. Many of these papers use much more robust data and advanced econometric models in their analysis, resulting in conclusions that are more empirically sound. Although this section did not find a definite link between liberalization and inequality, and liberalization and poverty, we can still make the following conclusions:

1. Overall income inequality did decrease during the year of liberalization
2. The data suggests weakly that liberalization may have resulted in increased inequality in the urban sector
3. The data suggests weakly that liberalization may have resulted in decreased inequality in the rural sector
4. Absolute poverty as reflected by the HDI, decreased during the year of liberalization

11.5 Survey of Various Quantitative Approaches in Literature

The methodology used in this research lead to inconclusive results due limitations of data, and perhaps the simplicity of the regression model. This section explores similar literature, and whether or not others have shown the link between liberalization and inequality, and liberalization and poverty in an empirical fashion.

11.5.1 Literature on Economic Liberalization and Income Inequality

According to [2], analysis using a distributed lag model is better in showing empirically the relationship between trade liberalization and inequality.

In econometrics a distributed lag model is a model for time series data in which a regression equation is used to predict current values of a dependent variable based on both the current values of an explanatory variable and the lagged (past period) values of this explanatory variable. This is used because sometimes the effects of a policy change are not felt immediately, but rath distributed over time periods. Trade liberalization does not have an instantaneous response on income inequality, but rather a gradual response spread over many time periods.

The general distributed lag model can be with one explanatory variable and one dependent variable can be written as:

$$Y_t = f_t\left(x_t, x_{t-1}, x_{t-2} \ldots\right) = e_t$$

Using this model [2], assumes that trade liberalization can be represented using export growth and that a Poisson random variable is appropriate for small vales of x. The model in [2] then can be written as:

$$z_t = \left[e^{-a_2} a_1 \left(u_t + a_2 u_{t-1} + \frac{a_2^2 u_{t-2}}{2!} + \frac{a_2^3 u_{t-3}}{3!} + \ldots \right) + a_3 \right] + \epsilon_t$$

zt is the growth rate (log difference) of the inequality indicator in period t as measured by either the Gini coefficient or the CV. The variable u_t is the growth rate of national exports as measured by either nominal national exports or exports as a percent of GDP. The coefficient a1 measures the effect of an increase in national exports on inequality. Agarwal et al. [2] solved this equation for various Gini coefficient data, CV data, and export data and concluded that: in some cases, liberalization has reduced income inequality throughout the years in a distributed fashion.

However, using distributed lag models, the conclusion for each state is different, and there are some problems with the quality of the data [1].

Similarly, in [16], a empirical strategy based on regression was used to determine that liberalization induced productivity at the firm level gets passed on as industry wages. This in turn decreases the wage inequality between skilled and unskilled workers in India.

In a paper by [19], there was sufficient evidence to conclude that income inequality was increasing along with the presence of persistent poverty. However, there is no causation or link directed towards economic liberalization. Thus, the overall increase of inequality may be attributed for factors besides trade liberalization.

11.5.2 Literature on Economic Liberalization and Poverty

According to [15], wage increases in the urban informal sector brought by trade reform had a favourable impact on urban poverty reduction. Using a simple empirical model and generalized least squares regression, [15] has shown this to be the case. The main result is that trade liberalization in sectors that compete with imports "raises informal wage across occupational types, and expands production and employment in the informal industrial segment". Since many people stricken by poverty are employed in the informal sector, this improves the development situation of the poor.

Using more robust and complete data extracted from National Sample Survey Organization in India (NSSO), [8] has shown that growth in India has tended to decrease levels of absolute poverty in both the pre-liberalization era and post-liberalization era using indicators such as headcount index of persons below the poverty line, and squared poverty gap index. Using the headcount index as a poverty measure, [8] found the rate of poverty decline increased post liberalization, suggesting liberalization might be a factor that was crucial in alleviating poverty.

It is critical to note that [8] simply observed this trend, and did not link it economic liberalization. There is no formal empirical linkage between liberalization and poverty reduction.

11.6 Cause and Effect of Inequality

In the regression analysis in this paper, there was a weak statistic inference that trade liberalization had an effect on inequality and poverty. Either the observed sample data is badly conditioned, or various other exogenous factors besides liberalization results in inequality. This section discusses some possible exogenous factors that may be at play.

11.6.1 Causes of Economic Inequality

There are some well-defined causes of economic inequality that are exogenous to the analysis in this paper. For example, the labour market can be a significant factor in determining the wage for different occupations, dictated by the supply and demand of different types of occupations. In a pure market economy, the wages are entirely determined by the market, which may skew wages down in occupations where a large amount of supply is available. This will result in income inequalities between professions in a market economy.

A person's innate ability and level of education may also play a significant role in determining wages paid in the labour market. It is expected that people with lower education, due to lack or access or otherwise, will experience lower wages in the job market. It is also fair to assume that people with higher abilities, perhaps in terms of intelligence will function more effectively within society and command higher wages. The proportion of people with high functioning abilities is assumed to be low compared to the general population, thus these few individuals could potentially command significantly higher wages, thus creating income inequality.

Technological development in the last several decades has automated many labors and manufacturing oriented tasks, and in turn has created a demand for high technology skills to create more technological products. The demand for skilled labour has increased, and this has not been met adequately with supply.

Finally, trade liberalization theoretically can reduce wages in highly developed countries because low wage workers in poorer countries will perform the same production tasks as workers in developed countries. This in turn can have a positive effect on wages in developing countries, such as India.

11.6.2 Effect of Economic Inequality

According to [20], rising inequality can cause capital flight, rich people will spend much of their incomes on imported luxury goods. Thus, the rich will not save and invest in the local economy, "representing a substantial drain on resources". According to classical growth theories, this will be sure to hamper growth, as economic growth depends on accumulation of savings and capital. Additionally [20] argues that higher inequality tends to overemphasize higher education at the expense of primary education, thus creating more inequality.

High levels of inequality have a negative effect on social cohesion. According to [20] high levels of inequality strengthens the political power of the rich and hence their bargaining power. High inequality leads to rent seeking behaviours, and failure of populist policies. Additionally, crime rates, mental health problems and teen-age pregnancies are lower in countries like Japan and Finland compared to countries with greater inequality such as the US and UK [22].

To complete the discuss about inequality, some mitigating factors that may alleviate economic inequality include: income redistribution via progressive taxation, bridging the educational divide between rich and poor, subsidization of goods and services that are frequently used by everybody, and nationalization of goods and services such as healthcare.

11.7 Conclusions and Future Research

In this research we hypothesized that increased growth in India due to neoclassical economic liberalization policies should lead to a reduction in absolute poverty levels and income inequality. Based on the empirical analysis in the research we cannot say with certainty that there is a reduction in poverty and inequality, due to statistical weakness of the regression models used in this research. The regression analysis suffered from either lack of data, or extremely dispersed data, possibly due to factors exogenous to the regression model. These factors may be other causes of economic inequality discussed in the previous section. The empirical analysis in the research suggests that:

1. Overall income inequality and poverty decreased during the year of liberalization, but is not proven to be strongly correlated with liberalization
2. Weak evidence suggests that inequality increased in the Indian urban sector and decreased in the rural sector due to liberalization

A review of literature strengthens the empirical analysis by confirming that generally income inequality decreases due to economic liberalization. This does not imply that overall inequality decreased, but rather the effect of liberalization has a tendency to reduce inequality. As mentioned before, many factors outside liberalization may be responsible for changes in inequality. Further literature review confirms that economic liberalization does tend to decrease poverty levels holding all other factors that affect poverty constant.

Future areas of research will involve developing a robust model that will more accurately test statistically the effect of liberalization of many indicators of poverty and inequality not covered in this research. More sophisticated regression techniques, along with multiple regression methods can be used to test the effect of various other factors besides liberalization that effect poverty and inequality, to determine which factor has the greatest effect on development.

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Chapter 12
Analyzing the Effect of Choice and Availability in Healthcare on Health Outcomes in Canada – A Pre-COVID-19 Environment

Rohit Narayan and Satyendra Narayan

Abstract This research hypothesizes that greater availability of healthcare services, and greater choice in healthcare facilities results in better health when controlling for a variety of socio-economic factors within the Canadian context. This research will model access to healthcare services using density of general and specialist physicians relative to population size, and the geographic density of healthcare facilities. Choice in healthcare is modeled by the number of healthcare facilities in each health region, when normalized by the population in that health region.

Various health outcomes will be used as benchmarks to test this hypothesis, including self- reported general health, self-reported mental health, influenza immunization rates, body mass index (BMI), and incidence of diabetes, cardiovascular disease and hypertension.

From the empirical results, choice in the healthcare system does not have an impact on the selected health outcomes. Increased availability of healthcare generally improves health outcomes, but this is dependent on the health outcome in question, and the provincial region being analyzed.

Keywords Health economics · Pre-COVID healthcare · Healthcare access · Health outcomes · Canadian healthcare · Pre-COVID Canadian healthcare

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R. Anandan et al. (eds.), *How COVID-19 is Accelerating the Digital Revolution*,
https://doi.org/10.1007/978-3-030-98167-9_12

12.1 Introduction

12.1.1 Overview of Healthcare in Canada

Healthcare in Canada is delivered via a publicly funded system that is paid by the taxpayer, but delivered via private entities. Access to primary health care services is intended to be available to all citizens and permanent residents across all socioeconomic groups with minimal upfront costs. Canada is fairly unique in the world due to the fact that it has a national health insurance system which assures access to all citizens, regardless of their ability to pay. As guided by the Canada Health Act, each province is responsible for administering healthcare under federal guidelines [20]. As a result, the provinces handle the administration and physician reimbursement for services. The provincial governments administer and deliver health services in divided geographic health regions. Health regions can be thought of as administrative areas defined by each provincial ministry of health.

The supply of healthcare and the associated wait times have been a significant issue of public interest, particularly in non-urban areas. Although government administered healthcare is theoretically available to all, there remains challenges in the utilization of services. Currently long wait times, lack of available physicians, rising population to physician ratios, and physician brain drain have contributed to a shortage of available services in Canada [17]. Coupled with geographic challenges in accessing distant healthcare facilities, it is clear that there are imperfections in the delivery of healthcare to all Canadians. In 2006, Canada's physician-to-population ratio ranked 26th among 28 developed nations that maintain universal access health care [17]. Additionally, 6.6% of Canadians reported being unable to find a family doctor in 2010 [17]. Nadeem [17] also suggests that lack of physicians in Canada is a serious problem negatively affecting the health of Canadians. In this context, this research aims to explore the relationship between choices and availability in healthcare and the resulting health outcomes in Canada.

12.1.2 Overview of Chapter

This research will use measures such as physician density and geographic distance to healthcare facilities as a proxy for availability of healthcare services. The density of healthcare facilities will serve as a proxy for choice. This research will attempt to examine the effect of availability and choice on health outcomes. It is hypothesized that greater availability of healthcare services, and greater choice in healthcare facilities results in better health when controlling for a variety of socio-economic factors. This research will examine the extent to which health outcomes are affected at the health region level, a finer level of analysis than current literature which examines health outcomes at the provincial level. Self-reported general health and self-reported mental health are used as direct indicators of health outcomes.

Other measures such as body mass index (BMI), influenza immunization, diabetes, cardiovascular disease, and hypertension will be used as proxies for health outcomes.

This research will begin by discussing the current literature on the topic both in Canada and in various other countries. The data and methodology will be discussed, and various empirical models will be presented to analyze the topic at hand. The empirical model results will be presented, and conclusions will be derived on whether greater availability and choice in healthcare results in better health outcomes when controlling for a variety of socio-economic factors.

12.1.3 Review of Literature

Although it is difficult to compare Canada's healthcare to other countries due to structural differences between the healthcare systems, analyzing the literature on healthcare systems in other countries can provide key insights on analyzing the Canadian system. Health economics in Canada is an emerging field of study, as recent problems within the healthcare system have gained the public focus.

The main focus in Canada has been towards the reduction of wait times for procedures and emergency department visits. A policy report by Barua et al. [3] illustrates that wait times in Canada is increasing rapidly and must be addressed to ensure timely access to healthcare services for a variety of procedures. A study by Kulkarni et al. [13] concluded that for patients who underwent cystectomy for bladder cancer in Ontario between 1992 and 2004, higher wait times for this procedure was associated with a lower overall survival rate. Similarly, a study by Jewett et al. [12] concluded that Canadian wait times for urological surgeries, such as for renal cancer, are beyond the recommended thresholds set by national and international expert bodies, thus resulting in overall poorer tumor control. Another study by Braybrooke et al. [4] showed that for posterior lumbar spinal surgery, a longer wait for surgery was associated with less improvement in outcome following surgery. Clearly wait times have an effect on certain health outcomes, and wait times are expected to be correlated with the public access to healthcare. It may be fair to hypothesize that increasing public access to healthcare services effectively increases healthcare supply, which may serve to reduce wait times and improve health outcomes.

Most literature shows evidence that there is a positive effect on health outcomes when access to healthcare is increased. A study by Macinkko et al. [15] suggests that increased access to family physicians decreases infant mortality, mortality related to cancers, heart disease, and increases life expectancy across time periods and jurisdictions in the United States. Macinkko et al. [15] also concluded that an increase in one primary care physician per 10,000 population is associated with a reduction of mortality by 5.3% or 49 lives per 10,000 population. Another study by Roetzheim [22] concluded that higher dermatologist and family physician supply is associated with earlier detection of a melanoma – a deadly form of skin cancer which is lethal if not diagnosed early. Another study by Roetzheim [21] concluded that a higher supply of primary care physicians decreased the odds of late state diagnosis of colorectal cancer. However, there is some contradiction by other research. A thesis by Franz [8] examines the relationship between physician density in the United States and population health. Franz [8] concludes that there is insufficient evidence to claim that an increase in physician density would increase population health in the United States. A study by Arild and Tor Helge [1] examined the impact of economic conditions and access to primary health care on health outcomes in Norway. Arild and Tor Helge [1] rejected the significant relationship between mortality and the number of GPs per capita found in most previous studies in Norway. However, Arild and Tor Helge [1] found there is a significant effect of the composition of GPs, where an increase in the number of contracted GPs reduces mortality rates when compared with GPs employed directly by the municipality. There has been some research on the effect of specialist physicians compared to general physicians on health outcomes. A study by Baicker and Chandra [2] suggests that greater supply of specialist physicians is associated with higher costs and inadequate care. On the other hand, a study by Nash [18] showed that treatment of acute myocardial infarction (heart attack) by a cardiologist lowers risk of mortality than if treated by a general practitioner. This research will also examine the effect of specialist physicians on health outcomes in Canada.

A study of the structural economics and delivery of healthcare is also important in understanding access to healthcare services, which may affect health outcomes. In the United States, the managed care model is a healthcare plan or system that seeks to control medical costs by contracting with a network of providers, and by requiring preauthorization for visits to specialists. A thesis by Grefer [10] concluded that the density of physicians is negatively correlated with the prevalence of managed care facilities. These structural differences between healthcare systems make cross country comparisons difficult. Additionally, the structural supply of healthcare may be affected by exogenous factors. For example, a study by Correia and Veiga [7] found that geographic disparities in physician density are high, and appear to be due mainly to geographic income inequality.

This research is based on the work of Sarma and Peddigrew [23], which examines the extent to which the density of family physicians influences health outcomes in Canada. Sarma and Peddigrew [23] finds that increased density of physicians positively impacts self-reported health on the order of 2–4%. The analysis by Sarma and Peddigrew [23] is performed on a national and provincial basis, and provides some evidence that increasing density of physicians positively impacts health outcomes. This research continues the work of Sarma and Peddigrew [23] and analyzes health outcomes at a finer provincial and regional level, by examining individual health regions. This research also uses different metrics of health outcomes, and models various factors of choice and availability of healthcare not present in Sarma and Peddigrew [23].

12.2 Methodology and Data

This research hypothesizes that greater availability of healthcare services and greater choice in healthcare facilities results in better health when controlling for a variety of socio-economic factors. The determinants of access to health care are complex, and involve the interaction between the supply of healthcare services and the competition or demand for these services. Geographical factors which constrain access to healthcare services are important in determining whether an individual is able to reach locations that offer healthcare services. This research will model access to healthcare services using the density of general and specialist physicians, and the geographic density of healthcare facilities. Family physicians per 100,000 and specialist physicians per 100,000 are used as a proxy for density of physicians. The geographical density is determined from the number of healthcare facilities within 10, 20, 30, 50, and 100 km from the center of each health region. Choice in healthcare can be interpreted as the number of healthcare facilities that a person has access to, or alternatively as the number of competitors. It is another measure of healthcare supply, and is modeled by the total number of healthcare facilities in each health region, when normalized by population in that health region. This research examines the effects of choice and availability on health outcomes on a health region level.

The data for this research comes from the Canadian Community Health Survey (CCHS), performed by Statistics Canada. This is a cross-sectional survey that collects information related to health status, health care utilization and health determinants for the Canadian population. The survey contains large sample of respondents and is designed to provide reliable estimates at the health region level. Physician density at a provincial level is obtained from the Canadian Institute of Health Information (CIHI) reports that are available on their website. A list of healthcare facilities is sourced from DMTI Spatial Inc, using a product called Enhanced Points of Interest which is a national database of approximately 1 million Canadian business and recreational points of interest. This data was checked against official listing of healthcare facilities entitled Guide to Canadian health care facilities published by the Canadian Hospital Association [6]. Geographical data from Health Statistics Division of Statistics Canada provided boundaries for health regions in Canada. Using these sources, the various geographical density variables were generated.

Several measures of health outcomes were used, the two primary measures being self-reported general health and self-reported mental health. These ordinal measures ranged from 1 to 5, where 1 indicates health is poor, 2 if health is fair, 3 if health is satisfactory, 4 if health is good, and 5 if health is excellent. Various other measures that reflect health status were also used such as influenza immunization rates, body mass index (BMI), incidence of diabetes, cardiovascular disease and hypertension.

Many control variables that are probable in their effect on health status are also included in the model. Age and squared age are continuous variables used, as this is expected to be highly correlated with health status. Other controls include gender, marital status, education status, employment status, income, and geographic location. Gender and marital status is captured by a single dummy variable for that equals 1 if female or married respectively, and 0 otherwise. Educational status is captured by 3 dummy variables that represent 4 categories of education in the CCHS. These categories include individuals who graduated with post-secondary education, individuals with some post-secondary education who did not graduate, and individuals who graduated from high school. The reference or base category for education are individuals who did not graduate from high school. Employment status is a dummy variable that equals 1 if the person has been employed part-time or full-time within the past 3 months, 0 otherwise. Income is controlled via 4 dummy variables that control for 5 income categories in the CCHS. The base category is individuals whose household income is below 20,000. The remaining income categories are individuals whose household income is between \$20,000–\$39,999, \$40,000–\$59,999, \$60,000–\$79,999, and \$80,000+. Geographic differences were modeled using several dummy variables indicating the various health regions in Canada. Four provinces were analyzed in detail: Ontario, British Columbia, Quebec, and Nova Scotia. The health regions that served as base categories which were omitted in the model were Toronto, Vancouver, Montreal, and Zone 1 respectively. The choices of these omissions reflected the fact that these were the most populous health regions in each province.

Several models were constructed using regression analysis, where the dependent variables reflected health status. Self-reported general health, and self-reported mental health are ordered categorical variables, therefore an ordered logit model is employed. For dichotomous dependent variables, a logistical regression is employed. The results are presented as odds ratios for easier interpretation. Marginal effects were calculated, but not presented due space restrictions, and the limited value added after interpreting odds ratios. The analysis was performed in STATA software, and all regression results were weighted using the provided survey weights, and corrected for heteroscedasticity using the robust command in STATA. This option estimates the standard errors using the Huber-White sandwich estimators which compensate for heteroscedasticity, and erroneous observations that exhibit large residuals.

12.2.1 Body Mass Index (BMI)

Body mass index (BMI) is a measure of human body shape and is dimensionless quantity defined as the ratio between mass and height. The quantity is designed to be a simply measure that describes various levels of obesity. It assesses a person's body weight excess or deficiency relative to their height. Although commonly used, it does not account for weight deviations due to muscularity. According to the World Health Organization, the categorical descriptions for various ranges of BMI are given below (Table 12.1).

Table 12.1 BMI categories [26]

Category	BMI range
Very severely underweight	less than 15
Severely underweight	from 15.0 to 16.0
Underweight	from 16.0 to 18.5
Normal (healthy weight)	from 18.5 to 25
Overweight	from 25 to 30
Obese Class I (Moderately obese)	from 30 to 35
Obese Class II (Severely obese)	from 35 to 40
Obese Class III (Very severely obese)	over 40

The BMI ranges are based on the relationship between body weight and disease/death [25]. Therefore, individuals with higher BMI are at risk for many health conditions that are detrimental to health status. Some conditions of risk include: hypertension, diabetes, heart disease, stroke, sleep problems, and some types of cancers [19]. From the literature it is clear that BMI is very highly correlated with health status. Although control of an individual's BMI is ultimately dependent on each person, access to health professionals may have an educational effect, which may induce people to correct abnormally high BMI and its associated health issues. A healthcare provider can also assist individuals in performing this often-difficult task.

12.2.2 Alternate Measures of Health Status

Three common diseases are used as alternate measures of health status, as they are highly reflective of an individual's lifestyle choices [24]. Just as BMI is ultimately dependent on each individual, these three diseases are predominately caused or exacerbated by poor diet, inadequate exercise, and other negative health choices [24]. Similar to BMI, access to health professionals may have an educational effect, which may induce people to prevent or manage these diseases. The three conditions are: diabetes mellitus, hypertension, and cardiovascular disease.

Diabetes mellitus or simply diabetes is a group of metabolic diseases that involve a lack of control of blood sugar (glucose) due to a variety of physiological dysfunctions. Type 1 diabetes is an autoimmune condition where the body destroys insulin secreting cells in the pancreas, resulting in tissue degradation, ketoacidosis (acid blood), polyuria (abnormally high urine volume), polydipsia (increased thirst) and polyphagia (increased hunger) [24]. Type 2 diabetes is a general term for a family of diseases that result from insulin resistance, or an abnormal body response to insulin, and is associated with obesity, polyuria, and atherosclerosis (buildup of fatty plaque inside blood vessels) which leads to heart disease and stroke [24]. Based on the physiological effects of this disease, it is expected that both types of diabetes should decrease the health status of individuals who are inflicted.

Hypertension is another term for high blood pressure which is a chronic medical condition that causes the heart to work harder to pump blood throughout the body, and may increase risk for stroke, heart attacks, kidney disease, and shortened lifespan [24]. Hypertension is classified as either primary or secondary hypertension; about 90–95% of cases are categorized as primary hypertension which means high blood pressure with no obvious underlying medical cause [5]. Hypertension in most cases is easily manageable using various medications, weight loss, and food choices [24]. Treatment of minor to moderate hypertension is quite manageable with the assistance of a physician or healthcare provider.

Cardiovascular disease or heart disease is a family of diseases involving the circulatory system (heart, arteries, veins) [24]. There are many underlying causes of this disease, and both diabetes and hypertension are strong factors that influence the onset of cardiovascular disease. It is also one of the leading causes of death worldwide, but the death rate has been dropping in developing countries like Canada due to improvements in treatment [9]. This disease can partially be avoided by proper diet, adequate exercise, abstaining from smoking, and maintaining a healthy body weight under the guidance of a healthcare practitioner [24].

It is important to emphasize that in most cases type 2 diabetes and minor hypertension can be cured, particularly if diagnosed and managed early during the onset of the disease [24], therefore access to healthcare services is critical in managing these diseases.

12.2.3 Influenza Immunization

Influenza or the" flu" is a family of infectious viral diseases which causes chills, fever, sore throat, muscle pains, headache (often severe), coughing, weakness/ fatigue and general discomfort [16]. Most cases of influenza pass after a few days, but some individuals (particularly high-risk individuals) may develop life-threatening complications (such as pneumonia) which can cause death [11]. As a result, the Canadian Task Force on Preventative Health-care recommends annual influenza immunization for high-risk individuals and elderly individuals [14]. In this research, it is assumed that the incident of influenza immunization increases with greater availability and choice. Therefore, influenza immunization is expected to reflect choice and availability of this procedure.

12.2.4 Summary of Model Variables

The Table 12.2 below summarizes the different independent and dependent variables in the regression models.

Table 12.2 Variable definitions

Variable	Definition
Dependent Variables	
Self-Perceived Health	=1 if general health is poor; =2 if general health is fair; =3 if general health is satisfactory; =4 if general health is good; =5 if general health is excellent
Self-Perceived Mental Health	=1 if general health is poor; =2 if general health is fair; =3 if general health is satisfactory; =4 if general health is good; =5 if general health is excellent
BMI	Body Mass Index (BMI) of respondent. Measure for human body health based on an individual's weight and height
High Blood Pressure	=1 if a respondent has high blood pressure; =0 otherwise
Diabetes	=1 if a respondent has diabetes; =0 otherwise
Heart Disease	=1 if a respondent has heart disease; =0 otherwise
Seasonal Flu Shot	=1 if a respondent had influenza immunization in past year; =0 otherwise
Independent Variables	
[Facilities within X km]	Vector: Number of healthcare facilities that fall within X km of gravity center of health region in which the respondent resides. X takes on values 10, 20, 30, 50, 100 km respectively
# of Facilities in H.R. Normalized	Density of healthcare facilities in each health region in which respondent resides
Family Physicians per 100,000	Number of general practitioners or family physicians per 100,000 population in the corresponding health region
Specialists per 100,000	Number of specialist physicians per 100,000 population in the corresponding health region
Age	Age of respondent in completed years
Age Squared	Squared Age
Female	=1 if female; =0 if male
Married	=1 if married; =0 if otherwise
Smoker	=1 if current and regular smoker; =0 if otherwise
Employed	=1 if employed full time or part time; =0 if other-wise
Educ: Graduated Post-Secondary	=1 if completed post-secondary education; =0 if otherwise
Educ: Some Post-Secondary	=1 if respondent has some post-secondary education, but not completed a degree/diploma; =0 if otherwise
Educ: Graduated Secondary	=1 if respondent graduated from secondary school; =0 if otherwise
Income: 20,000–39,999	=1 if household income is in the range of $20,000–39,999; =0 if otherwise
Income: 40,000–59,999	=1 if household income is in the range of $30,000–59,999; =0 if otherwise
Income: 60,000–79,999	=1 if household income is in the range of $60,000–79,999; =0 if otherwise
Income 80,000+	=1 if household income is above $80000, =0 if otherwise
[Provinces]	=1 if respondent lies in X province
[Health Regions]	=1 if respondent lies in X health region

12.2.5 Geographic Variables

As mentioned previously, a list of all healthcare centers was obtained from DMTI Spatial Inc, using a product called Enhanced Points of Interest. This includes hospitals, special care centers, nursing homes, and providers of group healthcare (groups of physicians). Using this data and geographic data from Health Statistics Division of Statistics Canada, the latitude and longitude of the gravity center of each health region and healthcare centers was extracted. The distance between the gravity center of each health region and each individual health center was calculated. Then this data was sorted to generate the number of health centers within various distances from the gravity center of each health region. Only the following distances were used in this analysis: 10, 20, 30, 50, and 100 km, as this provided sufficient data to model availability of healthcare services. Additionally, GIS software was used to calculate the number of healthcare facilities that are contained by the borders of each health region, and this was normalized by the population of the particular health region.

The analysis at the health region level was limited to 4 provinces: Ontario, British Columbia, Quebec, and Nova Scotia. This resulted from the improper use of the health region variable in the CCHS, as several health regions were improperly combined in the CCHS. A correction for issue using the GIS data is fairly complex, therefore provinces that exhibited this problem were omitted.

The Fig. 12.1 below shows the various health boundaries for Canada, and healthcare centers contained within each region. Clearly most health centers are located in populated areas close to the US border.

12.3 Empirical Results

This section presents the regression results performed in STATA. For self-reported health in Canada, analysis was performed at a granular level – that is province level geographic variables were employed. For the remaining models, the analysis was performed at the health region level. This section will summarize all regression results, please refer to the appendix for all the regression tables.

12.3.1 Self-Reported Health in Canada

The granular level model is intended to replicate the efforts of Sarma and Peddigrew [23] with updated data from 2010. The self-reported general health and self-reported mental health models were ordinal logistical models that took the form:

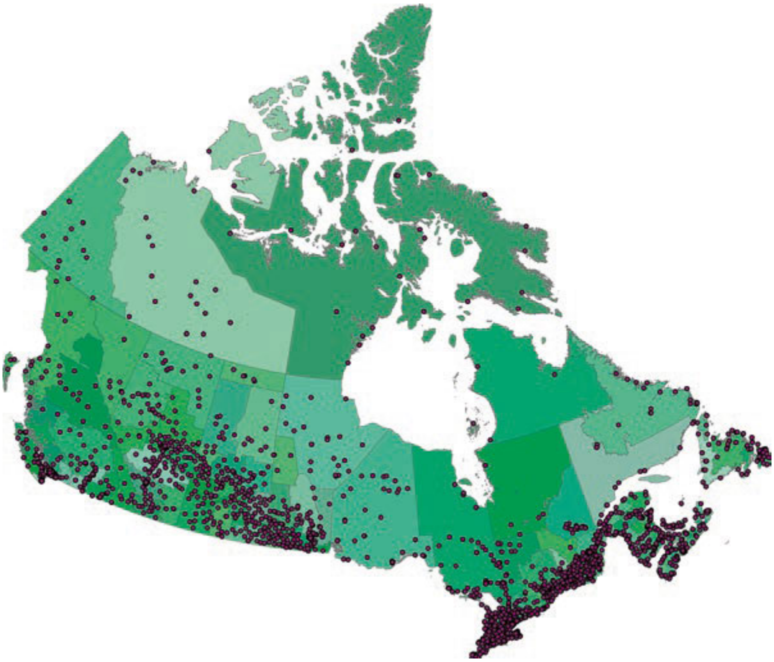

Fig. 12.1 Health regions and location of health centers in Canada

$$\begin{aligned}\left[\text{Self - Perceived Health}\right] &= \beta 0 + \beta 1\,\text{Physician Density} + \beta 2\,\text{Specialist Density} + \beta 3\,\text{Age} \\ &+ \beta 4\,\text{Age2} + \beta 5\,\text{Female} + \beta 6\,\text{Married} + \alpha\left[\text{Education}\right] + \gamma\left[\text{Income}\right] + \delta\left[\text{Province}\right]\end{aligned}$$

The density variables for general physician density and specialist density are found to be statistically insignificant. This deviates from Sarma and Peddigrew [23] which found that an additional general physician per 100,000 persons increased the odds of reporting better health status by 0.2%, and an additional specialist per 100,000 persons increase the odds of reporting better health by 0.1%, ceteris paribus. We do find that holding all things constant that increased age decreases the likelihood of reporting excellent general health by 10%, and mental health by approximately 25%. Relative to incomes below $20,000, incomes above $40,000 appear to increase the likelihood of reporting both general and mental health by at least 40%. Being female increases the probability of reporting excellent general health by 9.1% but decreases the probability of excellent mental health status by 12%. The effect of marriage is only significant in the case of mental health, where it increases the odds of reporting mental health by 21%.

Similar to the findings on income, education is found to have a strongly positive effect on health status at high significance levels. Relative to people who did not graduate high school, it is found that the odds of reporting better general health are increased by 77% for post-secondary graduates, 34% for people with some post-secondary education, and 27.6% for people who graduated from high school. Similarly, the odds of reporting better mental health increased by 53% for post-secondary graduates, 25% for people with some post-secondary education, and 36% for people who graduated from high school. Employed individuals are 20.5% more likely to report better general health, and 17.4% more likely to report better mental health.

Provincial variables appear to limited in their significance. However, it is found that residents of Quebec are 17.7% more likely to report better general health, and 27.8% more likely to report better mental health. Residents of Manitoba are 22% less likely to report excellent general health, and 29% less likely to report excellent mental health. Perhaps intra-provincial cultural differences or the differences in the delivery of healthcare may be at play, and this could be the subject of further research.

At the granular level, it is found that variables which reflect availability of healthcare are statistically insignificant, and only socio-economic factors play a role in reporting excellent general and mental health.

12.3.2 Self-Reported General Health

Self-reported general health was analyzed at the regional level using an ordered logistical regression model as follows. Additional variables that reflect choice and availability of healthcare services are included that were not in Sarma and Peddigrew [23].

$$\begin{aligned}\left[\text{Self - Perceived General Health}\right] &= \beta 0 + \beta 1\,\text{Physician Density} + \beta 2\,\text{Specialist Density}\\ &+ \beta 3\,\text{Age} + \beta 4\,\text{Age2} + \beta 5\,\text{Female} + \beta 6\,\text{Married} + \alpha\left[\text{Education}\right] + \gamma\left[\text{Income}\right]\\ &+ \delta\left[\text{Health Region}\right] + \beta 7\,\text{Number of Facilities in Health Region Normalized}\\ &+ \beta 8\,\text{Has Doctor} + \zeta\left[\text{Density of Health Facilities}\right] + \beta 9\,\text{Smoker}\end{aligned}$$

The density variables which are general physicians per 100,000 population and specialists per 100,000 population are found to be statistically insignificant in all provinces. Similarly, the density of healthcare facilities (number of facilities within X km), is not found to be significant across any of the provinces. Therefore, measures of availability of healthcare do not play a role in affecting self-reported general health. In the province of Ontario, the variable reflecting choice (number of facilities in each health region normalized by population) is significant, but has no effect on the odds of reporting better health status.

Many socioeconomic factors are found to significantly affect general health. In the province of Ontario, increasing education affected health status in a quasi-exponential fashion. Relative to individuals who did not graduate from high school, the odds of reporting better general health increased by 22% for high school graduates, 26.3% for individuals with some post-secondary education, and 63.2% for post-secondary graduates. Similarly, it was found that higher income increased the odds of reporting better general health. Being employed increased the odds of reporting better general health by 18.3%. A similar trend for education, income, and employment was found across in the other provinces. Another interesting fact revealed from the model, is that across all 4 provinces the odds of reporting better health decreases by approximately 38% for smokers.

In Ontario, living in the Haliburton-Kawartha-Pine Ridge District Health Unit decreases the odds by approximately 55% of reported excellent general health status, relative to Toronto. Similarly, living in Peel Region decreases the odds of reporting excellent general health by 42%. In contrast, living in the Oxford County Health Unit increases the odds of reported better general health by nearly 50%. In British Columbia, no such geographical health region effects were found to be significant relative to individuals living in Vancouver. In Quebec, living in Region du Saguenay, Region de la Capitale Nationale, and Region de la Montrgie increases the odds of reporting better general health by 88%, 29.7%, and 35.3% respectively (relative to Montreal). In Nova Scotia, residents of Zone 2 have decreased odds of reporting better general health by nearly 40%, relative to Zone 1.

12.3.3 Self-Reported Mental Health

Self-reported mental health was analyzed at the regional level using an ordered logistical regression model as follows.

$$\begin{aligned}\left[\text{Self - Perceived Mental Health}\right] &= \beta 0 + \beta 1\,\text{Physician Density} + \beta 2\,\text{Specialist Density}\\ &+ \beta 3\,\text{Age} + \beta 4\,\text{Age2} + \beta 5\,\text{Female} + \beta 6\,\text{Married} + \alpha\left[\text{Education}\right] + \gamma\left[\text{Income}\right]\\ &+ \delta\left[\text{Health Region}\right] + \beta 7\,\text{Number of Facilities in Health Region Normalized}\\ &+ \beta 8\,\text{Has Doctor} + \zeta\left[\text{Density of Health Facilities}\right] + \beta 9\,\text{Smoker}\end{aligned}$$

The density variable denoting general physicians per 100,000 population played an unusual but statistically significant role in the province of Nova Scotia. Residents of Nova Scotia were 0.5% less likely to report better mental health status for an additional general physician per 100,000 population. Mental health was also affected by the density variable for specialist physicians per 100,000 population in three out of four provinces. The odds increased by 0.9% in Ontario, 0.8% in British Columbia, and 0.9% in Nova Scotia for reporting better mental health with an additional specialist physician per 100,000 population. The density of healthcare facilities (number of facilities within X km), was not found to be significantly and affect mental health outcomes in any of the provinces. The number of facilities in each health region normalized by population also did not play a role in affecting mental health outcomes. It is clear that only in some cases did the measures for healthcare availability play a role increasing mental health outcomes.

Socioeconomic factors mirrored their effects to self-reported general health. As expected, increased income and education increased the odds of reported better mental health. Unique to mental health, being female actually decreased the odds of reporting better mental health by 12.5%, 12.4%, 23.6%, and 23.5% in Ontario, British Columbia, Quebec, and Nova Scotia respectively. Being married also increases the odds of reporting better mental health by 17.6%, 17.1%, 18.5%, and 17.1% in Ontario, British Columbia, Quebec, and Nova Scotia respectively. In each of the four provinces the odds of reporting better mental health decreases by approximately 23% for smokers.

Regional effects of health regions were sparse and mostly insignificant for the most part. Residents of the Sudbury and District Health Unit in Ontario were 36% less likely to report better mental health relative to the base category of Toronto. In contrast, Quebec residents of Region de la Capital Nationale, Region de l'Abitibi-Tomiscamingue, Region de la Cote-Nord, Region de la Gaspsieles-de-la-Madeleine and Region de la Montrgie are more likely to report better mental health by 39.5%, 37.8%, 103.9%, 51.2% and 36.0% relative to Region de Montreal.

12.3.4 Body Mass Index

BMI was analyzed at the regional level using a normal least squares regression corrected for heteroscedasticity. The model takes the form:

$$\begin{aligned}\text{BMI} = {} & \beta 0 + \beta 1 \text{Physician Density} + \beta 2 \text{Specialist Density} + \beta 3 \text{Age} + \beta 4 \text{Age2} \\ & + \beta 5 \text{Female} + \beta 6 \text{Married} + \alpha \left[\text{Education}\right] + \gamma \left[\text{Income}\right] + \delta \left[\text{Health Region}\right] \\ & + \beta 7 \text{Number of Facilities in Health Region Normalized} + \beta 8 \text{Has Doctor} \\ & + \zeta \left[\text{Density of Health Facilities}\right] + \beta 9 \text{Smoker}\end{aligned}$$

The density variable for general physicians per 100,000 population was found to be statistically significant, but roughly decreased BMI by only 0.025 for a unit increase in density across all four provinces. This effect is not significant from viewpoint of health, as the change in BMI is too small. Similarly, the density of healthcare centers and number of facilities per health region exhibited statistical significance across the provinces, but had a non-significant effect on BMI from a health viewpoint.

Socioeconomic factors had a very interesting effect on this health outcome. As expected, a unit increase in age resulted in greater BMI by approximately 1.4 across the provinces. Interesting to note that smoking and being female decreased BMI by approximately 0.5 and 1.6 respectively across the provinces. This suggests that BMI is an imperfect measure of health outcome, and may not be suited to cross-gender comparisons. In particular, it may not capture the health consequences of smoking. It is also interesting to note that education played very little role in reducing BMI until individuals reached a very high level of education. Across the provinces, BMI decreased by roughly 0.6 only when individuals achieved post-secondary education. Lesser amounts of education had much small coefficients, and were found to be statistically insignificant. Income levels were not found to be statistically significant in their effect on BMI.

There were some regional effects of health regions that are notable. In Ontario the residents of the City of Ottawa Health Unit and Oxford County Health Unit exhibited lower BMI by 0.757 and 1.345 respectively (relative to Toronto). The odds of general health in Oxford County Health Unit were previously found to be greater, suggesting that residents of this health unit are healthier than residents of other regions. In British Columbia, residents of Fraser North, Fraser South, Richmond, and North Shore were found to have significantly lower BMI relative to residents of Vancouver. Similarly in Quebec, residents of Region du Bas-Saint-Laurent, Region du Saguenay Lac-Saint-Jean, Region de la Capitale Nationale, Region de la Mauricie et du Centre- du-Quebec and Region de l'Outaouais were found to have significantly lower BMI relative to Region de Montreal. In Nova Scotia, residents of Zone 2 were found to have an increased BMI by 2.292 relative to residents of Zone 1.

12.3.5 Alternate Measures of Health

Three alternate measures of health include: diabetes, cardiovascular disease, and hypertension. These were measured at the regional level using a logistical regression model as follows:

$$\begin{aligned}\text{Health Measure} = {} & \beta 0 + \beta 1\,\text{Physician Density} + \beta 2\,\text{Specialist Density} + \beta 3\,\text{Age} \\ & + \beta 4\,\text{Age2} + \beta 5\,\text{Female} + \beta 6\,\text{Married} + \alpha\left[\text{Education}\right] \\ & + \gamma\left[\text{Income}\right] + \delta\left[\text{Health Region}\right] \\ & + \beta 7\,\text{Number of Facilities in Health Region Normalized} + \beta 8\,\text{Has Doctor} \\ & + \beta 9\,\text{Facilities within10km} + \beta 10\,\text{Smoker}\end{aligned}$$

In Ontario, an additional general physician per 100,000 population decreased the odds of reporting diabetes and hypertension by 3.1% and 2.6% respectively. In contrast, an additional specialist physician per 100,000 population increased the odds of reporting hypertension by 1%. In Quebec and Nova Scotia, it was found that an increase in general physician density decreased the odds of diabetes by 2.5%. No other statistically significant effects were found for physician density or specialist density. The choice variable – number of facilities in health region normalized by population – did not affect any alternate health outcomes, nor was it statistically significant.

In all provinces, increased age raised the likelihood of reporting diabetes and hypertension by over 100%, but did not have a significant effect on cardiovascular disease. In each of the provinces, being female cut the odds of reporting diabetes and cardiovascular disease in half, and hypertension by approximately 25%.

Increased education tended to significantly decrease the odds of reporting any of the 3 conditions, but the results were not consistently statistically significant. Increased incomes above $80,000 tended to decrease the likelihood of reporting diabetes and hypertension by approximately 60% and 50%, across all four provinces. Being employed decrease the odds of reporting diabetes and cardiovascular disease by roughly 36% and 32% in each of the four provinces.

Regional effects of health regions were significant in quite a few cases. In the case of Ontario, the base health region was Toronto. Relative to Toronto, residents of the District of Algoma Health Unit were 67% less likely to report hypertension. In Brant County Health Unit, residents were less likely to report diabetes, cardiovascular disease, and hypertension by 71.4%, 75.6%, and 63.7% respectively. In contrast residents of Haliburton-Kawartha-Pine Ridge District Health Unit were a whopping 607% more likely to report cardiovascular disease and 27.5% more likely to report hypertension. Residents of Chatham-Kent Health Unit were less likely report diabetes and hypertension by 57% and 51% respectively. Residents of the Leeds, Grenville and Lanark District Health Unit, were less likely to report hypertension by 52%. Residents of Middlesex- London Health Unit were less likely to report diabetes and cardiovascular disease by 68.2% and 83.7% respectively. Residents of North Bay Parry Sound District Health Unit and Oxford County Health Unit were found to be less likely to report diabetes by 58.2% and 77.8% respectively. Note that residents of Oxford County Health Unit reported lower BMI and were more likely to report better general health. Residents of Simcoe Muskoka District Health Unit were 50.3% less likely to report diabetes. In British Columbia base category for health regions was Vancouver. Relatively to Vancouver, residents of East Kootenay were 56.4% less likely to report hypertension. Residents of Okanagan were less likely to report diabetes and cardiovascular disease by 58.5% and 76.7% respectively. Residents of Thompson/Cariboo and South Vancouver Island were found less likely to report cardiovascular disease by 84.7% and 77% respectively. Residents of North Shore/Coast Garibaldi were less likely to report both cardiovascular disease and hypertension by 81.1% and 60% respectively. In the province of Nova Scotia, the base category was Zone 1. Relative to Zone 1, residents of Zone 5 were 144% more likely to report hypertension, and residents of Zone 6 were 119% more likely to report diabetes.

12.3.6 Influenza Immunization

Influenza immunization was also analyzed at the regional level and employed a logistical regression model as follows:

$$\begin{aligned}
&\text{Influenza Immunization} = \beta 0 + \beta 1\,\text{Physician Density} + \beta 2\,\text{Specialist Density} + \beta 3\,\text{Age} \\
&+\beta 4\,\text{Age2} + \beta 5\,\text{Female} + \beta 6\,\text{Married} + \alpha\left[\text{Education}\right] + \gamma\left[\text{Income}\right] + \delta\left[\text{Health Region}\right] \\
&+\beta 7\,\text{Number of Facilities in Health Region Normalized} + \beta 8\,\text{Has Doctor} \\
&+\zeta\left[\text{Density of Health Facilities}\right] + \beta 9\,\text{Smoker}
\end{aligned}$$

An additional general physician per 100,000 population was not found to be statistically significant across any of the four provinces. However, an additional specialist per 100,000 population increases the odds of receiving influenza immunization in Ontario, British Columbia, and Nova Scotia by 5.5%, 6%, and 7% respectively. The density of healthcare facilities – number of facilities within X km – was not found to be significant across any of the provinces. The number of facilities in each health region normalized by population also did not play a role in affecting the odds of receiving the influenza immunization.

Socioeconomic factors played less of a role in affecting the odds of receiving the influenza immunization when compared to other measures of health status, as not very many socioeconomic variables were significant. Being female in Ontario, British Columbia, and Nova Scotia decrease the odds of receiving the influenza immunization by about 40–45%. Age, education, employment, and income were not found to have a statistically significant effect.

Regional effects of health regions showed extreme results in each of the provinces. In Ontario relative to Toronto, residents of Halton Regional Health Unit and Windsor-Essex County Health Unit were many times more likely to receive the influenza immunization. In contrast, residents of Huron County Health Unit and The Eastern Ontario Health Unit were many times less likely to receive the influenza immunization. Regional effects in British Columbia were difficult to analyze, as many observations predicted failure perfectly, or exhibited collinearity. This occurred because variables for each health region were zero every time influenza immunization was also zero. In Quebec, residents of the Region de la Capitale Nationale were more than 9 times more likely to receive influenza immunization relative to residents of Montreal. Note that from previous sections, residents of Region de la Capitale Nationale were also more likely to report better mental and general health outcomes. In Nova Scotia, residents of Zone 2 were much less likely to receive the immunization relative to Zone 1.

12.4 Discussion, Conclusions, and Future Research

12.4.1 Discussion and Future Research

There are some methodological problems in using ordinal choices in survey data. There are no precise differences between the ordinal choices, and the relative differences between each ordinal choice is unclear. It may also be the case the ordinal variables do not capture the wide range of health status reported by individuals. It may also be the case an ordinal ranking of health status is in appropriate, and it makes sense to partition the outcomes into a dichotomous variable. Further investigation is required to prove that this is the case.

The density of healthcare facilities – number of facilities within X km – was calculated from the gravity center of each health region. That is, the shape of each health region was mathematically averaged to find the center of each health region.

In rare instances, for irregularly shaped health regions, this resulted in the gravity center being outside the borders of the health region. Therefore, it is also important to emphasize, that the gravity center is substantially different from the geographic center of most health regions. This limitation may have served to skew results for this variable, particularly for irregular shaped health regions in rural areas.

The CCHS did not adequately represent the health regions as defined by Health Canada and the various provincial ministers. Often several health regions defined by the provincial ministries would be amalgamated into one large health region in the CCHS. This led to issues in generating the geographic variables used in the models, thus any provinces that caused issues was removed from the analysis. The provinces of Saskatchewan, Manitoba, PEI, Newfoundland exhibited this issue to varying levels of extent. Alberta recently restructured its health boundaries, which created significant mismatch between the new health boundaries and regions in the CCHS. Also, the CCHS combined the northern territories, while excluding Nunavut.

In order to ensure that the CCHS data sufficiently represented the covered population accurately, the models were all weighted using the included probability weights. The weights represented the inverse of the probability of each observation being sampled. However, standard survey techniques of calculating reliable variance estimates were not employed at this time due to the lack of availability of replicate weights in the dataset. Further study should employ variance estimation methods such as: Taylor Linearization, balanced repeated replication (BRR), jackknife, or bootstrap. The variance estimation methods coupled with the corresponding replicate weights allow us to obtain much more accurate standard errors of the estimates in the CCHS. This may significantly change the inference of many variables, and provide greater insight into the question of the effect of availability and choice on health outcomes. Although these variance estimation methods are built into STATA, they are not compatible with complex survey data where weighting needs to be applied.

Finally, there is myriad of factors that are unaccounted for given the limited availability of data on this subject. Assuming the population is not genetically homogeneous, genetic factors between groups of individuals between regions can result in radically different health outcomes.

Quality of care can vary significantly between regions, particularly in urban vs. rural areas, where higher standard facilities may only be available in urban areas. Unobserved socioeconomic factors may also play a role, as well as other unaccounted for factors.

12.4.2 Conclusions

This research initially hypothesized that greater availability of healthcare services and greater choice in healthcare facilities results in better health when controlling for a variety of socioeconomic factors. The research modeled access to healthcare services using density of physicians and specialists, and the geographic density of healthcare facilities. Choice in healthcare was modeled as the number of healthcare facilities that a person has access to, which is the number of facilities in each health region normalized by population. The analysis was performed at the regional level in four provinces: Ontario, British Columbia, Quebec, and Nova Scotia.

Based on the various models constructed in this research, the indicator of choice – number of facilities in each health region normalized by population was found to be either statistically insignificant, or too small to realistically affect health outcomes. The indicator of availability of healthcare – the density of healthcare facilities – was also found to be statistically insignificant, or too small to realistically affect health outcomes. The indicators of availability of healthcare services – density of general physicians and specialist physicians – were found to affect health outcomes only in the case of certain health outcomes. Therefore, the results can be summarized by the various health outcomes as follows:

Self-Reported General Health
At the provincial level and the health region level, the density variables for general physician density and specialist density are found to be statistically insignificant. Socioeconomic factors dominate in explaining effects on self-reported general health.

Self-Reported Mental Health
In Nova Scotia, it was found that increased physician density decreased the likelihood of reported better mental health outcomes by 0.5%. Increased density of specialist physicians increased the odds of better mental health by 0.9% in Ontario, 0.8% in British Columbia, and 0.9% in Nova Scotia. Socioeconomic factors also played a strong role in explaining mental health.

BMI
Physician density decreased BMI by 2.5% in all four provinces, but this change is too small to make a real-world difference in health. Specialist density was not found to have any effect on BMI. Socioeconomic factors played less of a role in explaining BMI.

Diabetes, Cardiovascular Disease, and Hypertension
In Ontario increased general physician density decreased the odds of reporting diabetes and hypertension by 3.1% and 2.6% respectively. Specialist physician density increased the odds of reporting hypertension by 1%. In Quebec and Nova Scotia, it was found that increased general physician density decreased the odds of diabetes by 2.5%. No other statistically significant effects were found for general physician density or specialist density. Socioeconomic factors played a strong role in explaining these health outcomes.

Influenza Immunization
Increased general physician density was statistically insignificant across all 4 provinces, but increased specialist physician density increased the odds of receiving the influenza immunization in Ontario, British Columbia, and Nova Scotia by 5.5%, 6%, and 7% respectively.

Therefore, it is clear from the results, that choice in healthcare does not have an impact on the chosen health outcomes. Increased availability of healthcare generally improves health outcomes, but this is dependent on the health outcome in question, and the provincial region being analyzed.

Finally, regional effects of living in a particular health region did reveal some slight trends. From the various models, it appears that residents of Oxford Country and Region de la Capitale Nationale exhibit better health outcomes over a variety of measures. Relative to Toronto residents, residents of Oxford County Health Unit were found to be less likely to report diabetes by 58.2%, had a lower BMI by approximately 1.345, and 50% more likely to report better general health. Similarity, residents of Region de la Capitale National (relative to Montreal) were 26.7% more likely to report better general health, 39.5% more likely to report better mental health, reported lower BMI, and were nine times more likely to receive an influenza immunization.

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